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(54) Title: HOMOLOGY MODELS OF THE GLUCOCORTICOID RECEPTOR

(57) Abstract

A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three–dimensional image, the method comprising: (i) providing an amino acid sequence and an x–ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor; (ii) modifying said x–ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand; (iii) verifying the accuracy of the homology model by comparing it with experimentally–determined binding properties of a number of ligands for the glucocorticoid receptor; and (iv) if required modifying the homology model for greater consistency with those binding properties.

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HOMOLOGY MODELS OF THE GLUCOCORTICOID RECEPTOR

INTRODUCTION

Technical Field

This invention relates to combined computational and chemical methods of obtaining improved homology models of the human glucocorticoid receptor and to computational methods using such models for the design of ligands that bind to the glucocorticoid receptor.

BACKGROUND

Nuclear Receptors

The glucocorticoid receptor is a member of a superfamily of soluble proteins, the nuclear receptors. Unlike receptors associated with or integrated in the cell membrane the nuclear receptors reside in the cytoplasm or the cell nucleus. The members of the nuclear receptor superfamily have in common the ability to bind specifically their respective cognate ligands as well as DNA-elements. The ligands include physiologically-relevant ligands that are small molecules such as steroid hormones (androgens, oestrogen, mineralocorticoids, progestagens, and glucocorticoids), vitamins A and D, as well as pharmacologically important synthetic hormone mimetics that can act as agonists and/or antagonists. Upon ligand binding the receptor-ligand complex is able to modulate the transcription of genes that are controlled by that particular receptor's physiologic ligand. Depending on the nature of a specific target gene, it can be either up- or down-regulated via a classical mechanism that involves the interaction of the receptor-ligand complex with specific DNA-sequences upstream of target genes or by non-classical mechanisms such as protein-protein interactions between the receptor-ligand complex and other proteins involved in a signal transduction. The nuclear receptors bind DNA by means of a protein fold that contains cysteine residues coordinated to zinc atoms, the so-called zinc finger.

The zinc-finger motif has been used to identify and to clone members of the nuclear hormone receptor family. The nuclear receptors have 5 regions: the N-terminal A-B domain that contains an activation function; the DNA-binding domain; DBD(C); the hinge D; the ligand binding domain, LBD(E), and the F-domain (that is specific for the estrogen receptor). The 3D structures for the DNA-binding domains of the GR, oestrogen receptor (ER), thyroid hormone receptor (THR) and retinoic acid receptor (RAR), have earlier been determined by X-ray crystallography or NMR spectroscopy.

More recently, the 3D-structures of the ligand-LBD complexes of some nuclear receptors, (THR, RAR, ER and progesterone receptor (PR)) have been published. The overall fold of the LBD of these nuclear receptors is an anti-parallel alpha-helical sandwich. This fold does not occur in any other known protein. Therefore it has previously not been possible to homology-model nuclear receptor LBDs correctly. A prerequisite for homology modelling is that the target and template structures have a similar tertiary structure. The sequence homology between the LBD's of various nuclear hormone receptors is low to moderate (10-50%) which alone does not guarantee that the LBDs of other members of this family will share similar tertiary folds. However, all these nuclear hormone receptors share a common function (transcriptional regulation), ID organisation (vide ante; A-E(f) region organisation), and many but not all are activated by ligand (i.e. endogenous hormones). In addition the structures of the LBDs of all members of the nuclear hormone family that have been solved to date share a common fold (antiparallel alpha-helical sandwich). Taken together, this evidence suggests that other members of this family are also likely to share this fold and therefore it should be possible to create homology models for the LBDs of these nuclear hormone receptors.

The conformation of the C-terminal a-helix (helix-12) in the X-ray crystallographic structure of ER-a complexed with raloxifene together with the PR-based GR-homology model was used to produce a GR homology model for the study of antagonist binding.

Glucocorticoids

Glucocorticoids are steroid hormones that mediate some of the body's responses to stress. The primary function of glucocorticoids is to protect the organism from the potentially harmful defence mechanisms induced by different forms of stress. Two such potentially harmful stress reactions are the induction of hypoglycaemia by insulin and the inflammatory response. Increased levels of glucocorticoids will increase the blood levels of glucose as well as exerting and anti-inflammatory action.

The mobilisation of blood glucose by glucocorticoids results from their induction of gluconeogenesis primarily by the induction of key enzymes in intermediary metabolism. For instance tyrosine amino-transferase and other transaminases are induced which results in redirection of energy in the amino acid to carbohydrate metabolism. One of the key regulatory enzymes in the gluconeogenic pathway, phospho-*enol*-pyruvate carboxykinase (PEPCK), is also induced by the glucocorticoids. The mechanism of induction of these enzymes is mediated by the DNA-binding of the steroid-activated glucocorticoid receptor (GR) which results in increased transcription of the genes for these enzymes.

In contrast, the anti-inflammatory effects of glucocorticoids involve the inhibition of the expression of a large number of proteins induced within the inflammatory response cascade. Examples of such proteins are cytokines (e.g. IL-2, IL-8), ezymes (e.g. collagenase I, iNOS, cyclooxygenase-2) and adhesion molecules. The principle mechanism involved is the repression of the transcriptional activation of these genes induced by various intermediary transcriptional factors (e.g. AP-1, NF-xB). Glucocorticoids prevent the induction of these genes by protein-protein interaction between the steroid-activated GR and the intermediary activating transcriptional factors.

The initial step in the mechanism of action of glucocorticoids is their binding to a specific soluble cytoplasmic receptor protein, the glucocorticoid receptor (GR). Thereafter a chaperone protein, HSP 90 is released from the GR, and the hormone receptor complex translocatese to the cell nucleus. GR belongs to the superfamily of nuclear receptors that have a zinc-finger DNA-binding motif. This motif enables ligand activated GR to bind to glucocorticoid response elements (GREs) situated on DNA upstream of GR-regulated genes. The transcription of those genes is then up- or down-regulated in response to the hormone. The Kd for binding of dexamethasone to GR is ~ 7nM and the natural hormone

cortisol binds with ~ 10% of that affinity. In the PR based GR model an alternative orientation of the side chain of Thr-739 is found which enables it to hydrogen bond to both the C-20 keto group and the C21b hydroxyl group. However, it is not currently known if the C-20 carbonyl contributes to affinity.

Homology Modelling

Homology modelling involves the replacement of the differing amino acids in a related template protein structure in order to produce a model of the target protein structure. The basic assumption and requirement is that the template and target have a similar three-dimensional structure. The usefulness of a homology model is to be judged on the ability of such a model to explain the biochemical data for the target structure. A homology model can never be correct in all details, but it should capture one or more of the essential characteristics of the protein. Before a determination of the three-dimensional structure of the target is available the only way to evaluate a homology model is to assess its explanatory power. That the model is reasonable from a protein structure standpoint of view is not enough, since it can be very different from the target, especially if it was made from an unsuitable template. Therefore we have in the present invention tried to validate our model by checking it and refining it against as much experimentally-derived biochemical data available for the glucororticoid receptor as possible. For the same purpose we have also docked representative glucocorticoids in the banana shaped cavity of the homology model and minimised the resultant steroid-protein complexes with molecular mechanics. The experimental binding affinities for GR obtained in this invention were correlated with the computed protein interaction energies.

The first homology model in accordance with this invention was based on the thyroid hormone receptor (THR).

TR was initially used for homology modeling of GR. Because of the higher degree of sequence homology of the LBDs of GR vs ER (26%) than with THR (13%), and because of the close similarity of the preferred ligands of ER and GR (i.e. steroids), ER will be a better template than THR and therefore ER was then used as a preferred template for GR homology modelling in the present invention. For similar reasons a progesterone receptor (PR) was also used as a preferred template for GR modelling in the present invention.

Glucocorticoid Structure - Activity Relationships

Synthetic glucocorticoids were investigated at an early stage for their anti-inflammatory properties. The ranking order of GR binding affinities correlates well with both the metabolic and anti-inflammatory effects of glucocorticoids. A combination of experimental, QSAR and computational chemistry studies have produced the following concept of important features for ligand binding to the glucocorticoid receptor.

The C-3 and C-20 keto groups of glucocorticoids are regarded as important for binding since their reduction to hydroxyl reduces binding affinity. This has been interpreted as suggestive of hydrogen bond donors located at corresponding positions in the receptor structure. Certain pyrazolosteroids, such as deacycortivazol, bind with high affinity although they do not have the C-3 keto group. There are also steroids without the C-20 keto group that have high affinity for GR, so neither the C-3 nor the C-20 keto group appear to be absolute requirements of glucocorticoids for high affinity GR binding.

The C-11 and C-21 hydroxyl groups are likewise as important for binding, and therefore suggest the existence of complementary hydrogen bond acceptors-donors in the receptor.

The replacement of the C-11ß hydroxyl with a keto group is detrimental to binding whereas a chlorine substituent at this position does not lead to loss of binding affinity. A C-17 *a* hydroxyl group increases affinity of glucocorticoids for the human receptor, but decreases the affinity for the rat receptor.

Hydrophobic pockets of limited size appear to exist in GR corresponding to the C-6*a* and C-9*a* positions of glucocorticoids, since small halogen atoms and methyl substituents here increase binding affinity, whereas bromine or methoy substituents in the C-0 position decrease ligand binding affinity.

It may be concluded from thermodynamic analysis that the ligand binding cavity of GR is predominantly hydrophobic since the binding enthalpy decreases when the temperature increases, which indicates that the driving force for binding is hydrophobic in nature. Surface area calculations indicate that both faces of the steroid are in contact with the protein, i.e. it is completely enclosed by the binding cavity.

An important feature of GR binding is the presence of the 4,5-diene double bond in the A-ring of the steroid. A second double bond in the A-ring, the 1-2,diene, further enhances the binding affinity. This double bond causes the A-ring to tilt downwards (toward the α-face of the steroid) from the main plane of the molecule. This downward bend of the A-ring was parameterized as the distance of the C-3 to C-17 carbon atoms (A- to D-ring distance) in the QSAR study of Wolff et al. It was found in that study that the shorter this distance was, the higher the affinity of the glucocorticoid was for the glucocorticoid receptor, i.e. the more bent the steroid is out of its main plane, the higher its affinity is for the glucocorticoid receptor.

Taken together, the structure-activity relationships presented above clearly indicate that the receptor imposes strict steric requirements on ligand binding.

UTILITY OF THE INVENTION

The glucocorticoid receptor models described in this application can be used to design new glucocorticoid receptor ligand, that can be agonists and/or antagonists. Glucocorticoid receptor agonists are useful for treatment of inflammation and immunosuppressive therapy. Glucocorticoid antagonists are expected to be useful in treatment of hypertension, diabetes, obesity, glaucoma, depression, AIDS and for wound healing.

The glucocorticoid receptor models can be used in design of new glucocorticoids in various ways. De novo drug design can be carried out by identification of features in the binding site that can be important for binding with respect to shape, charge, and hydrogen bonding properties. Ligand fragments with complementary properties to receptor features can be optimised for binding, in the same manner, by replacement of ligand fragments by better ones. Both these processes can be carried out manually or with de novo drug design programs, like LUDI and LEAPFROG given the coordinates of the glucocorticoid receptor models described herein.

The models can also be used with molecular mechanics, or 3D-quantitative structure activity relationship programs to assess the protein binding affinity of virtual glucocorticoid receptor ligands in order to prioritise their synthesis.

In summary, the homology models according to the invention will be useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for glucocorticoid receptor by means of molecular mechanics scoring functions.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig 1 is a structure of a glucocorticosteroid, dexamethasone, with atom numbering.

Fig 2a is the final alignment used between the rat thyroid hormone receptor α_1 and β sequences and the glucocorticoid receptor.

Fig 2b is the final alignment used between the estrogen receptor and sequence and the glucocorticoid receptor.

Fig 3 is a ribbon drawing of the ligand binding domain of the glucocorticoid receptor with a ligand depicted as a space-filling model.

Fig 4 shows cross-sections of a glucocorticoid receptor ligand within the binding site of the glucocorticoid receptor. The van de Waals radii of the ligand atoms as well as the water-excluded surface of the glucocorticoid receptor-model is shown as dots.

Fig 5 shows a drawing of a glucocorticoid receptor ligand with its interactions, with residues in the binding site that are critical for ligand binding.

Fig 6 sequence alignment used for homology modelling of GR from ER and TR.

Fig 7 structure of eight representative glucocorticoids used for experimental GR-binding assays and correlation with their computed protein interaction energies.

Fig 8 Graphs showing the progression of the improved correlation between calculated protein-interatction energy with the experimental free binding energy; (i) molecular mechanics ligand-protein interaction energy, (ii) inclusion of terms for ligand solvation, (iii) inclusion of terms for ligand solvation and strain energy, (iv) scaling of the individual components with respect to each other by means of PLS. Triamcinolone is not included in (i); R^2=0.02 if it is included.

Fig 9 (a) RasMol representation of the main interactions with dexamethasone in the GR homology model.

(b) Sketch of the main interactions with dexamethasone in the GR homology model.

Figures 10 and 10b Orthographic views of mutations in GR LBD that affect transactivation and/or ligand binding (Table 4) displayed as balls on the α-carbons. The Figure being produced with RasMol.66.

Figure 11 Sequence alignment used for homology modelling of GR from PR.

Figure 12 The three dimentional coordinates of the GR model produced from ER using its X-ray crystallographic structure as a template.

Figure 13 The three dimensional coordinates of the GR model produced from PR using its X-ray crystallographic structure as a template.

Figure 14 Sequence alignment of ER and GR used for the conformation of the C-terminal-helix (helix 12) in a PR-based GR-model for the study of binding of antagonists. The three dimensional coordinates of the GR homology model using the rat TRa/T3 and human TRb/Triac crystallographic structures.

Figure 15 The three-dimensional coordinates of the GR model produced from PR using the conformation of the C-terminal a-helix (helix 12) such as is in the X-ray crystallographic structure of ER- a complexed with raloifene. A GR-specific antagonist is docked into the binding site.

DETAILED DESCRIPTION OF THE INVENTION

Homology Modelling Based on the Thyroid Receptor

Initial multiple sequence alignments of the ligand binder nuclear receptor sequences were obtained using the Pileup program from the Genetics Computer Group at Univ. of Wisconsin program package. For semi-automated homology modelling Modeler, as supplied with Quanta96 from Molecular Simulations Inc., was used. [8] The homology

modelling that we performed involved the replacement of the differing amino acids in a related protein structure (the template) in order to produce a model of the target protein structure. It is essential that the template and target have a similar three-dimensional structure. In manual homology modelling the side-chain positions of the amino-acids are then refined e.g. using rotamer libraries and energy minimisation. Loops can be copied from libraries of the other protein structures, and/or simulated by molecular dynamics. If the model does not exhibit a reasonable protein structure, or if it fails to account for the available biochemical data, the alignment is revised and the model is rebuilt. This process is preferably repeated until the model cannot be further improved. Serious manual homology modelling is thus a tedious enterprise, since the placing and refinement of the side chain positions has to be redone in each modelling cycle. Semi-automated homology modelling facilitates the interactive process since it automates the manual placement and refinement of the amino-acid side-chains as well as modelling of loops. In the present invention we used the program Modeler for this purpose. [15]

The initial sequence alignments were obtained from multiple sequence alignments of nuclear receptors. These alignments were used for the initial runs but they were adjusted for subsequent runs in order to produce a molecular model with a reasonable protein structure that also accounted for the available scientific data. The ligand was not included in the Modeler runs. Iterative Modeler runs, using sequence alignments taking account of the known scientific data, resulted in the final alignment (Fig. 2). The overall fold of the model is shown in Fig 3. In the water-excluded surface of the model a completely enclosed banana-shaped binding cavity can be observed. This accords with calculations that have shown that glucocorticosteroids should be completely enclosed by glucocorticoid receptor, and because it is known that the glucocorticoids with high affinity for glucocorticoid receptor are more bend out of their main-plane (have a shorter A to D-ring distance) than glucocorticoid receptor-ligands with lower affinities. cortisol was manually docked as a rigid body into the glucocorticoid receptor homology model by the best possible fits of its atomic van der Waals raadi to the water-excluded surface of the binding cavity (Fig 4). The amino acid residues in the cavity were mainly hydrophobic, except for two residues namely Arg-611 and Thr-739. These were located within 3A of the 21-OH and 19-OH of cortisol, and their side chain nitrogen atoms could constitute hydrogen bonding partners.

Furthermore, the backbone carbonyl of Leu-563 was within 3A of the 11-OH group of cortisol, and could thus be a possible hydrogen bond acceptor (Fig 5.).

A small cavity surrounded by carbonyl oxygen atoms near the C-3 of the ligand was observed. This cavity may contain water molecules. Therefore water-mediated hydrogen bonding may be involved in the binding of the C-3 carbonyl oxygen atom. Possibly cortivazol which does not have a C-3 carbonyl oxygen may displace the water molecules by its pyrazole ring which could fill the cavity, thus explaining its high binding affinity.

That C-11 chloro substituted glucocorticosteroids have similar affinities for glucocorticoid receptor as C-11 hydroxyl substituted glucocorticosteroids has been rationalized by the assumption that there exists an accessory hydrophobic pocket for such halogen substituents. [3] However this assumption may not be necessary, because in our model both the C-11 chloro or hydroxyl substituents may interact with a carbonyl oxygen, and carbonyl oxygens in other X-ray structures are known to interact with halogen atoms at less than the sum of their van der Waals radii. In the THR x-ray structure the ligand iodines thus interact with backbone carbonyl oxygens.[5]

That the binding cavity in this model is more bent than steroid makes sense in view of the classical structure-affinity relationships for glucocorticoid-steroids since it would preserve the rank order of affinities where the most bent glucocorticoid receptor-binding steroids (that have the shortest A-D ring distances) bind with the highest affinities to glucocorticoid receptor and the more planar ligands bind with lower affinities. It is known that the receptor-bound conformations of ligands frequently differ from their minimum energy conformations. It may thus be concluded that ligand binding to a receptor is a complex process where both the ligand and the binding site has to adjust for binding.

Warriar et al, have shown by point mutations that M565 and G567 are important for ligand specificity and binding, respectively. [12] In our glucocorticoid receptor model these residues are close to the binding site. Stromstedt et al have covalent affinity labelling with radiolabelled glucocorticoid receptor ligands and protein sequencing studies demonstrated three residues, namely Met-622, Cys-754 and Cys-656, to be in the vicinity of the binding site of the glucocorticoid receptor [13]. In our initial alignment two of these residues were in our glucocorticoid receptor-model in the vicinity of the ligand. We therefore improved the

alignment so that the third residue was nearer the binding site after homology modelling. However, this revision of the models did not affect the binding site. The final alignments are shown in Fig 2A and 2B.

Homology Modelling Based on the Estrogen and Progesterone Receptors

Materials

[^{3}H]TA was obtained from NEN-Dupont, unlabelled steroids from Sigma and cell culture media, fetal bovine serum and penicillin-streptomycin from Gibco-BRL.

Plasmids

The mammalian vector pCMVhGR, expressing the wild type hGR, was constructed by cutting out a BamHI-Xbal gragment from pUC18/ATG-NX and inserting it into pCMV4. This fragment contains the entire coding region of the human GR gene and about 400 bp of the 3'-untranslated sequence.

Mammalian Cell Culture and Transfection

COS-7 cells were grown in Dulbecco's modified Eagle's medium, supplemented with 10% fetal calf serum, penicillin (100 IU/mL) and streptomycin (100µg/mL), at 37°C in a humidified atmosphere with 5% CO2. For ligand binding assays and competition assays 10 cm plates containing cells at 60-80% confluency, plated out 1-3 days before transfection, were transfected with 10-15µg expression vector using the calcium phosphate method. Cells were incubated 48 hours after transfection before assays were performed.

Ligand Binding and Competition Assays

Cells were washed with and scraped in PBS and spun in a microfuge. They were then resuspended in a buffer consisting of 1mM EDTA, 20mM potassium phosphate p7.8, 10% glycerol, 20mM sodium molybdate and 1 mM DTT, homogenised with a glass homogenizer and the lysate was spun for 30 min at 100,000 xg at 4°C. For saturation analysis different concentrations of [^{3}H]TA(0.2-0.7 nM) were added and for competitive

binding assays 10nM [^{3}H]TA and increasing concentrations of different non-radiolabelled steroids were added. The extracts were incubated at 4°C overnight. Bound and free [^{3}H]TA were then separated by gel filtration on a Nick column (Pharmacia) and the amount of [^{3}H]TA bound was measured in a scintillation counter. Free [^{3}H]TA was calculated as total minus bound [^{3}H]TA. The level of unspecific binding was negligible as monitored by adding 200 fold excess non-radiolabelled TA to parallel incubations with the different concentrations of [^{3}H]TA.

Homology modelling and molecular dynamics

Initial multiple sequence alignments of the ligand binding nuclear receptor sequences were obtained using the Pileup program from the GCG program package. For semi-automated homology modelling, Modeler, as supplied with Quanta96, was run using the no optimism option, with the ER-α LBD/estradiol complex X-ray crystallographic structure (Brookhaven PDB accession number 1ERE) as the template. Hydrogen atoms were added to the homology model using the HBUILD routine in CHARMm. Sodium and chloride counterions were placed at the maxima and minima of the protein electrostatic potential near charged amino acid residues so as to achieve net neutrality of the system. The C- and N-termini were made neutral. The 3D molecular editor of QUANTA96 was used to build the various glucocorticoids. The constructed glucocorticoids were minimised in vacuo using Gasteiger - Huckel charges and a dielectric constant of 78. Partial atomic charges for the resulting structures were calculated by fitting the water-accessible surfaces of the molecules to their 6-31G* electrostatic potentials according to Singh and Kollamn, as implemented in Gaussian 94. The 6-31G* ESP charges were used for the ensuing protein-ligand interaction studies. The fit of dexamethasone in the binding site with the lowest ligand-protein interaction energy after minimization of various explored alternative starting orientations was chosen as an initial conformation for subsequent molecular dynamics. The minimisation was carried out with CHARM*m* and started with 200 initial cycles of steepest descent and continued by the adopted-basis Newton-Raphson algorithm until the root means square energy gradient was less than 0.01 kcal/Å. The default heuristic non-bonded list-update method and a distance dependent dielectric function (scaled with 1/r) were used. The protein-ligand interaction energies were when required calculated for each resulting minimised conformation. The system was subjected to molecular dynamics

using the Verlet and Shake algorithms using the same conditions as for the minimisation. The protein was surrounded by a 21 Å solvent cap of TIP3 waters centred on the ligand for the dynamics simulation. The initial dynamics simulation was for 10 ps using a step-size of 0.01 followed by 60 ps with a step-size of 0.02. The solvent cap was then removed and the remaining dexamethasone-GR complex structure resulting from the final trajectory after 70 ps of dynamics, was energy-minimised using the same constraints as described above and thereafter used for energy-minimisation with other ligands instead of dexamethasone.

The Modeler program was used, and it has been shown that it produces results as good as manual modelling at different levels of homology.

The initial sequence alignments were obtained from multiple sequence alignments of nuclear receptors. These alignments were used for the initial runs but they were adjusted for subsequent runs in order to produce a molecular model with a reasonable protein structure that also accounted for the available scientific data. The ligand was not included in the Modeler runs. Iterative Modeler runs, using sequence alignments considering the scientific data, resulted in the final alignment (Fig. 6). In the water-excluded surface of the model a completely enclosed banana-shaped binding cavity could be observed. This is reassuring, since it has been calculated that glucocorticoids should be completely enclosed by GR, and because it is known that the glucocorticoids with high affinity for GR are more bent out of their main plane (have a short A- to D-ring distance) than GR ligand with lower affinities. Dexamethasone was manually docked as a rigid body into the GR receptor homology model by the best possible fits of its atomic van der Waals radii to the water-excluded surface of the binding cavity. The initially selected position of dexamethasone within the homology model correspond to that of estradiol in the ER-α crystallographic complex (binding mode 1, Table 1). The dexamethasone molecule was also rotated 180 degrees about its long axis, such that the positions of the A- and D-rings were reversed (binding mode 5, Table 1) and thereafter at each of these two orientations, the molecule was rotated in steps 90 degrees about its short axis (binding modes 2-4 and 6-8, Table 1). An alternative orientation of the C-17-side chain corresponding to binding mode 1 was also investigated (binding mode 9, Table 1). The orientation with the most favourable protein ligand-interaction energy (Table 1) agrees with that of the ligand in the ER and PR X-ray crystallographic structures but not with the orientation of the

glucocorticoid in an earlier published GR model. The fit with the lowest ligand-protein interaction energy was chosen as a starting conformation for subsequent molecular dynamics. A water molecule was placed in the cavity near the C-3 carbonyl oxygen, based on the bridging water between the glutamate, arginine and 3'-OH of estradiol in the ER-α X-ray crystallographic structure. Side-chains of residues or water molecules within 5Å of the ligand were allowed to move freely, whereas the main chain C, Cα and N atoms within the same zone were restrained with a harmonic potential of 100 kcal/Å. The rest of the protein was kept rigid. These restraints were imposed because too much unrestrained minimisation and molecular dynamics has in blind tests been shown to cause the homology models to be more off the target than the template. The system was equilibrated with molecular dynamics together with the explicit solvent for 70 ps. The potential energy and temperature appeared stable during the last 10 ps of the trajectory. The solvent water was then removed and the remaining dexamethasone-GR complex structure resulting from the final trajectory after 70 ps of dynamics was energy-minimised using the same constraints as described above. The other ligand structures were then fit into the binding site in this same position and orientation as the best fit obtained for dexamethasone, and energy-minimised and used for correlation with the in this study experimentally determined IC_{50}s for human GR (Table 2).

Because a crystallographic structure of the progesterone receptor bound toan PR antagonist such as RU-38486 is not currently available, it is not certain how the conformation of PR changes when complexed with an PR antagonist. If RU-486 is docked into the binding cavity of the PR crystallographic structure or the GR homology model in an orientation analogous to progesterone in PR, there is insufficient space to accommodate its bulky 11-N,N-dimethylaniline substituent (i.e., it sterically clashes with helix-12). Therefore it is likely that H12 of GR is displace by RU-486 in analogy to the displacement of H12 by ER antagonists in estrogen receptor complexes. This displacement of H12 will then allow sufficient space to accommodate the 11-b-substituent of RU-486 and other GR antagonists with bulky 11-b-substituents. Therefore to produce an antagonistic GR homology model, H12 and the loop connect H11 and H12 in the PR based GR homology model was moved to where it is located in the ER -raloxifene complex by superimposition of the C-carbons according to the alignment in Fig 9. This was accomplished by splicing H12 and the loop between H11 and H12 from the ER -raloxifene complex X-ray crystallographic structure

into the GR-model, followed by mutation of the ER amino acid residues to the corresponding GR residues.

Table 1 Molecular Mechanics Interaction Energies For Various Biding Modes of Dexamethasone

Binding Mode *	Molecular Mechanics Interaction Energy (kcal/mol)
1	-82.5
2	-54.4
3	-73.6
4	-57
5	-64.9
6	-73.4
7	-64.2
8	-64.2
9	-79.6

*Binding mode 1 corresponds to that of estradiol in the ER-*a* crystallographic complex. Rotating the dexamethasone molecule in this binding mode by 180 degrees about its long axis, such that the positions of the A and D rings are reversed, results in binding mode 5. Binding modes 2-4 and 6-8 respectively, result from the progressive rotation of the molecule in steps of 90 degrees about its short axis at each of these two orientations. Binding modes 1 and 9 have a different orientation of the C-17 side.

Calculation of Solvation Energy

6-31G* electrostatic potential-fit charges and the corresponding CHARM*m* in vacuo optimised geometries of the steroids were used for calculation of solvent free energies with the GB/SA algorithm as implemented in the solvation module of the pseudoreceptor drug design software package PrGen. All calculations were run on Silicon Graphics R10000 workstations under IRIX 6.2/6.4.

Statistical Analysis

The sigmoidal dose-response curves obtained by competitive ligand binding assays were linearized with the log-logit function and the IC_{50} determined as the intersection with the X-axis (where logit=0) as described by Rodbard. The statistical analyses were performed using Microsoft Excel 5.0 and the partial least squares methodology as implemented in the QSAR module of Sybyl 6.4.

Molecular Mechanics Interaction Energies

Initially, the last frame of the molecular dynamics simulation performed with dexamethasone was energy minimised as described in Methods. It was noted that Thr-739 could possibly form a hydrogen bond with the steroid's 21-hydroxyl group by simple rotation of the amino acid's side-chain. The complex was then re-minimised following this alteration. As this lead to an improvement in the protein-ligand interaction energy, and the 21-hydroxyl is known to contribute to the affinity of glucocorticoid steroids, this complex was then used as a template to investigate the interactions of the other ligands with the protein. A spectrum of ligands was chosen to represent typical glucocorticoids ranging from natural ligand cortisol to potent synthetic ligands such as triamcinolone acetonide. The ligands were selected to include various combinations of common substituents of pharmacologically interesting GR-ligands such as Δ-1, 9α-fluoro and 16α-, 17α--substitutions (c.f. Fig 7 for the structures of the ligands used in the present study).

Table 2

Table 2. Relative binding of glucocorticoids to human GR.

Ligand	IC50±SD[a](nM)
Dessonide	7.0 ± 3.4
9α-F prednisolone	7.3 ± 7.0
TA	7.2 ± 1.8
Dexamethasone	12.5 ±7.1
9α-F cortisol	18 ± 1.7
Prednisolone	18.4 ±8.5
Cortisol	68.0 ±39.5
Triamcinolone	131.0 ±7

[a]n=3 for all compounds except for Ta where n=2

As can be seen from Table 2, the modifications of the cortisol structure employed here lead to quite significant alterations in binding affinity. Thus, this series of steroid ligands was well suited to challenge the explanatory powers of the model. Different orientations of the side chains of both ligands and amino acid residues were investigated and the model yielding the best correlation between molecular mechanics interaction energy and experimental data is analysed below and its interactions discussed with respect to the points described in the introduction.

It was not possible to obtain a useful correlation between the molecular mechanics interaction energy and the experimental free binding energy for all ligands (data now shown; R^2=0.10 vs. 0.45 when triamcinolone is excluded). Triamcinolone, which is the outlier, is the only ligand in this investigation having a 16α-hydroxyl substituent. In other studies, it has been shown that in order to reproduce experimental relative free energies of binding, ligand desolvation effects have to be taken into account. The GB/SA algorithm has been validated with a series of small substituted hydrocarbons. We have within the context of another study (Carlsson et al., manuscript in preparation) applied the PrGen solvation module to the Wolfenden data set which consists of the experimentally determined free energies of solvation in water of ten aromatic and cyclic molecules. Due to the greater degree of resemblance of the molecules in the Wolfenden data set to drug molecules, the solvation energies calculated by the solvation module of PrGen are scaled according to the equation resulting from the fit between that data set and the experimental data

$(\Delta Gsolv\ (GB/SA)=(\Delta Gsolv\ (PrGen)+0.25)/0.88; R^2=0.91$

with 6-31G* ESP charges calculated on the CHARM*m* in vacuo optimised geometries.

When a solvation correlation was included, the correlation between computed and experimental free energies for GR ligand binding was not improved (R^2 = 0.01 for all ligands vs. 0.45 when triamcinolone is excluded). The activity of triamcinolone was under-predicted in the correlation, as its C-15α-hydroxyl group was unable to make any hydrogen bonds with the protein but yet had the largest solvation penalty (Table 3). It was

then noted that Gln-642 could make a hydrogen bond with the C-16α hydroxyl oxygen atom of triamcinolone and the C-16 ether oxygen atoms.

Table 3: Summary of Ligand-Protein Interaction Energies (kcal/mol), Calculated Solvation Energies (kcal/mol), Ligand Strain Energies (kcal/mol) and Experimental Binding Affinities (kcal/mol) of the Glucocorticoids.

Ligand	Molecular Mechanics Interaction Energy (kcal/mol)	Scaled Calculated Solvation Energy (kcal/mol)	Ligand Strain Energy (kcal/mol)	Experimental free binding energy[a](kcal/mol) $-\Delta G_{bind\ (exptl.)}$
Desonide	-78.0	-26.32	5.66	11.55
9α-F prednisolone	-72.4	-23.33	3.08	11.53
TA	-78.7	-25.88	5.96	11.47
Dexamethasone	-74.3	-21.13	4.71	11.24
9α-F cortisol	-72.1	-20.35	3.42	11.04
Prednisolone	-73.9	-21.81	2.90	11.03
Cortisol	-70.6	-17.99	2.93	10.32
Triamcinolone	-82.9	-27.78	5.69	9.96

[a] $\Delta G_{bind\ (exptl.)}=RT \ln K^*_a$, $K^*_a=(1/K_d \text{ for } [^3H]TA)\,(IC_{50} \text{ for tested ligand}/IC_{50} \text{ unlabeled TA})$. K_d for TA = 0.66 nM.

of triamcinolone acetonide and desonide. Thus, the side chain of Gln-642 was rotated so as to achieve a hydrogen bond with the C16-oxygen substituent of these ligands and the complexes minimized. Although the other steroids do not possess a C16-substituent capable of acting as either a hydrogen bond donor or acceptor, Gln-642 in these complexes was also rotated to the same position as that in triamcinolone and the resulting complexes minimised. The amide nitrogen of Gln-642 formed hydrogen bonds (~3.1Å) with the S of Met-639 and also with the 16*α* oxygen atoms of triamcinolone, desonide and triamcinolone acetonide. A good correlation between the molecular mechanics interaction energy for all the ligands could then be achieved with this model if solvation and ligand strain energy (ligand strain energy is the difference in energy between the ligand conformation in the protein and when minimised in vacuo) corrections were included. Figure 8 shows the progressive improvement of the correlation with the addition of these corrections. the R^2 increases from 0.04 (0.49 without triamcinolone; Fig 8A) to 0.48 with the solvation penalty (Fig 8B) and further to 0.69 if the ligand strain energy penalty is also included (Fig 8C). When considering only molecular mechanics interaction energy together with ligand strain energy, the correlation coefficient is 0.1 (0.49 without triamcinolone). Thus it is the combination of the solvation and strain terms that results in good correlation with the experimental free energy binding data. A partial least squares analysis using the molecular mechanics interaction energy together with the solvation (not scaled according to Wolfenden data set) and strain energies was then performed, increasing the R^2 from 0.04 (molecular mechanics term only) to 0.80 (inclusion of solvation and strain energies, Fig. 3(iv)). The resulting equation was:

$$\Delta Gbind(calc)=0.384 - \Delta Ginter(MM)0.343 - \Delta Gsolv(PrGen) - 0.466 - \Delta Gstrain(MM) - 31.058.$$

The main interactions of dexamethasone with the protein are shown schematically in Fig. 4. In another model the C-17-side-chain of the ligands was rotated so as to enable the C20-keto group to form a hydrogen bond with the CD2 hydrogen of Tyr-735, but at the same time maintaining the hydrogen bond interaction between the C21-hydroxyl and Thr-739. Such hydrogen bond interactions have been reported in the literature and interestingly, Tyr-735 corresponds to His-524 in hER*α*, the residue which forms a hydrogen bond with the C-17-OH group of estradiol. The corresponding residue for the other members of the steroid hormone superfamily is either a phenylanaline or a tyrosine.

However, this model yielded a poor correlation (R^2<0.5) and was therefore discarded from further analysis.

It will be noted that whilst the description refers to a method of designing a GR homology model from rat thyroid hormone receptors and a Human Progesterone Receptor, the same process may be used to design a GR model from a Human Progesterone Receptor. Figure 11 shows the sequence alignment which would be used to design a GR from PR.

Explanation of the Glucocorticoids Structure-Activity Relationships

Reduction of the C-3 keto to a hydroxyl group reduces biding affinity

Tanenbaum et al have contrasted the hydrogen bonding interactions of the phenolic group of estradiol and the C-3 keto group of progesterone complexed with their respective receptors. Steroid receptors which bind 3-keto groups have a conserved glutamine corresponding to the sequence position of Gln-725 in hPR, but the equivalent residue in hERα is a glutamate residue (Glu-353). Hence, these residues are responsible for the discrimination by the steroid receptors of keto and hydroxy moieties as the arginine residues which form either direct (hPR) or direct and water mediated interactions (hERα) with the keto and hydroxyl functions are conserved throughout the steroid receptor family. Additionally, there is a conformational change (atomic displacement) associated with a change in hybridization from a sp^2C-3 keto to a sp^3 hydroxyl. Thus, as the ligand makes several hydrogen bonds with the receptor, a protein with functional groups at an optimum separation for simultaneous binding to the O-3 and O-20 keto oxygen atoms, and O-11, O-17 and O-21 hydroxyl oxygen atoms may bind less to a ligand which has a 3-hydroxyl group instead of a 3-keto group.

In our homology model, the C-3 keto groups of the glucocorticoid ligands form direct hydrogen bonds with Gln-570 and Arg-611. In contrast, in hPR Arg-766 directly contacts progesterone's C-3-keto group, and in hERα the equivalent interaction (Arg-394) with the phenolic oxygen of estradiol is also direct.

Reduction of the C-20 keto group reduces binding affinity

In the homology model, the C-20 keto group does not engage in hydrogen bonding, but does have a favourable electrostatic interaction with the sulfur of Met-560. For the eight glucocorticoids, the O-A distance is ~3Å. (Many examples of both intermolecular and intramolecular nonbonded sulfur-nucleophile close contacts in which the sulfur-nucleophile distance is less than the sum of the sulfur and nucleophile van de Waals radii have been reported in the crystallographic literature).

The C-11β- and C-21β- hydroxyl groups are important for binding

The main weakness of the present model is its inability to explain the importance of the C-11β-hydroxyl as the nearest potential hydrogen bond partner is the backbone carbonyl of Leu-563, with a distance of ~4Å. That C-11β-chloro substituted glucocorticoids have similar affinities for Gr as C-11β-hydroxyl substituted glucocorticoids has been rationalised by the assumption that there exists an accessory hydrophobic pocket for such halogen substituents. However this assumption may not be necessary, because in our model both the C-11 chloro or hydroxyl substituents may interact with the Leu-563 carbonyl oxygen, and carbonyl oxygens in other X-ray structures are known to interact with halogen atoms at less than the sum of their van de Waals radii. In the thyroid hormone receptor X-ray structure the ligand iodines interact thus with backbone carbonyl oxygens.

The C-21 hydroxyl forms a hydrogen bond (2.6Å) with Try-739 and also with the backbone carbonyl of Tyr-735 (2.9Å). Thr-730 corresponds to Thr-894 in hPR, but in the complex with progesterone (which lacks the C-21 hydroxyl group) no hydrogen bond could be made by this residue with the ligand.

A C-17α hydroxyl group increases affinity for the hGR, but decreases it for rat GR

The C-17α hydroxyl group in both cortisol and 9α-F cortisol forms a good hydrogen bond with Met-639 (oxygen-sulfur distance = ~3.2Å). However, from our model it appears that compounds possessing a 16-methyl substituent are unable to form a short hydrogen bond with this residue due to a steric repulsion between Met-639 and 16-Me. By comparing the sequences of rat and human GR, there were no species differences in the vicinity of Met-639. Thus the model is unable to explain the intolerance of the rat GR for a C17α-OH group.

Bromine or methoxy substituents in the C-9 position decrease ligand binding affinity

The C-9*a* fluorine of the ligands is in close contact with the CE2 carbon atom of Phe-623 (3.4Å). Thus, introducing a more bulky substituent would presumably result in the displacement of Phe-623 from a position in which it can form a "pi-teeing" interaction with the ligand's A-ring and/or displacement of the ligand from its preferred position, causing a disruption of its interactions with the receptor.

The ligand is completely enclosed by the hydrophobic binding cavity

In the model the ligand is completely enclosed by predominantly hydrophobic residues: Leu-563, Leu-566, Trp-600, Met-601, Met-604, Phe-623, Leu-723 and Leu-753. The ligands make many favourable hydrophobic contacts with the receptor, in particular the C18- and C19- methyl groups with Met-601 and Leu-732 respectively. Significantly, these residues are preserved in the hPR, human androgen receptor and human mineralocorticoid receptor, whose ligands also have C18- and C19- methyl groups, but not in hER whose natural ligands 17 β-estradiol lacks the C19-methyl group. Additionally, hydrophobic contact exist between the C16-methyl group of dexamethasone and the acetonide functions of desonide and triamcinolone acetonide with Tyr-735.

In order to assess the utility of the PR-based GR homology model modified to accommodate GR antagonists for the design of such drugs the compound 10e described Gebhard et al. Biorg. Med. Chem. Lett. 7(17) 2229, 1997 was used. The ligand was placed in the receptor with it steroid core in the same orientation as progesterone in PR and the complex minimized to gradient norm of 0.05 with the residues within 7 Å of the ligand treated as flexible while the remainder of the protein was held rigid. After minimization the carbonyl oxygen atom of the 2-oxo-1-pyrrolidinyl group was within hydrogen bonding distance (2.7 Å) to the hydroxyl oxygen atom of Thr-556, which corresponds to Ser-711 in PR. The distance from the steroid C-3 carbonyl oxygen atom to Arg-611 was 2.6 Å. Thus the model may be used to interpret and improve the binding of GR antagonists to GR.

A second double bond in the A-ring improves binding affinity

The fact that the binding cavity in this GR homology model is more bent than the steroid ligand is consistent with the classical structure-affinity relationship for glucocorticoids, since it would preserve the rank order of affinities where the most bent GR-binding steroids (those that have the shortest A- to D- ring distances) bind with the highest affinities to GR and the more planar ligands bind with lower affinities. It is known that the receptor bound conformation of ligands frequently differs from the minimum energy conformation of ligands. In the liganded RAR structure the 9-cis retinoic acid is more bent than the binding cavity whereas the all-trans retinoic acid is flatter than the binding cavity. It was thus concluded that ligand binding to a nuclear receptor is a complex process where both the ligand and the binding site have to adjust for binding. If our modelling has produced a correct impression of the ligand binding cavity, the above statement will be valid for GR as well.

Each of the pair cortisol and prednisolone, 9α-F, prednisolone represent ligands which differ only in whether they have a 1,2-diene double bond or not (Fig 7). In our model, the A-ring of the 1,2-unsaturated ligands adopt a 1α, 2β–half chair conformation which represents one of the ideal forms. Relative to the docked 9α-F prednisolone, the 3-C keto oxygen of the docked 9α-F cotrisol is displaced by 0.2Å. This leads to minor adjustments in its interactions with the protein so that the coordinates of the water oxygen atom and nitrogen of the Gln-570 side-chain differ by 0.1 Å as compared to those in the 9α-F prednisolone protein biding site. Additionally, displacements of the 11-O, 17-O, 20-O and 21-O oxygen atoms and 9α-F atom of between 0.1 to 0.2Å occur. Atomic movements of the same magnitude also occur for cotrisol with respect to prednisolone, with the exception of the 17-O and 20-O atoms which are displaced to a lesser extent, (0.04 Å vs. 0.1Å respectively). Prednisolone has a distinctly superior molecular mechanics interaction energy as compared to cortisol (~3 kcal/mol), but 9α-F cortisol has only a marginally better molecular mechanics interaction energy than 9α-F prednisolone (Table 3). These differences are attenuated (9α-F cortisol vs 9α-F prednisolone) or at least maintained (cortisol vs prednisolone) when ligand strain energy is added to the molecular mechanics

term (Table 3). Thus, the model does reflect the preference of GR for ligands with a 1,2-diene double bond relative to those that lack this feature.

The shorter the C-3 to C-17 distance the higher the affinity of a Glucocorticoid is for the Glucocorticoid Receptor

Although there is not a direct relationship between the C-3 to C-17 distance of the ligand in the homology model and ligand binding affinity (Table 4), it is notable that this distance is greatest for cortisol and its 9-fluorinated analog. When compared to the other ligands, both lack a 1,2-diene double bond in the A-ring and with the exception of triamcinolone, they have the highest free binding energies (together with prednisolone).

Explanation of Mutational Data

The HSP90 heat-shock protein is required for GR ligand binding, but as a part of activation of GR which is conceived as a steroid-induced conformation change of Gr necessary for DNA-binding and glucocorticoid dependent transcriptional regulation) it dissociates from the receptor. The HSP90 interaction sites on the GR surface have been mapped with peptide competition studies. It was found that the critical contact site is located in the region between residues 632-659 of mouse GR. In our model this region (626-653) in hGR) corresponds to S1-S2 hairpin β-sheets and H6-H7 α-helices which constitute a part of the protein surface and which also line the binding cavity. Thus. our GR model is consistent with what is known about the GR-HSP90 interactions.

A number of mutations of GR in various species have been described. Most of the mutations in the GR LBD completely disrupt the function of the receptor, presumably by perturbation of the fold of the LBD. Those detrimental mutations are not useful for validation of a GR homology mode. On the other hand, mutations in the LBD that affect ligand binding specificity and/or GR ligand-dependent activation/repression of transcription without totally activating the protein are of the greatest interest for our invention, validation of a GR homology model, since they ought to be located near the binding site. Such residues whose mutations modulate the function of GR are (in terms of the human GR sequence): P541, M565, G567, A573, M601, C638, D641, C643, M646, L653, C665, E668, V729, C736, T774, 764, F774, and these are shown as purple balls in

the receptor model in Fig. 10a and 10b. It can be seen that they seem to cluster around the ligand site and/or on H12 or its vicinity. Most of the mutations which are non-detrimental to protein activation are within 7Å of the ligand, i.e. on the parts closest to the binding site of the helices that line the binding cavity (Table 5). Most of the mutated side-chains had direct ligand contact before the mutation (c.f. the inventory of the residues lining the binding cavity). That those mutations affect ligand biding affinity and/or ligand-dependent transactivation is thus consistent with our mode.

Table 4

Summary of Ligand Binding Affinities and C-3/C-17 Distances (Å) within Homology Model

Ligand	-ΔGbind(exptl.) (kcal/mol)	C-3/C-17 (Å)
Desonide	11.55	8.21
9αF prednisolone	11.53	8.3
TA	11.47	8.24
Dexamethasone	11.24	8.28
9αF cortisol	11.04	8.45
Prednisolone	11.03	8.23
Cortisol	10.32	8.47
Triamcinolone	9.96	8.17

Table 5. Mutations affecting GR transactivation/ligand affinity within GR.

Mutation	Decreased affinity for DEX	Decreased transactivation with DEX
P541A	*nt*	> 100-fold
L563F	6-fold	15 – 60-fold
M601L	3-fold	*nt*
C638Y	Normal	Normal
C638G	10-fold INCREASED	10-fold INCREASED
C638W	Normal	Normal
D641G	Normal	no activity
D641V	Normal	no activity
C643R	*nt*	Slightly reduced
C643G	*nt*	2 – 3-fold
C643S	4-fold	*nt*
M646T	*nt*	Slightly reduced
L653S	Reduced	Reduced
C665A	*nt*	> 100-fold
C665S	*nt*	4-fold
M666I	4-fold	10 – 25-fold
E688K	Normal	no activity
V729I	2-fold	4-fold
C736S	2-fold	10-fold
C736G	*nt*	no activity
T744I	*nt*	Reduced
I747T	2-fold	50-fold
L753F	Normal	no activity
Y764N	2-fold	3 – 4-fold
F774A	6-fold	20-fold

DEX = dexamethasone

nt = not tested

Some mutated residues were remote from the ligand, or did not have direct ligand contact. These mutations were further scrutinised, in order to confirm that they do not invalidate our GR homology model. Mutations in residues <523 and residues >761 are in the hinge or on the C-terminal part of H12 that is not included in the template X-ray structure and outside our GR model so they cannot be used for model validation.

The P541A mutation in Gr results in that more than 100-fold increase in steroid concentration is needed to preserve biological activity, presumably due to decreased steroid affinity. Although this mutation is remove from the binding site it is at the very beginning of the strand between H1 and H3 (at the end of H1) and it may therefore be critical for its conformation. This strand (consisting of residues 540-560) delimits the binding site with residues 542-544. Therefore, a conformational change in this strand brought about by the P541A mutation could affect ligand binding from a distance.

The patient mutation V762I which reduces affinity for dexamethasone 2-fold and the C643S mutation, which reduces affinity 4-fold, are located in proximity of the ligand binding site but the side chains of the residues are not directed towards the steroid. Thus, these residues do not appear to be in direct contact with the steroid and secondary effects of these mutations would be required to explain the difference in ligand affinity. The L653S and F744A mutants that were reported by Garabedian and Yamamoto were tested in a yeast expression system, in which binding receptor binding assays were not performed so their effect may be exerted on transcription only, and need not necessarily directly affect ligand binding.

The I747T mutation reported by Roux is 9-10Å from the ligand, so it is difficult to explain why it decreases binding affinity with our model. The E688K mutation has been reported by Garabedian and Yamamoto to abolish transcriptional activity of Gr expressed in yeast and COS cells and to decrease the affinity for dexamethasone. This residue is located on H9, as far from the binding site as you can get in the GR LBD, located near H1 and facing outwards. It is here H1 connects to the hinge region to the DBD and thus it is plausible that the effect of this mutation is caused by disturbances of the interaction with DBD, rather than an direct effect on the binding site.

The C655A/S mutants required a 100-fold higher steroid concentration for biological activity of the mouse GR, but C665S in human GR has no effect on binding affinity. This residue in our model is located in H8, remove from the ligand, but since it does not affect binding affinity it does not have to be located near the binding site to validate our model. Hence, the inhibition of binding observed by Lee et al, by the mutation of the neighbouring residue, M666I, is then difficult to rationalise. However, their other mutation affecting binding affinity, L563F is near the C-ring of the steroid's α-face, and thus consistent with the model.

Warriar et al, have described that the point mutations M565R and A573Q greatly enhance the affinity of Gr for dexamethasone, whereas the G567A mutant fails to bind ligands efficiently. In our GR model these residues are relatively close to the binding site. The Cα's of M565, G567 and A573 are ~7Å from C1, 3Å from C2 to 11 Å from the C3-carbonyl of dexamethasone, respectively. IN our model G567 and A574 are facing the binding cavity, in contrast to M565, which is directed from it(and constitutes part of the protein surface). Thus the M565R mutation should not affect the ligand affinity of GR to a great extent if our model is correct. In the context of another study (Lind. U., Wright, A.P.H. and Carlstedt-Duke, J., ms. in preparation) a random combination of GR to mineralocorticoid receptor mutations (between residues 565-574) was created and screened for activity with glucocorticoids and mineralocorticoids. We found in agreement with Warriar et a., that the A573Q mutant had increased activity with dexamethasone, and that the G567A mutation inactivated GR. Finally, in contrast to Warriar et al, it was also found that the M565R mutant had no effect on the activity of dexamethasone which is in better agreement with the GR model proposed.

Thus, of the mutations described in the literature affecting ligand affinity, only two (M666I, 1747T) cannot easily be accounted for by the present GR-model.

Carlstedt-Duke et al have demonstrated three residues to be in the vicinity of the binding site of GR by covalent affinity labelling with radiolabelled Gr ligands with protein sequencing studies, Cys-638 is affinity-labelled through an electrophilic group of the 21-position in dexamethasone 21-mesylate reacting with a thiol. There is an absolute requirement for the C-20 carbonyl group for this labelling reaction. In our model the sulfur

of Cyc-638 is located 7Å from the hydroxyl oxygen on C-21 of dexamethasone. The Cys-736 sulfur is even closer, which may explain why this residue is preferentially labelled.

Regarding the other two affinity labels, the chemistry is not known following the photoactivation of UV-light of the bound TA ligand. IN our GR-model the C-18 and C-19 methyl groups of Ta are located within 4 Å of Cys-736S, and 5.6 Å of Met-604S, respectively. If the reaction mechanism involves direct binding to the A- or B-ring, the affinity labelling of Cys-736 would require that the ligand be flipped with respect to A- and B-ring location at the time of the reaction. These two support the orientation of the steroid. In an earlier GR model the orientation of the dexamethasone is reversed with respect to the location of the A- and D-rings. With that orientation the Cys-736 is closer to the A-ring, but the other two residues (Met-604 and Cys-638) involved in the covalent affinity labelling are much further away, as compared to our orientation of the steroid. Thus, the orientation of the steroid in our model is more congruent with the affinity labelling data previously known.

Figures 12 and 13 show the -ray crystalography data obtained from the GR models produced using the X-ray crystallographic structures of TR, ER and PR as templates.

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CLAIMS

1. A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three-dimensional image, the method comprising:

(i) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor,

(ii) modifying said x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand,

(iii) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receiptor, and

(iv) if required modifying the homology model for greater consistency with those binding properties.

2. A method according to claim 1, wherein amino acids lining the binding cavity of the glucocorticoid receptor are identified chemically and the information thus gained used to verify and if appropriate modify the homology model.

3. A method according to claim 2, wherein (v) amino acids lining the binding cavity of the glucocorticoid receptor are identified by chemically mutating the glucocorticoid receptor so as to change one amino acid thereof, and experimentally determining how the

mutation affects the binding properties of the receptor to one or more ligands known to bind to the unmutated receptor.

4. A method according to claim 3, wherein step (v) is repeated one or more times, each time changing a different amino acid of the glucocorticoid receptor.

5. A method according to claim 2, including: (vi) introducing a photolabile group into a ligand having affinity for the glucocorticoid receptor, and forming a complex of the modified ligand with the receptor, expose the resulting complex to light to cause it to decompose to form reactive groups which bind to adjacent amino acids of the receptor, break up the complex into peptide fragments, analysing fragments to identify those bound to reactive groups from the modified ligand and thus the amino acids lining the binding cavity of the receptor.

6. A method according to any preceding claim, wherein the homology model is compared with the structures of other, similar, proteins.

7. A method according to any preceding claim, wherein the homology model is checked and if necessary modified to ensure that it shows predominantly hydrophobic amino acids lining the binding cavity and predominantly hydrophilic amino acids exposed to the outside.

8. A method according to any preceding claim, wherein the thyroid, estrogen or progesterone receptor is a human receptor.

9. A homology model of the ligand binding domain of a glucocorticoid receptor designed in accordance with any preceding claim and having hydrogen bonding partners for the C-16 and C-21 OH groups of a glucocorticosteroid.

10. A homology model according to claim 9, showing a hydrophilic cavity positioned to interact with the C-3 carbonyl group of a glucocorticosteroid.

11. A homology model according to claims 8, 9 or 10, showing at least one small hydrophobic pocket capable of interacting with a methyl or halogen substituent at the C-6 and/or C-9 position of a glucocorticosteroid.

12. Use of a homology model according to any of claims 9 to 11 to identify or design ligands capable of binding to the ligand binding domain of a glucocorticoid receptor.

13. Use of a homology model according to any of claims 9 to 11 to identify or design glucocorticoid receptor antagonists or agonists.

14. A glucocorticoid receptor antagonist or agonist identified by use of a homology model according to any of claims 9 to 11.

15. A medicinal product comprising a glucocorticoid agonist according to claim 14 for treatment of inflammation or for use in immunosuppressive therapy.

16. A medicinal product comprising a glucocorticoid antagonist according to claim 14 for use in the treatment of hypertension, diabetes, obesity, glaucoma, depression, AIDS, and wounds.

17. A computer programmed with a homology model of the ligand binding domain of a glucocorticoid receptor according to any of claims 9 to 11.

18. A machine-readable data-storage medium on which has been stored in machine-readable form a homology model of the ligand binding domain of a glucocorticoid receptor according to any of claims 9 to 11.

19. The use of a homology model according to any of claims 9 to 11 as input to a computer programmed for drug design and/or database searching and/or molecular graphic imaging in order to identify new ligands for the glucocorticoid receptor.

20. A computational and chemical method of iteratively generating a homology model of the ligand binding domain of a glucocorticoid receptor, which homology model is capable of being displayed as a three-dimensional image, the method comprising:

(i) entering into a computer an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor;

(ii) modifying under computer control said x-ray crystallographic structure to take account of known differences between the amino acid configuration of the ligand

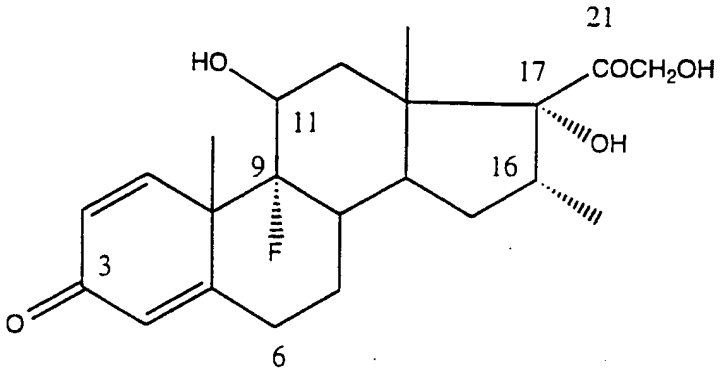
binding domains of the glucocorticoid receptor on the one hand and at least one of the thyroid, estrogen, or progesterone receptors on the other hand,

(iii) reconciling under computer control the resulting modified crystallographic structure with the chemically-determined binding properties of a number of ligands for the glucocorticoid receptor;

(iv) identifying by chemical means the amino acids that line the binding cavity of the ligand binding domain and reconciling under computer control the modified crystallographic structure with these;

(v) repeating steps (ii) and (iii).

Fig. 1



Dexamethasone

FIGURE 2A

```
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TRb_triac2      KPEPTDEEWELIKTVTEAHVATNAQGSAWKQKR-KFLPEDIG----------QVDLEAFS
erhum7          ----SLALSLTADQMVSALLDAEPPI-LYSEYDPTRP---------FSE------ASMMG
grmodel         ----PATLPQLTPTLVSLLEVIEPEV-LYAGYDSSVP---------DST------WRIMT

TR_t3cyatocys   EFTAIITPAITRVVDFAKKLPMFAELPCEDQIILLKGCCMEIMSLRAAVRYDPASD--TL
TRb_triac2      HFTAIITPAITRVVDFAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESE--TL
erhum7          LLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG--KL
grmodel         TLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLL

TR_t3cyatocys   TLSGEMAVKREQLKN-GGLGVVSDAIFALGKSLSAFALDDTEVALLQAVLLMST-----D
TRb_triac2      TLNGEMAVTRGQLKN-GGLGVVSDAIFDLGMSLSSFNLDDTEVALLQAVLLMSS-----D
erhum7          LFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFL
grmodel         CFAPDLIINEQRMTL-PCMYDQCKHMLYVSSELHRLQVSYEEYLCMKTLLLLS----SVP

TR_t3cyatocys   RAGLLCVDAIAASQAAYLLAFEHYVNHRK------HAIPHFWPKLLMKVTDLRMIGACHA
TRb_triac2      RPGLACVERIEKYQDSFLLAFEHYINYRK------HHVTHFWPKLLMKVTDLRMIGACHA
erhum7          SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGM
grmodel         KDGLKSQELFDEIRMTYIKELGKAIVKREGN---SSQNWQRFYQLTKLLDSMHEVVENLL

TR_t3cyatocys   SRFAHMKVECPTA---LFPPLFLEVF
TRb_triac2      SRFLHMKVACPTA---LFPPLFLAVFED
erhum7          EHLYSMKCKN---VVP-LYDLLLEMLDAHR
grmodel         NYCFQTFLD-K-TMSIEFPEMLAEIITNQI
```
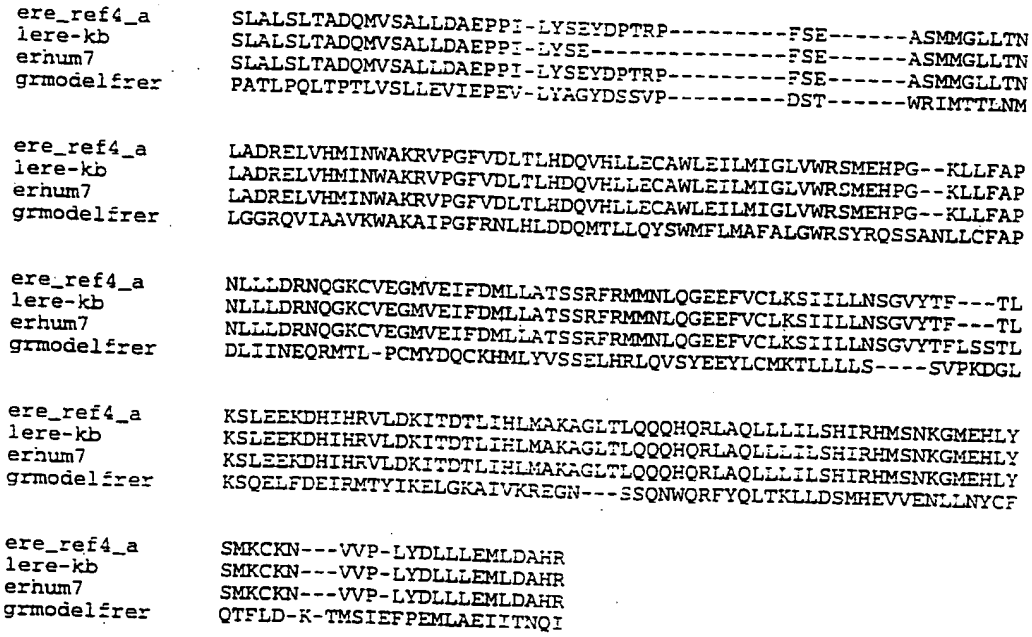

FIGURE 2B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lere-kb SLALSLTADQMVSALLDAEPPI-LYSE----------FSE------ASMMGLLTN
erhum7 SLALSLTADQMVSALLDAEPPI-LYSEYDPTRP---------FSE------ASMMGLLTN
grmodelfrer PATLPQLTPTLVSLLEVIEPEV-LYAGYDSSVP---------DST------WRIMTTLNM
ere_ref4_a LADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG--KLLFAP
lere-kb LADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG--KLLFAP
erhum7 LADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG--KLLFAP
grmodelfrer LGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLLCFAP
ere_ref4_a NLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF---TL
lere-kb NLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF---TL
erhum7 NLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF---TL
grmodelfrer DLIINEQRMTL-PCMYDQCKHMLYVSSELHRLQVSYEEYLCMKTLLLLS----SVPKDGL
ere_ref4_a KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLY
lere-kb KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLY
erhum7 KSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLY
grmodelfrer KSQELFDEIRMTYIKELGKAIVKREGN---SSQNWQRFYQLTKLLDSMHEVVENLLNYCF
ere_ref4_a SMKCKN---VVP-LYDLLLEMLDAHR
lere-kb SMKCKN---VVP-LYDLLLEMLDAHR
erhum7 SMKCKN---VVP-LYDLLLEMLDAHR
grmodelfrer QTFLD-K-TMSIEFPEMLAEIITNQI

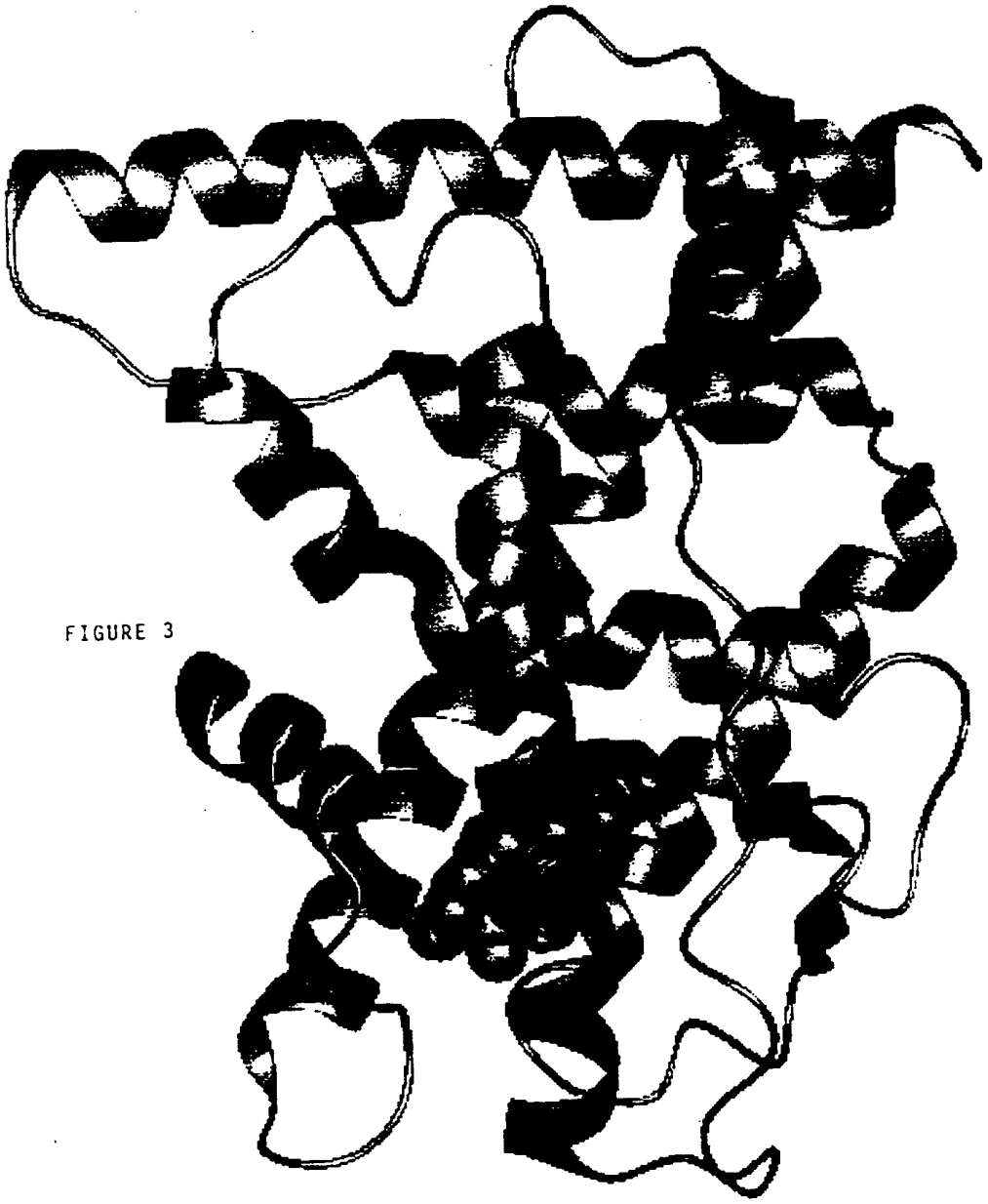
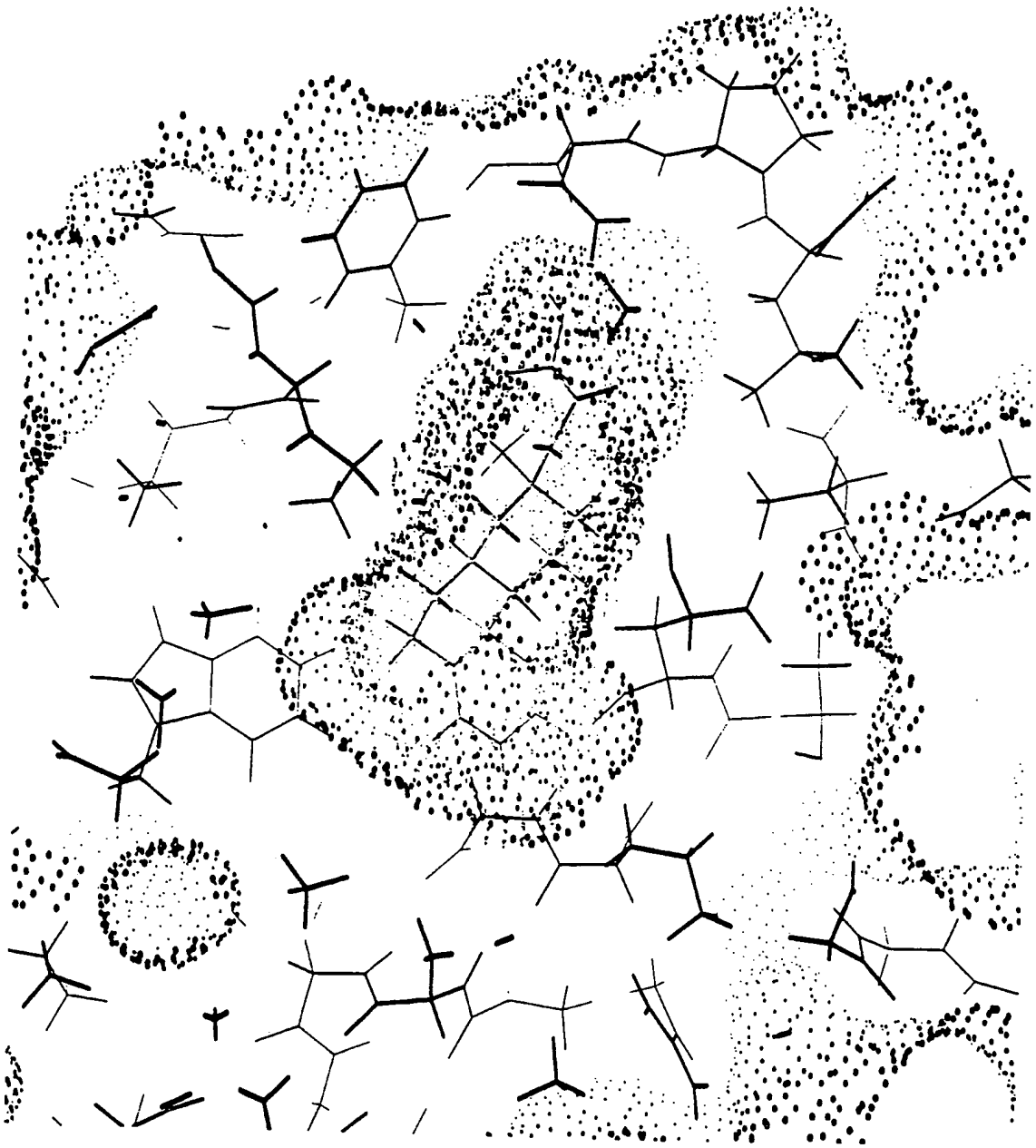


FIGURE 3

FIGURE 4



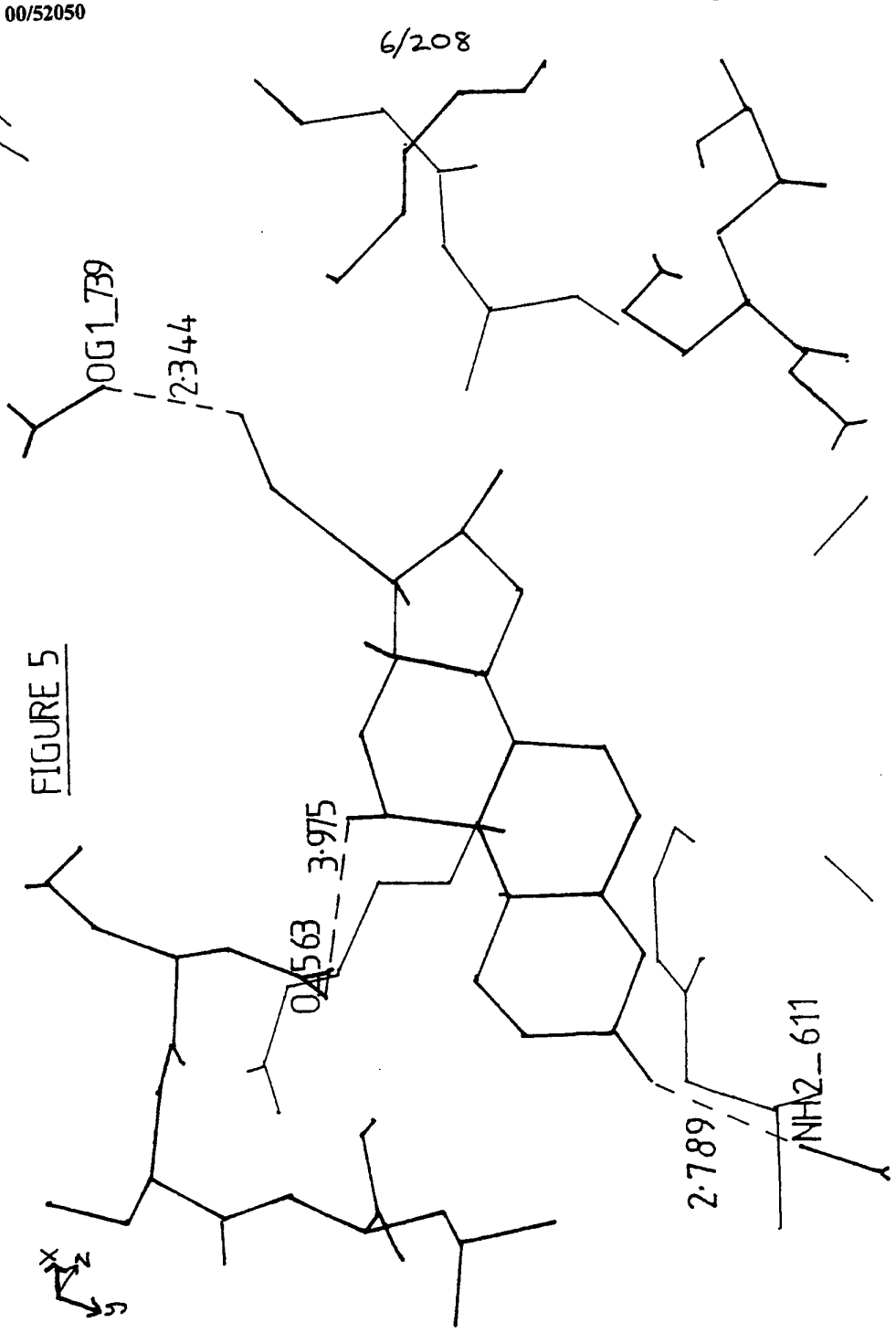


FIGURE 5

```
ER 305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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ER 365 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG--KLLFAPNLLLDRNQGKCVEGMV
GR 582 PGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLLCFAPDLIINEQRMTL-PCMY

ER 423 EIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKI
GR 643 DQCKHMLYVSSELHRLQVSYEEYLCMKTLLLLSSVPKDG----LKSQELFDEIRMTYIKE

ER 483 TDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKN--VVP-LYDL
GR 697 LGKAIVKREGN---SSQNWQRFYQLTKLLDSMHEVVENLLNYCFQTFLD-KTMSIEFPEM

ER 540 LLEMLDAHR
GR 753 LAEIITNQI
```

FIG. 6

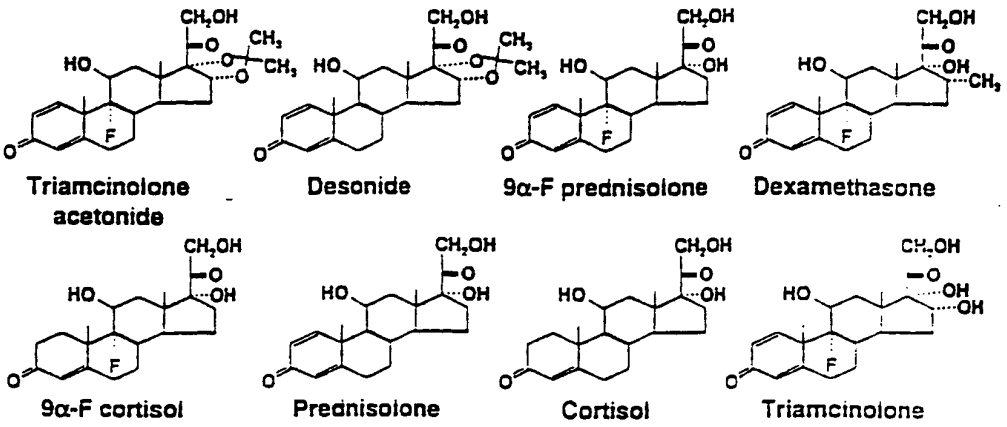

Triamcinolone acetonide
Desonide
9α-F prednisolone
Dexamethasone
9α-F cortisol
Prednisolone
Cortisol
Triamcinolone

FIG. 7

Fig 8(i).

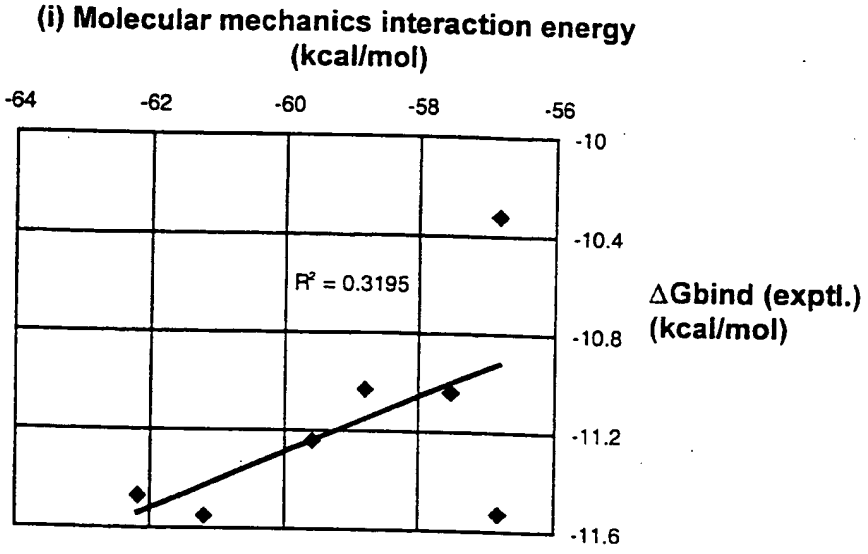


Fig 8(ii).

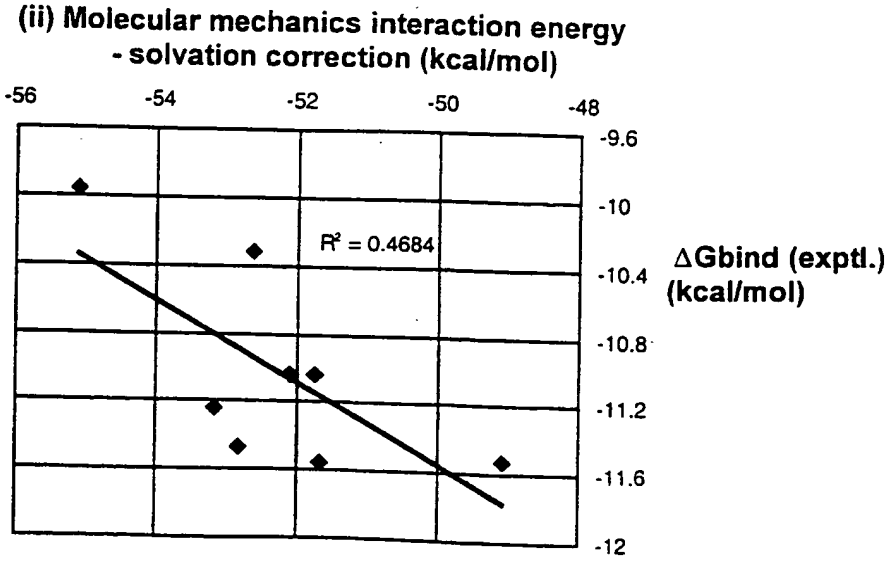


Fig 8(iii).

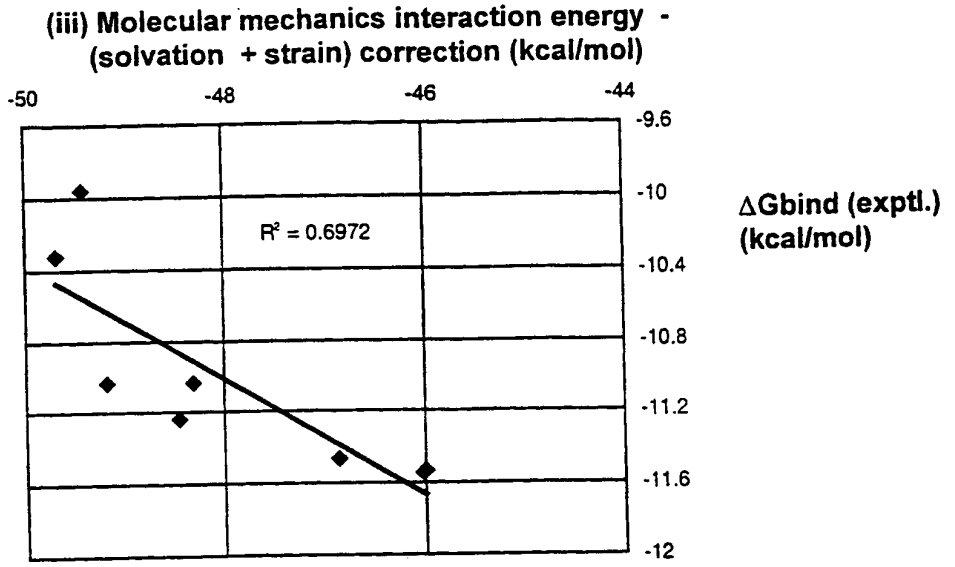


Fig 8(iv).

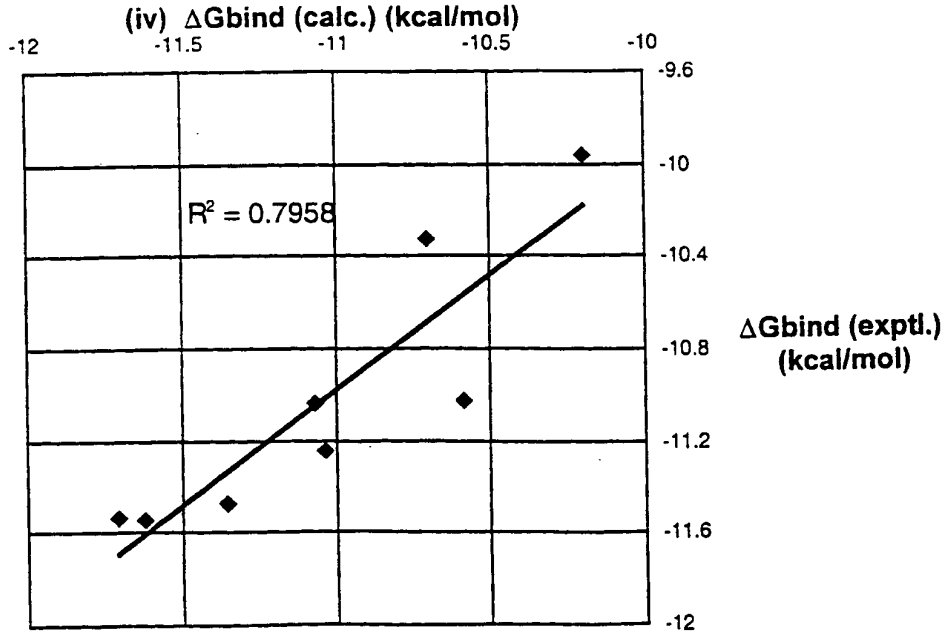


Figure 9: (a) RasMol representation of the main interactions with dexamethasone in the GR homology model.

(b) Sketch of the main interactions with dexamethasone in the GR homology model.

Figure 9a:

Figure 9b:

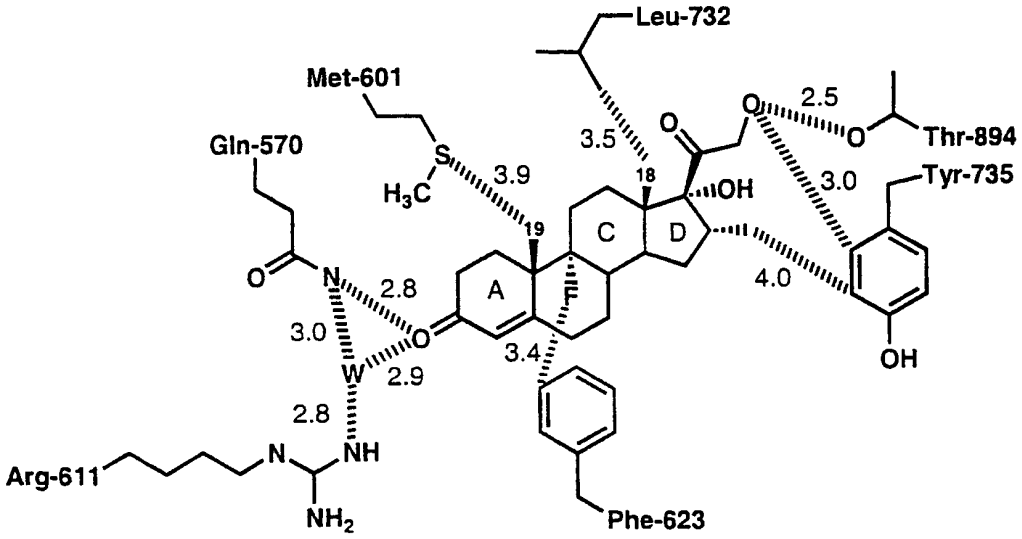

Leu-732
Met-601
Gln-570
Thr-894
Tyr-735
Arg-611
Phe-623
OH
A
C
D
F
18
19
2.5
3.5
3.9
3.0
2.8
4.0
3.4
2.9
NH
NH2

Figure 10a

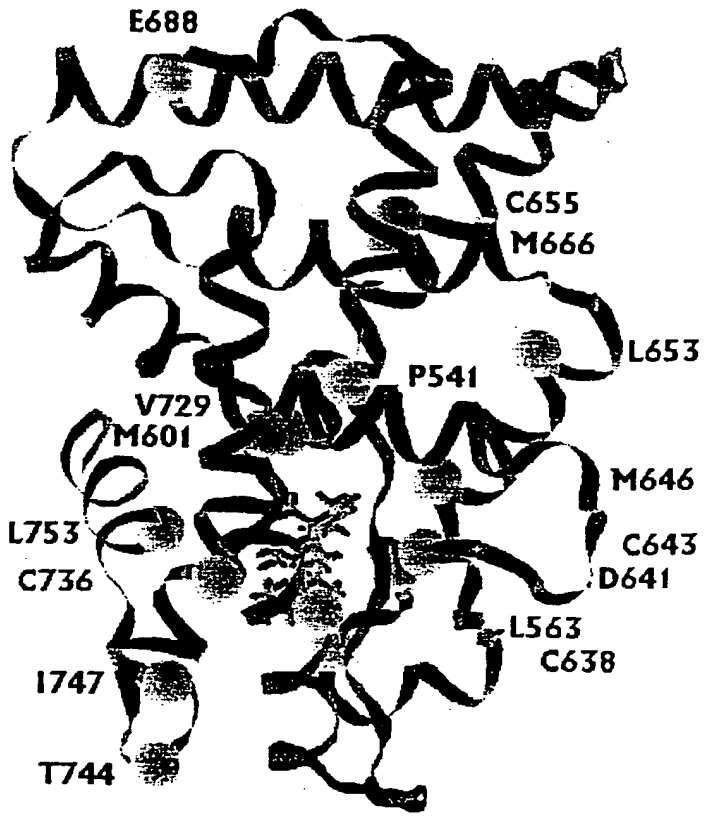
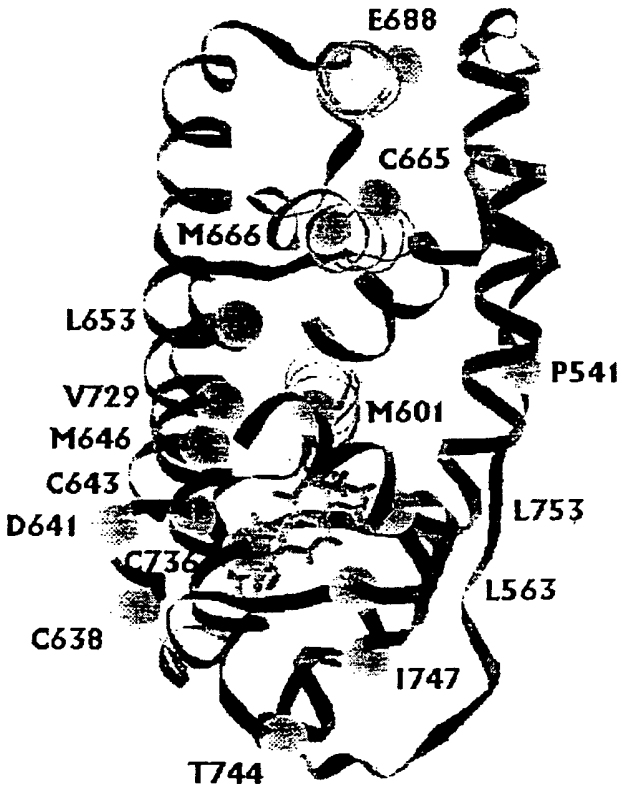

E688
C655
M666
L653
P541
V729
M601
M646
L753
C643
C736
D641
L563
C638
I747
T744

Figure 10b


E688
C665
M666
L653
P541
V729
M601
M646
C643
L753
D641
C736
L563
C638
I747
T744

progA
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWM
GRmodel
QLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVIAAVKWAKAIPGFRNLHLDDQMTLLQYSWM

progA
SLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIP
GRmodel
FLMAFALGWRSYRQSSANLLCFAPDLIINEQRMTLPCMYDQCKHMLYVSSELHRLQVSYEEYLCMKTLLLLSSVP

progA
LEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFP
GRmodel
KDGLKSQELFDEIRMTYIKELGKAIVKREGNSSQNWQRFYQLTKLLDSMHEVVENLLNYCFQTFLDKT-MSIEFP

progA EMMSEVIAAQLPKILAGMVKPLLFHK*
GRmodel EMLAEIITNQIPKYSNGNIKKLLFHQK*

Figure 11

Fig 12

```
REMARK  1 grfromer
ATOM      1  C25 CORTC  1      -6.118   0.501   0.557  1.00  0.00
ATOM      2  C26 CORTC  1      -5.161   1.475   0.031  1.00  0.00
ATOM      3  C27 CORTC  1      -4.017   1.077  -0.556  1.00  0.00
ATOM      4  C28 CORTC  1      -3.103   2.102  -1.174  1.00  0.00
ATOM      5  C29 CORTC  1      -1.725   2.081  -0.520  1.00  0.00
ATOM      6  C30 CORTC  1      -1.098   0.688  -0.620  1.00  0.00
ATOM      7  C31 CORTC  1      -2.015  -0.396  -0.015  1.00  0.00
ATOM      8  C32 CORTC  1      -3.481  -0.348  -0.549  1.00  0.00
ATOM      9  C33 CORTC  1      -1.345  -1.804  -0.010  1.00  0.00
ATOM     10  C34 CORTC  1       0.095  -1.803   0.562  1.00  0.00
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ATOM     12  C36 CORTC  1       0.223   0.626   0.150  1.00  0.00
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ATOM     14  C38 CORTC  1       2.589   1.090   0.347  1.00  0.00
ATOM     15  C39 CORTC  1       2.249  -0.345   0.791  1.00  0.00
ATOM     16  C40 CORTC  1       1.281  -0.984  -1.518  1.00  0.00
ATOM     17  C41 CORTC  1      -3.619  -0.828  -2.006  1.00  0.00
ATOM     18  C42 CORTC  1       3.489  -1.254   0.722  1.00  0.00
ATOM     19  C43 CORTC  1       3.976  -1.849  -0.588  1.00  0.00
ATOM     20  O6  CORTC  1      -7.096   0.859   1.135  1.00  0.00
ATOM     21  O7  CORTC  1      -1.342  -2.343  -1.318  1.00  0.00
ATOM     22  O8  CORTC  1       1.923  -0.291   2.164  1.00  0.00
ATOM     23  O9  CORTC  1       4.130  -1.424   1.716  1.00  0.00
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ATOM     26  C2  CORTC  1      -5.853  -0.959   0.270  1.00  0.00
ATOM     27  H1  CORTC  1      -5.413   2.513   0.111  1.00  0.00
ATOM     28 2H   CORTC  1      -3.538   3.095  -1.080  1.00  0.00
ATOM     29 3H   CORTC  1      -3.020   1.915  -2.245  1.00  0.00
ATOM     30 4H   CORTC  1      -1.800   2.387   0.522  1.00  0.00
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ATOM     36 0H1  CORTC  1       0.039  -1.632   1.634  1.00  0.00
ATOM     37  H11 CORTC  1      -0.041   0.700   1.208  1.00  0.00
ATOM     38 2H1  CORTC  1       1.001   2.576   0.593  1.00  0.00
ATOM     39 3H1  CORTC  1       1.263   2.094  -1.070  1.00  0.00
ATOM     40 4H1  CORTC  1       3.089   1.642   1.136  1.00  0.00
ATOM     41 5H1  CORTC  1       3.255   1.090  -0.518  1.00  0.00
ATOM     42 6H1  CORTC  1       1.927  -0.232  -1.968  1.00  0.00
ATOM     43 7H1  CORTC  1       0.373  -1.012  -2.114  1.00  0.00
ATOM     44 8H1  CORTC  1       1.701  -1.973  -1.671  1.00  0.00
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ATOM     47 1H2  CORTC  1      -4.607  -0.626  -2.414  1.00  0.00
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ATOM   59  C   ALA A 523  -25.170   5.680 -21.569  1.00  0.00
ATOM   60  O   ALA A 523  -25.779   6.716 -21.305  1.00  0.00
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ATOM   63 2HT  ALA A 523  -25.684   3.224 -23.685  1.00  0.00
ATOM   64  HA  ALA A 523  -26.802   4.813 -22.608  1.00  0.00
ATOM   65 1HB  ALA A 523  -25.353   3.249 -20.396  1.00  0.00
ATOM   66 2HB  ALA A 523  -26.799   2.709 -21.249  1.00  0.00
ATOM   67 3HB  ALA A 523  -26.860   4.142 -20.192  1.00  0.00
ATOM   68  N   THR A 524  -23.837   5.574 -21.425  1.00  0.00
ATOM   69  CA  THR A 524  -23.081   6.641 -20.839  1.00  0.00
ATOM   70  C   THR A 524  -23.327   7.904 -21.606  1.00  0.00
ATOM   71  O   THR A 524  -23.479   8.972 -21.015  1.00  0.00
ATOM   72  CB  THR A 524  -21.605   6.372 -20.834  1.00  0.00
ATOM   73  OG1 THR A 524  -20.927   7.391 -20.114  1.00  0.00
ATOM   74  CG2 THR A 524  -21.100   6.307 -22.283  1.00  0.00
ATOM   75  HN  THR A 524  -23.370   4.744 -21.729  1.00  0.00
ATOM   76  HA  THR A 524  -23.444   6.758 -19.818  1.00  0.00
ATOM   77  HB  THR A 524  -21.396   5.417 -20.352  1.00  0.00
ATOM   78  HG1 THR A 524  -20.005   7.175 -20.141  1.00  0.00
ATOM   79 1HG2 THR A 524  -20.958   7.310 -22.687  1.00  0.00
ATOM   80 2HG2 THR A 524  -21.825   5.791 -22.912  1.00  0.00
ATOM   81 3HG2 THR A 524  -20.142   5.788 -22.325  1.00  0.00
ATOM   82  N   LEU A 525  -23.397   7.817 -22.944  1.00  0.00
ATOM   83  CA  LEU A 525  -23.570   8.996 -23.745  1.00  0.00
ATOM   84  C   LEU A 525  -24.870   9.732 -23.529  1.00  0.00
ATOM   85  O   LEU A 525  -24.865  10.960 -23.499  1.00  0.00
ATOM   86  CB  LEU A 525  -23.420   8.705 -25.245  1.00  0.00
ATOM   87  CG  LEU A 525  -21.995   8.237 -25.583  1.00  0.00
ATOM   88  CD1 LEU A 525  -21.773   8.118 -27.099  1.00  0.00
ATOM   89  CD2 LEU A 525  -20.953   9.122 -24.879  1.00  0.00
ATOM   90  HN  LEU A 525  -23.329   6.923 -23.385  1.00  0.00
ATOM   91  HA  LEU A 525  -22.812   9.710 -23.422  1.00  0.00
ATOM   92 1HB  LEU A 525  -23.647   9.608 -25.812  1.00  0.00
ATOM   93 2HB  LEU A 525  -24.132   7.932 -25.535  1.00  0.00
ATOM   94  HG  LEU A 525  -21.818   7.266 -25.119  1.00  0.00
ATOM   95 1HD1 LEU A 525  -21.928   9.081 -27.587  1.00  0.00
ATOM   96 2HD1 LEU A 525  -22.478   7.406 -27.528  1.00  0.00
ATOM   97 3HD1 LEU A 525  -20.753   7.795 -27.307  1.00  0.00
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ATOM   98 1HD2 LEU A 525   -21.080  9.079 -23.798  1.00  0.00
ATOM   99 2HD2 LEU A 525   -21.069 10.159 -25.192  1.00  0.00
ATOM  100 3HD2 LEU A 525   -19.946  8.778 -25.115  1.00  0.00
ATOM  101  N  PRO A 526   -25.994  9.073 -23.434  1.00  0.00
ATOM  102  CA PRO A 526   -27.215  9.811 -23.205  1.00  0.00
ATOM  103  C  PRO A 526   -27.475 10.277 -21.807  1.00  0.00
ATOM  104  O  PRO A 526   -28.343 11.129 -21.629  1.00  0.00
ATOM  105  CB PRO A 526   -28.359  8.964 -23.770  1.00  0.00
ATOM  106  CG PRO A 526   -27.711  7.626 -24.150  1.00  0.00
ATOM  107  CD PRO A 526   -26.240  7.996 -24.368  1.00  0.00
ATOM  108 1HD PRO A 526   -25.584  7.152 -24.155  1.00  0.00
ATOM  109 2HD PRO A 526   -26.063  8.330 -25.390  1.00  0.00
ATOM  110  HA PRO A 526   -27.163 10.776 -23.710  1.00  0.00
ATOM  111 1HB PRO A 526   -28.804  9.443 -24.642  1.00  0.00
ATOM  112 2HB PRO A 526   -29.142  8.821 -23.024  1.00  0.00
ATOM  113 1HG PRO A 526   -27.821  6.892 -23.352  1.00  0.00
ATOM  114 2HG PRO A 526   -28.155  7.214 -25.056  1.00  0.00
ATOM  115  N  GLN A 527   -26.761  9.739 -20.807  1.00  0.00
ATOM  116  CA GLN A 527   -26.993 10.096 -19.439  1.00  0.00
ATOM  117  C  GLN A 527   -26.834 11.582 -19.328  1.00  0.00
ATOM  118  O  GLN A 527   -26.010 12.175 -20.021  1.00  0.00
ATOM  119  CB GLN A 527   -25.919  9.467 -18.537  1.00  0.00
ATOM  120  CG GLN A 527   -26.244  9.400 -17.051  1.00  0.00
ATOM  121  CD GLN A 527   -26.605  7.951 -16.765  1.00  0.00
ATOM  122  OE1 GLN A 527   -27.358  7.323 -17.507  1.00  0.00
ATOM  123  NE2 GLN A 527   -26.039  7.397 -15.658  1.00  0.00
ATOM  124  HN GLN A 527   -26.049  9.072 -21.023  1.00  0.00
ATOM  125  HA GLN A 527   -27.984  9.731 -19.171  1.00  0.00
ATOM  126 1HB GLN A 527   -25.002 10.042 -18.655  1.00  0.00
ATOM  127 2HB GLN A 527   -25.737  8.453 -18.888  1.00  0.00
ATOM  128 1HG GLN A 527   -27.087 10.046 -16.805  1.00  0.00
ATOM  129 2HG GLN A 527   -25.384  9.692 -16.449  1.00  0.00
ATOM  130 1HE2 GLN A 527   -25.549  7.978 -15.009  1.00  0.00
ATOM  131 2HE2 GLN A 527   -26.104  6.416 -15.480  1.00  0.00
ATOM  132  N  LEU A 528   -27.646 12.238 -18.474  1.00  0.00
ATOM  133  CA LEU A 528   -27.439 13.647 -18.292  1.00  0.00
ATOM  134  C  LEU A 528   -26.548 13.763 -17.108  1.00  0.00
ATOM  135  O  LEU A 528   -26.401 12.807 -16.350  1.00  0.00
ATOM  136  CB LEU A 528   -28.701 14.500 -18.039  1.00  0.00
ATOM  137  CG LEU A 528   -29.630 14.017 -16.911  1.00  0.00
ATOM  138  CD1 LEU A 528   -30.808 14.986 -16.720  1.00  0.00
ATOM  139  CD2 LEU A 528   -30.129 12.591 -17.179  1.00  0.00
ATOM  140  HN LEU A 528   -28.370 11.756 -17.981  1.00  0.00
ATOM  141  HA LEU A 528   -26.948 13.992 -19.201  1.00  0.00
ATOM  142 1HB LEU A 528   -29.278 14.529 -18.962  1.00  0.00
ATOM  143 2HB LEU A 528   -28.381 15.512 -17.802  1.00  0.00
ATOM  144  HG LEU A 528   -29.065 13.946 -15.982  1.00  0.00
ATOM  145 1HD1 LEU A 528   -31.397 15.063 -17.634  1.00  0.00
ATOM  146 2HD1 LEU A 528   -30.440 15.981 -16.471  1.00  0.00
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ATOM  147 3HD1 LEU A 528   -31.464  14.629 -15.926  1.00  0.00
ATOM  148 1HD2 LEU A 528   -29.370  11.859 -16.903  1.00  0.00
ATOM  149 2HD2 LEU A 528   -30.352  12.463 -18.238  1.00  0.00
ATOM  150 3HD2 LEU A 528   -31.023  12.388 -16.590  1.00  0.00
ATOM  151  N   THR A 529   -25.953  14.955 -16.901  1.00  0.00
ATOM  152  CA  THR A 529   -25.011  15.088 -15.833  1.00  0.00
ATOM  153  C   THR A 529   -25.630  14.696 -14.530  1.00  0.00
ATOM  154  O   THR A 529   -24.911  14.143 -13.703  1.00  0.00
ATOM  155  CB  THR A 529   -24.318  16.430 -15.759  1.00  0.00
ATOM  156  OG1 THR A 529   -23.408  16.443 -14.668  1.00  0.00
ATOM  157  CG2 THR A 529   -25.318  17.588 -15.674  1.00  0.00
ATOM  158  HN  THR A 529   -26.168  15.736 -17.487  1.00  0.00
ATOM  159  HA  THR A 529   -24.272  14.301 -15.982  1.00  0.00
ATOM  160  HB  THR A 529   -23.757  16.618 -16.675  1.00  0.00
ATOM  161  HG1 THR A 529   -23.922  16.603 -13.887  1.00  0.00
ATOM  162 1HG2 THR A 529   -25.690  17.702 -14.656  1.00  0.00
ATOM  163 2HG2 THR A 529   -26.171  17.398 -16.325  1.00  0.00
ATOM  164 3HG2 THR A 529   -24.837  18.523 -15.963  1.00  0.00
ATOM  165  N   PRO A 530   -26.897  14.913 -14.259  1.00  0.00
ATOM  166  CA  PRO A 530   -27.417  14.458 -13.003  1.00  0.00
ATOM  167  C   PRO A 530   -27.432  12.964 -12.906  1.00  0.00
ATOM  168  O   PRO A 530   -27.159  12.442 -11.828  1.00  0.00
ATOM  169  CB  PRO A 530   -28.805  15.078 -12.859  1.00  0.00
ATOM  170  CG  PRO A 530   -28.734  16.338 -13.737  1.00  0.00
ATOM  171  CD  PRO A 530   -27.709  15.980 -14.825  1.00  0.00
ATOM  172 1HD  PRO A 530   -28.205  15.633 -15.732  1.00  0.00
ATOM  173 2HD  PRO A 530   -27.083  16.837 -15.072  1.00  0.00
ATOM  174  HA  PRO A 530   -26.763  14.779 -12.192  1.00  0.00
ATOM  175 1HB  PRO A 530   -29.018  15.333 -11.820  1.00  0.00
ATOM  176 2HB  PRO A 530   -29.580  14.397 -13.208  1.00  0.00
ATOM  177 1HG  PRO A 530   -29.706  16.569 -14.173  1.00  0.00
ATOM  178 2HG  PRO A 530   -28.407  17.203 -13.159  1.00  0.00
ATOM  179  N   THR A 531   -27.761  12.252 -14.004  1.00  0.00
ATOM  180  CA  THR A 531   -27.830  10.823 -13.907  1.00  0.00
ATOM  181  C   THR A 531   -26.461  10.248 -13.760  1.00  0.00
ATOM  182  O   THR A 531   -26.269   9.282 -13.024  1.00  0.00
ATOM  183  CB  THR A 531   -28.499  10.141 -15.059  1.00  0.00
ATOM  184  OG1 THR A 531   -29.816  10.643 -15.223  1.00  0.00
ATOM  185  CG2 THR A 531   -28.587   8.645 -14.709  1.00  0.00
ATOM  186  HN  THR A 531   -27.953  12.714 -14.870  1.00  0.00
ATOM  187  HA  THR A 531   -28.377  10.609 -12.989  1.00  0.00
ATOM  188  HB  THR A 531   -27.947  10.324 -15.981  1.00  0.00
ATOM  189  HG1 THR A 531   -30.229  10.607 -14.371  1.00  0.00
ATOM  190 1HG2 THR A 531   -29.305   8.479 -13.906  1.00  0.00
ATOM  191 2HG2 THR A 531   -27.616   8.280 -14.373  1.00  0.00
ATOM  192 3HG2 THR A 531   -28.913   8.073 -15.577  1.00  0.00
ATOM  193  N   LEU A 532   -25.463  10.834 -14.449  1.00  0.00
ATOM  194  CA  LEU A 532   -24.140  10.293 -14.341  1.00  0.00
ATOM  195  C   LEU A 532   -23.728  10.336 -12.904  1.00  0.00
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ATOM  196 O   LEU A 532   -23.216  9.356 -12.375 1.00 0.00
ATOM  197 CB  LEU A 532   -23.037 11.072 -15.092 1.00 0.00
ATOM  198 CG  LEU A 532   -22.979 10.907 -16.625 1.00 0.00
ATOM  199 CD1 LEU A 532   -24.194 11.521 -17.322 1.00 0.00
ATOM  200 CD2 LEU A 532   -21.656 11.457 -17.184 1.00 0.00
ATOM  201 HN  LEU A 532   -25.643 11.632 -15.025 1.00 0.00
ATOM  202 HA  LEU A 532   -24.200  9.278 -14.735 1.00 0.00
ATOM  203 1HB LEU A 532   -22.076 10.760 -14.688 1.00 0.00
ATOM  204 2HB LEU A 532   -23.173 12.130 -14.877 1.00 0.00
ATOM  205 HG  LEU A 532   -22.929  9.846 -16.866 1.00 0.00
ATOM  206 1HD1 LEU A 532   -24.165 12.609 -17.261 1.00 0.00
ATOM  207 2HD1 LEU A 532   -25.113 11.182 -16.844 1.00 0.00
ATOM  208 3HD1 LEU A 532   -24.204 11.243 -18.376 1.00 0.00
ATOM  209 1HD2 LEU A 532   -20.824 11.200 -16.528 1.00 0.00
ATOM  210 2HD2 LEU A 532   -21.702 12.543 -17.261 1.00 0.00
ATOM  211 3HD2 LEU A 532   -21.455 11.028 -18.166 1.00 0.00
ATOM  212 N   VAL A 533   -23.988 11.475 -12.229 1.00 0.00
ATOM  213 CA  VAL A 533   -23.557 11.670 -10.872 1.00 0.00
ATOM  214 C   VAL A 533   -24.106 10.569 -10.040 1.00 0.00
ATOM  215 O   VAL A 533   -23.395  9.938  -9.260 1.00 0.00
ATOM  216 CB  VAL A 533   -24.181 12.876 -10.230 1.00 0.00
ATOM  217 CG1 VAL A 533   -23.646 13.000  -8.794 1.00 0.00
ATOM  218 CG2 VAL A 533   -23.999 14.111 -11.119 1.00 0.00
ATOM  219 HN  VAL A 533   -24.495 12.205 -12.688 1.00 0.00
ATOM  220 HA  VAL A 533   -22.473 11.779 -10.901 1.00 0.00
ATOM  221 HB  VAL A 533   -25.266 12.772 -10.216 1.00 0.00
ATOM  222 1HG1 VAL A 533   -22.558 12.936  -8.781 1.00 0.00
ATOM  223 2HG1 VAL A 533   -24.039 12.193  -8.175 1.00 0.00
ATOM  224 3HG1 VAL A 533   -23.932 13.961  -8.368 1.00 0.00
ATOM  225 1HG2 VAL A 533   -24.952 14.421 -11.548 1.00 0.00
ATOM  226 2HG2 VAL A 533   -23.317 13.886 -11.940 1.00 0.00
ATOM  227 3HG2 VAL A 533   -23.606 14.942 -10.533 1.00 0.00
ATOM  228 N   SER A 534   -25.416 10.334 -10.198 1.00 0.00
ATOM  229 CA  SER A 534   -26.127  9.359  -9.430 1.00 0.00
ATOM  230 C   SER A 534   -25.601  8.002  -9.723 1.00 0.00
ATOM  231 O   SER A 534   -25.351  7.212  -8.813 1.00 0.00
ATOM  232 CB  SER A 534   -27.617  9.334  -9.788 1.00 0.00
ATOM  233 OG  SER A 534   -28.224  8.203  -9.192 1.00 0.00
ATOM  234 HN  SER A 534   -25.918 10.863 -10.882 1.00 0.00
ATOM  235 HA  SER A 534   -25.993  9.621  -8.381 1.00 0.00
ATOM  236 1HB SER A 534   -27.748  9.267 -10.868 1.00 0.00
ATOM  237 2HB SER A 534   -28.113 10.229  -9.415 1.00 0.00
ATOM  238 HG  SER A 534   -27.556  7.532  -9.137 1.00 0.00
ATOM  239 N   LEU A 535   -25.397  7.716 -11.018 1.00 0.00
ATOM  240 CA  LEU A 535   -24.957  6.413 -11.399 1.00 0.00
ATOM  241 C   LEU A 535   -23.671  6.165 -10.706 1.00 0.00
ATOM  242 O   LEU A 535   -23.473  5.109 -10.102 1.00 0.00
ATOM  243 CB  LEU A 535   -24.674  6.303 -12.907 1.00 0.00
ATOM  244 CG  LEU A 535   -24.196  4.904 -13.334 1.00 0.00
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ATOM 245 CD1 LEU A 535 -25.299 3.852 -13.143 1.00 0.00
ATOM 246 CD2 LEU A 535 -23.613 4.922 -14.757 1.00 0.00
ATOM 247 HN LEU A 535 -25.552 8.416 -11.715 1.00 0.00
ATOM 248 HA LEU A 535 -25.748 5.719 -11.114 1.00 0.00
ATOM 249 1HB LEU A 535 -23.909 7.031 -13.174 1.00 0.00
ATOM 250 2HB LEU A 535 -25.584 6.545 -13.454 1.00 0.00
ATOM 251 HG LEU A 535 -23.326 4.625 -12.741 1.00 0.00
ATOM 252 1HD1 LEU A 535 -26.177 4.101 -13.739 1.00 0.00
ATOM 253 2HD1 LEU A 535 -25.602 3.810 -12.097 1.00 0.00
ATOM 254 3HD1 LEU A 535 -24.943 2.872 -13.461 1.00 0.00
ATOM 255 1HD2 LEU A 535 -23.017 5.821 -14.917 1.00 0.00
ATOM 256 2HD2 LEU A 535 -24.416 4.915 -15.493 1.00 0.00
ATOM 257 3HD2 LEU A 535 -22.967 4.058 -14.910 1.00 0.00
ATOM 258 N LEU A 536 -22.765 7.147 -10.741 1.00 0.00
ATOM 259 CA LEU A 536 -21.475 6.943 -10.168 1.00 0.00
ATOM 260 C LEU A 536 -21.618 6.859 -8.676 1.00 0.00
ATOM 261 O LEU A 536 -20.951 6.066 -8.012 1.00 0.00
ATOM 262 CB LEU A 536 -20.499 8.054 -10.577 1.00 0.00
ATOM 263 CG LEU A 536 -19.042 7.574 -10.561 1.00 0.00
ATOM 264 CD1 LEU A 536 -18.532 7.270 -9.152 1.00 0.00
ATOM 265 CD2 LEU A 536 -18.892 6.367 -11.503 1.00 0.00
ATOM 266 HN LEU A 536 -22.991 8.022 -11.168 1.00 0.00
ATOM 267 HA LEU A 536 -21.118 5.975 -10.521 1.00 0.00
ATOM 268 1HB LEU A 536 -20.606 8.893 -9.889 1.00 0.00
ATOM 269 2HB LEU A 536 -20.751 8.399 -11.579 1.00 0.00
ATOM 270 HG LEU A 536 -18.412 8.343 -11.006 1.00 0.00
ATOM 271 1HD1 LEU A 536 -18.391 6.197 -9.016 1.00 0.00
ATOM 272 2HD1 LEU A 536 -19.253 7.612 -8.409 1.00 0.00
ATOM 273 3HD1 LEU A 536 -17.573 7.760 -8.985 1.00 0.00
ATOM 274 1HD2 LEU A 536 -19.327 6.584 -12.479 1.00 0.00
ATOM 275 2HD2 LEU A 536 -19.408 5.501 -11.089 1.00 0.00
ATOM 276 3HD2 LEU A 536 -17.838 6.132 -11.648 1.00 0.00
ATOM 277 N GLU A 537 -22.536 7.666 -8.113 1.00 0.00
ATOM 278 CA GLU A 537 -22.768 7.706 -6.696 1.00 0.00
ATOM 279 C GLU A 537 -23.166 6.342 -6.225 1.00 0.00
ATOM 280 O GLU A 537 -22.698 5.872 -5.189 1.00 0.00
ATOM 281 CB GLU A 537 -23.943 8.637 -6.345 1.00 0.00
ATOM 282 CG GLU A 537 -24.259 8.742 -4.852 1.00 0.00
ATOM 283 CD GLU A 537 -23.474 9.909 -4.274 1.00 0.00
ATOM 284 OE1 GLU A 537 -23.662 10.204 -3.064 1.00 0.00
ATOM 285 OE2 GLU A 537 -22.684 10.526 -5.036 1.00 0.00
ATOM 286 HN GLU A 537 -23.079 8.261 -8.706 1.00 0.00
ATOM 287 HA GLU A 537 -21.848 8.061 -6.233 1.00 0.00
ATOM 288 1HB GLU A 537 -24.832 8.274 -6.858 1.00 0.00
ATOM 289 2HB GLU A 537 -23.713 9.633 -6.717 1.00 0.00
ATOM 290 1HG GLU A 537 -23.970 7.826 -4.336 1.00 0.00
ATOM 291 2HG GLU A 537 -25.324 8.916 -4.699 1.00 0.00
ATOM 292 N VAL A 538 -24.056 5.672 -6.979 1.00 0.00
ATOM 293 CA VAL A 538 -24.556 4.390 -6.568 1.00 0.00

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ATOM  294 C   VAL A 538   -23.516  3.314 -6.628 1.00 0.00
ATOM  295 O   VAL A 538   -23.511  2.405 -5.803 1.00 0.00
ATOM  296 CB  VAL A 538   -25.740  3.907 -7.362 1.00 0.00
ATOM  297 CG1 VAL A 538   -26.863  4.951 -7.249 1.00 0.00
ATOM  298 CG2 VAL A 538   -25.309  3.563 -8.796 1.00 0.00
ATOM  299 HN  VAL A 538   -24.374  6.073 -7.838 1.00 0.00
ATOM  300 HA  VAL A 538   -24.831  4.491 -5.519 1.00 0.00
ATOM  301 HB  VAL A 538   -26.082  2.947 -6.975 1.00 0.00
ATOM  302 1HG1 VAL A 538  -26.456  5.961 -7.298 1.00 0.00
ATOM  303 2HG1 VAL A 538  -27.383  4.843 -6.297 1.00 0.00
ATOM  304 3HG1 VAL A 538  -27.571  4.833 -8.069 1.00 0.00
ATOM  305 1HG2 VAL A 538  -24.340  3.064 -8.798 1.00 0.00
ATOM  306 2HG2 VAL A 538  -25.221  4.472 -9.391 1.00 0.00
ATOM  307 3HG2 VAL A 538  -26.035  2.893 -9.256 1.00 0.00
ATOM  308 N   ILE A 539   -22.595  3.403 -7.604 1.00 0.00
ATOM  309 CA  ILE A 539   -21.645  2.358 -7.858 1.00 0.00
ATOM  310 C   ILE A 539   -20.761  2.121 -6.681 1.00 0.00
ATOM  311 O   ILE A 539   -20.295  1.000 -6.483 1.00 0.00
ATOM  312 CB  ILE A 539   -20.732  2.669 -8.999 1.00 0.00
ATOM  313 CG1 ILE A 539   -21.553  3.171 -10.195 1.00 0.00
ATOM  314 CG2 ILE A 539   -19.883  1.418 -9.276 1.00 0.00
ATOM  315 CD1 ILE A 539   -22.880  2.440 -10.388 1.00 0.00
ATOM  316 HN  ILE A 539   -22.572  4.225 -8.171 1.00 0.00
ATOM  317 HA  ILE A 539   -22.221  1.458 -8.073 1.00 0.00
ATOM  318 HB  ILE A 539   -20.088  3.512 -8.747 1.00 0.00
ATOM  319 1HG2 ILE A 539  -20.519  0.571 -9.534 1.00 0.00
ATOM  320 2HG2 ILE A 539  -19.307  1.150 -8.391 1.00 0.00
ATOM  321 3HG2 ILE A 539  -19.207  1.600 -10.112 1.00 0.00
ATOM  322 1HG1 ILE A 539  -20.957  3.053 -11.099 1.00 0.00
ATOM  323 2HG1 ILE A 539  -21.757  4.231 -10.055 1.00 0.00
ATOM  324 1HD1 ILE A 539  -23.096  1.801 -9.532 1.00 0.00
ATOM  325 2HD1 ILE A 539  -22.838  1.811 -11.276 1.00 0.00
ATOM  326 3HD1 ILE A 539  -23.694  3.158 -10.486 1.00 0.00
ATOM  327 N   GLU A 540   -20.503  3.188 -5.897 1.00 0.00
ATOM  328 CA  GLU A 540   -19.615  3.196 -4.766 1.00 0.00
ATOM  329 C   GLU A 540   -19.648  1.908 -3.999 1.00 0.00
ATOM  330 O   GLU A 540   -20.702  1.356 -3.687 1.00 0.00
ATOM  331 CB  GLU A 540   -19.933  4.348 -3.798 1.00 0.00
ATOM  332 CG  GLU A 540   -18.850  4.602 -2.757 1.00 0.00
ATOM  333 CD  GLU A 540   -17.667  5.258 -3.455 1.00 0.00
ATOM  334 OE1 GLU A 540   -16.780  5.783 -2.731 1.00 0.00
ATOM  335 OE2 GLU A 540   -17.633  5.248 -4.715 1.00 0.00
ATOM  336 HN  GLU A 540   -20.968  4.044 -6.122 1.00 0.00
ATOM  337 HA  GLU A 540   -18.603  3.298 -5.158 1.00 0.00
ATOM  338 1HB  GLU A 540  -20.864  4.119 -3.282 1.00 0.00
ATOM  339 2HB  GLU A 540  -20.076  5.258 -4.378 1.00 0.00
ATOM  340 1HG  GLU A 540  -18.526  3.664 -2.305 1.00 0.00
ATOM  341 2HG  GLU A 540  -19.219  5.265 -1.975 1.00 0.00
ATOM  342 N   PRO A 541   -18.462  1.416 -3.745 1.00 0.00
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ATOM  343 CA  PRO A 541   -18.293  0.176 -3.033 1.00 0.00
ATOM  344 C   PRO A 541   -18.481  0.367 -1.567 1.00 0.00
ATOM  345 O   PRO A 541   -18.484  1.503 -1.097 1.00 0.00
ATOM  346 CB  PRO A 541   -16.882 -0.311 -3.354 1.00 0.00
ATOM  347 CG  PRO A 541   -16.552  0.357 -4.695 1.00 0.00
ATOM  348 CD  PRO A 541   -17.375  1.652 -4.680 1.00 0.00
ATOM  349 1HD PRO A 541   -16.771  2.496 -4.348 1.00 0.00
ATOM  350 2HD PRO A 541   -17.774  1.874 -5.670 1.00 0.00
ATOM  351 HA  PRO A 541   -19.038 -0.548 -3.364 1.00 0.00
ATOM  352 1HB PRO A 541   -16.851 -1.398 -3.438 1.00 0.00
ATOM  353 2HB PRO A 541   -16.177 -0.009 -2.580 1.00 0.00
ATOM  354 1HG PRO A 541   -15.486  0.569 -4.776 1.00 0.00
ATOM  355 2HG PRO A 541   -16.837 -0.280 -5.532 1.00 0.00
ATOM  356 N   GLU A 542   -18.639 -0.749 -0.833 1.00 0.00
ATOM  357 CA  GLU A 542   -18.786 -0.718  0.588 1.00 0.00
ATOM  358 C   GLU A 542   -17.432 -0.466  1.160 1.00 0.00
ATOM  359 O   GLU A 542   -16.420 -0.621  0.479 1.00 0.00
ATOM  360 CB  GLU A 542   -19.285 -2.049  1.175 1.00 0.00
ATOM  361 CG  GLU A 542   -18.347 -3.227  0.897 1.00 0.00
ATOM  362 CD  GLU A 542   -18.417 -3.551 -0.591 1.00 0.00
ATOM  363 OE1 GLU A 542   -19.469 -3.240 -1.210 1.00 0.00
ATOM  364 OE2 GLU A 542   -17.422 -4.104 -1.128 1.00 0.00
ATOM  365 HN  GLU A 542   -18.654 -1.633 -1.300 1.00 0.00
ATOM  366 HA  GLU A 542   -19.496  0.078  0.809 1.00 0.00
ATOM  367 1HB GLU A 542   -20.264 -2.273  0.751 1.00 0.00
ATOM  368 2HB GLU A 542   -19.396 -1.937  2.253 1.00 0.00
ATOM  369 1HG GLU A 542   -18.653 -4.102  1.470 1.00 0.00
ATOM  370 2HG GLU A 542   -17.321 -2.969  1.160 1.00 0.00
ATOM  371 N   VAL A 543   -17.388 -0.040  2.437 1.00 0.00
ATOM  372 CA  VAL A 543   -16.125  0.195  3.068 1.00 0.00
ATOM  373 C   VAL A 543   -15.795 -1.069  3.786 1.00 0.00
ATOM  374 O   VAL A 543   -16.621 -1.625  4.509 1.00 0.00
ATOM  375 CB  VAL A 543   -16.144  1.314  4.072 1.00 0.00
ATOM  376 CG1 VAL A 543   -16.445  2.627  3.331 1.00 0.00
ATOM  377 CG2 VAL A 543   -17.163  0.980  5.175 1.00 0.00
ATOM  378 HN  VAL A 543   -18.237  0.111  2.944 1.00 0.00
ATOM  379 HA  VAL A 543   -15.421  0.427  2.269 1.00 0.00
ATOM  380 HB  VAL A 543   -15.179  1.381  4.574 1.00 0.00
ATOM  381 1HG1 VAL A 543  -17.412  2.575  2.831 1.00 0.00
ATOM  382 2HG1 VAL A 543  -15.684  2.816  2.575 1.00 0.00
ATOM  383 3HG1 VAL A 543  -16.475  3.458  4.036 1.00 0.00
ATOM  384 1HG2 VAL A 543  -16.736  0.284  5.896 1.00 0.00
ATOM  385 2HG2 VAL A 543  -18.048  0.516  4.741 1.00 0.00
ATOM  386 3HG2 VAL A 543  -17.449  1.886  5.709 1.00 0.00
ATOM  387 N   LEU A 544   -14.569 -1.575  3.578 1.00 0.00
ATOM  388 CA  LEU A 544   -14.209 -2.815  4.187 1.00 0.00
ATOM  389 C   LEU A 544   -13.656 -2.531  5.543 1.00 0.00
ATOM  390 O   LEU A 544   -13.348 -1.387  5.870 1.00 0.00
ATOM  391 CB  LEU A 544   -13.131 -3.564  3.395 1.00 0.00
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ATOM 392 CG LEU A 544 -13.493 -3.682 1.906 1.00 0.00
ATOM 393 CD1 LEU A 544 -13.254 -2.350 1.187 1.00 0.00
ATOM 394 CD2 LEU A 544 -12.800 -4.861 1.224 1.00 0.00
ATOM 395 HN LEU A 544 -13.915 -1.086 3.001 1.00 0.00
ATOM 396 HA LEU A 544 -15.118 -3.413 4.244 1.00 0.00
ATOM 397 1HB LEU A 544 -13.010 -4.562 3.814 1.00 0.00
ATOM 398 2HB LEU A 544 -12.184 -3.035 3.493 1.00 0.00
ATOM 399 HG LEU A 544 -14.541 -3.965 1.807 1.00 0.00
ATOM 400 1HD1 LEU A 544 -12.442 -1.797 1.660 1.00 0.00
ATOM 401 2HD1 LEU A 544 -14.151 -1.732 1.230 1.00 0.00
ATOM 402 3HD1 LEU A 544 -12.980 -2.527 0.147 1.00 0.00
ATOM 403 1HD2 LEU A 544 -12.938 -5.775 1.802 1.00 0.00
ATOM 404 2HD2 LEU A 544 -11.729 -4.672 1.142 1.00 0.00
ATOM 405 3HD2 LEU A 544 -13.220 -5.022 0.232 1.00 0.00
ATOM 406 N TYR A 545 -13.553 -3.581 6.380 1.00 0.00
ATOM 407 CA TYR A 545 -12.972 -3.450 7.684 1.00 0.00
ATOM 408 C TYR A 545 -11.713 -4.251 7.646 1.00 0.00
ATOM 409 O TYR A 545 -11.640 -5.275 6.970 1.00 0.00
ATOM 410 CB TYR A 545 -13.835 -4.014 8.827 1.00 0.00
ATOM 411 CG TYR A 545 -14.981 -3.088 9.051 1.00 0.00
ATOM 412 CD1 TYR A 545 -14.854 -2.036 9.929 1.00 0.00
ATOM 413 CD2 TYR A 545 -16.172 -3.259 8.384 1.00 0.00
ATOM 414 CE1 TYR A 545 -15.902 -1.174 10.148 1.00 0.00
ATOM 415 CE2 TYR A 545 -17.220 -2.390 8.588 1.00 0.00
ATOM 416 CZ TYR A 545 -17.085 -1.346 9.471 1.00 0.00
ATOM 417 OH TYR A 545 -18.154 -0.448 9.677 1.00 0.00
ATOM 418 HN TYR A 545 -13.890 -4.474 6.084 1.00 0.00
ATOM 419 HA TYR A 545 -12.808 -2.384 7.838 1.00 0.00
ATOM 420 1HB TYR A 545 -13.248 -4.092 9.742 1.00 0.00
ATOM 421 2HB TYR A 545 -14.213 -5.002 8.566 1.00 0.00
ATOM 422 HD1 TYR A 545 -13.921 -1.887 10.453 1.00 0.00
ATOM 423 HE1 TYR A 545 -15.795 -0.361 10.851 1.00 0.00
ATOM 424 HD2 TYR A 545 -16.286 -4.081 7.693 1.00 0.00
ATOM 425 HE2 TYR A 545 -18.149 -2.530 8.055 1.00 0.00
ATOM 426 HH TYR A 545 -17.937 0.394 9.299 1.00 0.00
ATOM 427 N ALA A 546 -10.676 -3.791 8.370 1.00 0.00
ATOM 428 CA ALA A 546 -9.426 -4.489 8.363 1.00 0.00
ATOM 429 C ALA A 546 -9.603 -5.756 9.130 1.00 0.00
ATOM 430 O ALA A 546 -10.566 -5.900 9.884 1.00 0.00
ATOM 431 CB ALA A 546 -8.282 -3.699 9.022 1.00 0.00
ATOM 432 HN ALA A 546 -10.780 -2.958 8.915 1.00 0.00
ATOM 433 HA ALA A 546 -9.188 -4.688 7.318 1.00 0.00
ATOM 434 1HB ALA A 546 -8.514 -3.481 10.064 1.00 0.00
ATOM 435 2HB ALA A 546 -8.131 -2.752 8.505 1.00 0.00
ATOM 436 3HB ALA A 546 -7.360 -4.281 8.998 1.00 0.00
ATOM 437 N GLY A 547 -8.672 -6.714 8.923 1.00 0.00
ATOM 438 CA GLY A 547 -8.686 -7.983 9.595 1.00 0.00
ATOM 439 C GLY A 547 -8.822 -7.661 11.039 1.00 0.00
ATOM 440 O GLY A 547 -8.298 -6.649 11.499 1.00 0.00

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ATOM   441 HN  GLY A 547     -7.938  -6.529   8.269  1.00  0.00
ATOM   442 1HA GLY A 547     -7.748  -8.499   9.398  1.00  0.00
ATOM   443 2HA GLY A 547     -9.540  -8.560   9.243  1.00  0.00
ATOM   444 N   TYR A 548     -9.453  -8.584  11.790  1.00  0.00
ATOM   445 CA  TYR A 548     -9.937  -8.318  13.111  1.00  0.00
ATOM   446 C   TYR A 548     -8.940  -7.624  13.981  1.00  0.00
ATOM   447 O   TYR A 548     -9.107  -6.440  14.269  1.00  0.00
ATOM   448 CB  TYR A 548    -10.356  -9.629  13.804  1.00  0.00
ATOM   449 CG  TYR A 548    -11.182  -9.322  15.003  1.00  0.00
ATOM   450 CD1 TYR A 548    -12.506  -8.985  14.848  1.00  0.00
ATOM   451 CD2 TYR A 548    -10.694  -9.538  16.272  1.00  0.00
ATOM   452 CE1 TYR A 548    -13.324  -8.828  15.942  1.00  0.00
ATOM   453 CE2 TYR A 548    -11.507  -9.384  17.370  1.00  0.00
ATOM   454 CZ  TYR A 548    -12.825  -9.031  17.205  1.00  0.00
ATOM   455 OH  TYR A 548    -13.666  -8.889  18.330  1.00  0.00
ATOM   456 HN  TYR A 548     -9.589  -9.497  11.406  1.00  0.00
ATOM   457 HA  TYR A 548    -10.789  -7.645  13.015  1.00  0.00
ATOM   458 1HB TYR A 548     -9.472 -10.187  14.114  1.00  0.00
ATOM   459 2HB TYR A 548    -10.938 -10.245  13.118  1.00  0.00
ATOM   460 HD1 TYR A 548    -12.908  -8.841  13.856  1.00  0.00
ATOM   461 HE1 TYR A 548    -14.358  -8.545  15.808  1.00  0.00
ATOM   462 HD2 TYR A 548     -9.663  -9.831  16.406  1.00  0.00
ATOM   463 HE2 TYR A 548    -11.110  -9.540  18.362  1.00  0.00
ATOM   464 HH  TYR A 548    -13.522  -8.040  18.727  1.00  0.00
ATOM   465 N   ASP A 549     -7.850  -8.294  14.395  1.00  0.00
ATOM   466 CA  ASP A 549     -6.948  -7.558  15.232  1.00  0.00
ATOM   467 C   ASP A 549     -5.683  -8.324  15.365  1.00  0.00
ATOM   468 O   ASP A 549     -5.629  -9.359  16.027  1.00  0.00
ATOM   469 CB  ASP A 549     -7.494  -7.335  16.654  1.00  0.00
ATOM   470 CG  ASP A 549     -6.584  -6.355  17.379  1.00  0.00
ATOM   471 OD1 ASP A 549     -5.576  -5.914  16.766  1.00  0.00
ATOM   472 OD2 ASP A 549     -6.885  -6.035  18.561  1.00  0.00
ATOM   473 HN  ASP A 549     -7.680  -9.244  14.136  1.00  0.00
ATOM   474 HA  ASP A 549     -6.780  -6.599  14.742  1.00  0.00
ATOM   475 1HB ASP A 549     -7.515  -8.276  17.204  1.00  0.00
ATOM   476 2HB ASP A 549     -8.502  -6.924  16.613  1.00  0.00
ATOM   477 N   SER A 550     -4.609  -7.821  14.744  1.00  0.00
ATOM   478 CA  SER A 550     -3.373  -8.521  14.881  1.00  0.00
ATOM   479 C   SER A 550     -2.645  -7.794  15.955  1.00  0.00
ATOM   480 O   SER A 550     -3.151  -6.823  16.517  1.00  0.00
ATOM   481 CB  SER A 550     -2.526  -8.504  13.598  1.00  0.00
ATOM   482 OG  SER A 550     -1.473  -9.449  13.698  1.00  0.00
ATOM   483 HN  SER A 550     -4.671  -6.983  14.202  1.00  0.00
ATOM   484 HA  SER A 550     -3.625  -9.547  15.149  1.00  0.00
ATOM   485 1HB SER A 550     -2.088  -7.518  13.447  1.00  0.00
ATOM   486 2HB SER A 550     -3.140  -8.766  12.736  1.00  0.00
ATOM   487 HG  SER A 550     -0.895  -9.291  12.962  1.00  0.00
ATOM   488 N   SER A 551     -1.439  -8.267  16.297  1.00  0.00
ATOM   489 CA  SER A 551     -0.702  -7.585  17.309  1.00  0.00
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ATOM   490  C   SER A 551     -0.469  -6.217  16.768  1.00  0.00
ATOM   491  O   SER A 551      0.342  -6.026  15.864  1.00  0.00
ATOM   492  CB  SER A 551      0.641  -8.274  17.608  1.00  0.00
ATOM   493  OG  SER A 551      1.360  -7.589  18.614  1.00  0.00
ATOM   494  HN  SER A 551     -1.064  -9.080  15.851  1.00  0.00
ATOM   495  HA  SER A 551     -1.328  -7.572  18.202  1.00  0.00
ATOM   496 1HB  SER A 551      1.258  -8.293  16.710  1.00  0.00
ATOM   497 2HB  SER A 551      0.469  -9.293  17.954  1.00  0.00
ATOM   498  HG  SER A 551      2.271  -7.596  18.352  1.00  0.00
ATOM   499  N   VAL A 552     -1.170  -5.219  17.339  1.00  0.00
ATOM   500  CA  VAL A 552     -1.031  -3.881  16.855  1.00  0.00
ATOM   501  C   VAL A 552      0.410  -3.529  16.975  1.00  0.00
ATOM   502  O   VAL A 552      0.852  -2.649  16.236  1.00  0.00
ATOM   503  CB  VAL A 552     -1.932  -2.839  17.492  1.00  0.00
ATOM   504  CG1 VAL A 552     -1.754  -2.760  19.016  1.00  0.00
ATOM   505  CG2 VAL A 552     -1.651  -1.508  16.776  1.00  0.00
ATOM   506  HN  VAL A 552     -1.786  -5.414  18.102  1.00  0.00
ATOM   507  HA  VAL A 552     -1.238  -3.931  15.787  1.00  0.00
ATOM   508  HB  VAL A 552     -2.970  -3.084  17.269  1.00  0.00
ATOM   509 1HG1 VAL A 552     -0.784  -2.330  19.269  1.00  0.00
ATOM   510 2HG1 VAL A 552     -1.805  -3.757  19.454  1.00  0.00
ATOM   511 3HG1 VAL A 552     -2.526  -2.127  19.453  1.00  0.00
ATOM   512 1HG2 VAL A 552     -1.522  -1.666  15.705  1.00  0.00
ATOM   513 2HG2 VAL A 552     -0.738  -1.057  17.163  1.00  0.00
ATOM   514 3HG2 VAL A 552     -2.487  -0.821  16.916  1.00  0.00
ATOM   515  N   PRO A 553      1.160  -4.153  17.874  1.00  0.00
ATOM   516  CA  PRO A 553      2.572  -3.997  17.780  1.00  0.00
ATOM   517  C   PRO A 553      2.839  -4.634  16.475  1.00  0.00
ATOM   518  O   PRO A 553      2.831  -5.855  16.329  1.00  0.00
ATOM   519  CB  PRO A 553      3.197  -4.627  19.024  1.00  0.00
ATOM   520  CG  PRO A 553      1.990  -5.107  19.854  1.00  0.00
ATOM   521  CD  PRO A 553      0.789  -4.348  19.267  1.00  0.00
ATOM   522 1HD  PRO A 553     -0.128  -4.931  19.343  1.00  0.00
ATOM   523 2HD  PRO A 553      0.641  -3.389  19.764  1.00  0.00
ATOM   524  HA  PRO A 553      2.820  -2.936  17.724  1.00  0.00
ATOM   525 1HB  PRO A 553      3.789  -3.899  19.578  1.00  0.00
ATOM   526 2HB  PRO A 553      3.846  -5.461  18.758  1.00  0.00
ATOM   527 1HG  PRO A 553      1.855  -6.185  19.760  1.00  0.00
ATOM   528 2HG  PRO A 553      2.123  -4.872  20.910  1.00  0.00
ATOM   529  N   ASP A 554      3.070  -3.759  15.508  1.00  0.00
ATOM   530  CA  ASP A 554      3.109  -4.093  14.145  1.00  0.00
ATOM   531  C   ASP A 554      4.536  -4.346  13.841  1.00  0.00
ATOM   532  O   ASP A 554      5.427  -3.941  14.583  1.00  0.00
ATOM   533  CB  ASP A 554      2.635  -2.882  13.334  1.00  0.00
ATOM   534  CG  ASP A 554      1.951  -3.364  12.080  1.00  0.00
ATOM   535  OD1 ASP A 554      1.372  -2.506  11.363  1.00  0.00
ATOM   536  OD2 ASP A 554      1.967  -4.600  11.845  1.00  0.00
ATOM   537  HN  ASP A 554      3.225  -2.805  15.764  1.00  0.00
ATOM   538  HA  ASP A 554      2.451  -4.948  13.993  1.00  0.00
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ATOM   539 1HB  ASP A 554      3.485  -2.257  13.058  1.00  0.00
ATOM   540 2HB  ASP A 554      1.931  -2.288  13.917  1.00  0.00
ATOM   541  N   SER A 555      4.776  -5.073  12.743  1.00  0.00
ATOM   542  CA  SER A 555      6.104  -5.349  12.312  1.00  0.00
ATOM   543  C   SER A 555      6.030  -5.073  10.856  1.00  0.00
ATOM   544  O   SER A 555      4.938  -4.848  10.338  1.00  0.00
ATOM   545  CB  SER A 555      6.514  -6.816  12.521  1.00  0.00
ATOM   546  OG  SER A 555      5.603  -7.675  11.852  1.00  0.00
ATOM   547  HN  SER A 555      4.005  -5.430  12.216  1.00  0.00
ATOM   548  HA  SER A 555      6.759  -4.692  12.884  1.00  0.00
ATOM   549 1HB  SER A 555      6.503  -7.065  13.582  1.00  0.00
ATOM   550 2HB  SER A 555      7.511  -6.991  12.116  1.00  0.00
ATOM   551  HG  SER A 555      5.751  -7.557  10.923  1.00  0.00
ATOM   552  N   THR A 556      7.183  -5.076  10.161  1.00  0.00
ATOM   553  CA  THR A 556      7.172  -4.781   8.758  1.00  0.00
ATOM   554  C   THR A 556      6.244  -5.759   8.124  1.00  0.00
ATOM   555  O   THR A 556      5.354  -5.390   7.362  1.00  0.00
ATOM   556  CB  THR A 556      8.511  -4.981   8.118  1.00  0.00
ATOM   557  OG1 THR A 556      9.474  -4.118   8.704  1.00  0.00
ATOM   558  CG2 THR A 556      8.382  -4.706   6.612  1.00  0.00
ATOM   559  HN  THR A 556      8.045  -5.284  10.623  1.00  0.00
ATOM   560  HA  THR A 556      6.860  -3.741   8.659  1.00  0.00
ATOM   561  HB  THR A 556      8.845  -6.009   8.258  1.00  0.00
ATOM   562  HG1 THR A 556      9.460  -3.314   8.202  1.00  0.00
ATOM   563 1HG2 THR A 556      7.884  -3.753   6.435  1.00  0.00
ATOM   564 2HG2 THR A 556      7.791  -5.488   6.135  1.00  0.00
ATOM   565 3HG2 THR A 556      9.369  -4.661   6.152  1.00  0.00
ATOM   566  N   TRP A 557      6.412  -7.044   8.467  1.00  0.00
ATOM   567  CA  TRP A 557      5.573  -8.072   7.932  1.00  0.00
ATOM   568  C   TRP A 557      4.169  -7.891   8.395  1.00  0.00
ATOM   569  O   TRP A 557      3.224  -7.991   7.617  1.00  0.00
ATOM   570  CB  TRP A 557      5.970  -9.465   8.426  1.00  0.00
ATOM   571  CG  TRP A 557      7.251  -9.979   7.837  1.00  0.00
ATOM   572  CD1 TRP A 557      7.419 -10.886   6.838  1.00  0.00
ATOM   573  CD2 TRP A 557      8.561  -9.507   8.186  1.00  0.00
ATOM   574  NE1 TRP A 557      8.755 -11.037   6.572  1.00  0.00
ATOM   575  CE2 TRP A 557      9.468 -10.184   7.380  1.00  0.00
ATOM   576  CE3 TRP A 557      8.975  -8.580   9.100  1.00  0.00
ATOM   577  CZ2 TRP A 557     10.812  -9.953   7.466  1.00  0.00
ATOM   578  CZ3 TRP A 557     10.331  -8.349   9.190  1.00  0.00
ATOM   579  CH2 TRP A 557     11.232  -9.022   8.391  1.00  0.00
ATOM   580  HN  TRP A 557      7.138  -7.288   9.111  1.00  0.00
ATOM   581  HA  TRP A 557      5.663  -8.018   6.847  1.00  0.00
ATOM   582 1HB  TRP A 557      5.178 -10.169   8.173  1.00  0.00
ATOM   583 2HB  TRP A 557      6.086  -9.437   9.509  1.00  0.00
ATOM   584  HE3 TRP A 557      8.270  -8.051   9.724  1.00  0.00
ATOM   585  HD1 TRP A 557      6.621 -11.408   6.331  1.00  0.00
ATOM   586  HE1 TRP A 557      9.139 -11.653   5.914  1.00  0.00
ATOM   587  HZ2 TRP A 557     11.514 -10.477   6.836  1.00  0.00
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ATOM  588 HZ3 TRP A 557     10.696  -7.625   9.903  1.00  0.00
ATOM  589 HH2 TRP A 557     12.287  -8.814   8.492  1.00  0.00
ATOM  590 N   ARG A 558      4.005  -7.601   9.693  1.00  0.00
ATOM  591 CA  ARG A 558      2.695  -7.561  10.258  1.00  0.00
ATOM  592 C   ARG A 558      1.909  -6.485   9.583  1.00  0.00
ATOM  593 O   ARG A 558      0.749  -6.681   9.224  1.00  0.00
ATOM  594 CB  ARG A 558      2.762  -7.263  11.763  1.00  0.00
ATOM  595 CG  ARG A 558      1.578  -7.783  12.573  1.00  0.00
ATOM  596 CD  ARG A 558      1.839  -7.698  14.077  1.00  0.00
ATOM  597 NE  ARG A 558      0.831  -8.545  14.771  1.00  0.00
ATOM  598 CZ  ARG A 558      1.075  -9.869  14.997  1.00  0.00
ATOM  599 NH1 ARG A 558      2.205 -10.454  14.502  1.00  0.00
ATOM  600 NH2 ARG A 558      0.195 -10.607  15.736  1.00  0.00
ATOM  601 HN  ARG A 558      4.803  -7.413  10.266  1.00  0.00
ATOM  602 HA  ARG A 558      2.236  -8.533  10.079  1.00  0.00
ATOM  603 1HB ARG A 558      2.822  -6.184  11.897  1.00  0.00
ATOM  604 2HB ARG A 558      3.672  -7.710  12.161  1.00  0.00
ATOM  605 1HG ARG A 558      1.386  -8.820  12.301  1.00  0.00
ATOM  606 2HG ARG A 558      0.693  -7.196  12.330  1.00  0.00
ATOM  607 1HD ARG A 558      1.725  -6.677  14.440  1.00  0.00
ATOM  608 2HD ARG A 558      2.827  -8.082  14.328  1.00  0.00
ATOM  609 HE  ARG A 558     -0.032  -8.142  15.074  1.00  0.00
ATOM  610 1HH1 ARG A 558     2.857  -9.913  13.970  1.00  0.00
ATOM  611 2HH1 ARG A 558     2.379 -11.425  14.670  1.00  0.00
ATOM  612 1HH2 ARG A 558    -0.745 -10.289  15.857  1.00  0.00
ATOM  613 2HH2 ARG A 558     0.491 -11.465  16.155  1.00  0.00
ATOM  614 N   ILE A 559      2.516  -5.305   9.292  1.00  0.00
ATOM  615 CA  ILE A 559      1.827  -4.119   8.731  1.00  0.00
ATOM  616 C   ILE A 559      1.497  -4.396   7.283  1.00  0.00
ATOM  617 O   ILE A 559      0.366  -4.265   6.822  1.00  0.00
ATOM  618 CB  ILE A 559      2.656  -2.787   8.783  1.00  0.00
ATOM  619 CG1 ILE A 559      1.967  -1.560   8.132  1.00  0.00
ATOM  620 CG2 ILE A 559      4.060  -2.914   8.240  1.00  0.00
ATOM  621 CD1 ILE A 559      0.721  -1.051   8.861  1.00  0.00
ATOM  622 HN  ILE A 559      3.453  -5.200   9.578  1.00  0.00
ATOM  623 HA  ILE A 559      0.895  -4.007   9.286  1.00  0.00
ATOM  624 HB  ILE A 559      2.893  -2.543   9.804  1.00  0.00
ATOM  625 1HG2 ILE A 559     4.120  -2.765   7.164  1.00  0.00
ATOM  626 2HG2 ILE A 559     4.412  -3.883   8.472  1.00  0.00
ATOM  627 3HG2 ILE A 559     4.748  -2.270   8.777  1.00  0.00
ATOM  628 1HG1 ILE A 559     1.714  -1.773   7.093  1.00  0.00
ATOM  629 2HG1 ILE A 559     2.672  -0.731   8.090  1.00  0.00
ATOM  630 1HD1 ILE A 559    -0.007  -1.846   9.020  1.00  0.00
ATOM  631 2HD1 ILE A 559     0.242  -0.254   8.293  1.00  0.00
ATOM  632 3HD1 ILE A 559     0.983  -0.634   9.833  1.00  0.00
ATOM  633 N   MET A 560      2.586  -4.806   6.598  1.00  0.00
ATOM  634 CA  MET A 560      2.513  -5.064   5.177  1.00  0.00
ATOM  635 C   MET A 560      1.384  -6.043   4.913  1.00  0.00
ATOM  636 O   MET A 560      0.660  -5.940   3.937  1.00  0.00
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ATOM   637  CB  MET A 560      3.840  -5.628   4.656  1.00  0.00
ATOM   638  CG  MET A 560      3.772  -5.929   3.156  1.00  0.00
ATOM   639  SD  MET A 560      3.305  -4.449   2.226  1.00  0.00
ATOM   640  CE  MET A 560      2.780  -5.201   0.678  1.00  0.00
ATOM   641  HN  MET A 560      3.463  -4.907   7.078  1.00  0.00
ATOM   642  HA  MET A 560      2.274  -4.111   4.702  1.00  0.00
ATOM   643 1HB  MET A 560      4.106  -6.536   5.201  1.00  0.00
ATOM   644 2HB  MET A 560      4.639  -4.912   4.848  1.00  0.00
ATOM   645 1HG  MET A 560      3.035  -6.709   2.967  1.00  0.00
ATOM   646 2HG  MET A 560      4.718  -6.332   2.808  1.00  0.00
ATOM   647 1HE  MET A 560      3.583  -5.175  -0.059  1.00  0.00
ATOM   648 2HE  MET A 560      1.926  -4.659   0.276  1.00  0.00
ATOM   649 3HE  MET A 560      2.462  -6.227   0.842  1.00  0.00
ATOM   650  N   THR A 561      1.254  -6.972   5.877  1.00  0.00
ATOM   651  CA  THR A 561      0.230  -7.957   5.717  1.00  0.00
ATOM   652  C   THR A 561     -1.132  -7.338   5.753  1.00  0.00
ATOM   653  O   THR A 561     -1.942  -7.591   4.863  1.00  0.00
ATOM   654  CB  THR A 561      0.253  -9.015   6.778  1.00  0.00
ATOM   655  OG1 THR A 561      1.491  -9.710   6.754  1.00  0.00
ATOM   656  CG2 THR A 561     -0.907  -9.991   6.513  1.00  0.00
ATOM   657  HN  THR A 561      1.885  -7.023   6.651  1.00  0.00
ATOM   658  HA  THR A 561      0.384  -8.408   4.737  1.00  0.00
ATOM   659  HB  THR A 561      0.134  -8.564   7.763  1.00  0.00
ATOM   660  HG1 THR A 561      2.165  -9.061   6.598  1.00  0.00
ATOM   661 1HG2 THR A 561     -1.011 -10.185   5.445  1.00  0.00
ATOM   662 2HG2 THR A 561     -1.845  -9.567   6.872  1.00  0.00
ATOM   663 3HG2 THR A 561     -0.720 -10.942   7.012  1.00  0.00
ATOM   664  N   THR A 562     -1.371  -6.504   6.773  1.00  0.00
ATOM   665  CA  THR A 562     -2.671  -5.876   6.947  1.00  0.00
ATOM   666  C   THR A 562     -3.073  -5.043   5.712  1.00  0.00
ATOM   667  O   THR A 562     -4.151  -5.207   5.157  1.00  0.00
ATOM   668  CB  THR A 562     -2.575  -5.035   8.237  1.00  0.00
ATOM   669  OG1 THR A 562     -2.067  -5.838   9.297  1.00  0.00
ATOM   670  CG2 THR A 562     -3.945  -4.514   8.686  1.00  0.00
ATOM   671  HN  THR A 562     -0.606  -6.273   7.377  1.00  0.00
ATOM   672  HA  THR A 562     -3.391  -6.686   7.073  1.00  0.00
ATOM   673  HB  THR A 562     -1.920  -4.166   8.084  1.00  0.00
ATOM   674  HG1 THR A 562     -1.128  -6.023   9.203  1.00  0.00
ATOM   675 1HG2 THR A 562     -4.389  -3.856   7.939  1.00  0.00
ATOM   676 2HG2 THR A 562     -3.856  -3.947   9.613  1.00  0.00
ATOM   677 3HG2 THR A 562     -4.638  -5.336   8.866  1.00  0.00
ATOM   678  N   LEU A 563     -2.142  -4.157   5.310  1.00  0.00
ATOM   679  CA  LEU A 563     -2.440  -3.258   4.196  1.00  0.00
ATOM   680  C   LEU A 563     -2.561  -4.047   2.878  1.00  0.00
ATOM   681  O   LEU A 563     -3.452  -3.801   2.073  1.00  0.00
ATOM   682  CB  LEU A 563     -1.381  -2.149   4.098  1.00  0.00
ATOM   683  CG  LEU A 563     -1.569  -0.984   5.091  1.00  0.00
ATOM   684  CD1 LEU A 563     -1.720  -1.439   6.549  1.00  0.00
ATOM   685  CD2 LEU A 563     -0.413   0.017   4.954  1.00  0.00
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ATOM  686 HN  LEU A 563   -1.264 -4.106  5.796 1.00 0.00
ATOM  687 HA  LEU A 563   -3.410 -2.801  4.390 1.00 0.00
ATOM  688 1HB LEU A 563   -1.439 -1.707  3.105 1.00 0.00
ATOM  689 2HB LEU A 563   -0.382 -2.579  4.191 1.00 0.00
ATOM  690 HG  LEU A 563   -2.487 -0.461  4.821 1.00 0.00
ATOM  691 1HD1 LEU A 563  -0.876 -2.055  6.857 1.00 0.00
ATOM  692 2HD1 LEU A 563  -2.635 -2.010  6.700 1.00 0.00
ATOM  693 3HD1 LEU A 563  -1.775 -0.581  7.219 1.00 0.00
ATOM  694 1HD2 LEU A 563  -0.560  0.881  5.602 1.00 0.00
ATOM  695 2HD2 LEU A 563  -0.326  0.384  3.930 1.00 0.00
ATOM  696 3HD2 LEU A 563   0.540 -0.440  5.222 1.00 0.00
ATOM  697 N   ASN A 564   -1.646 -5.027  2.717 1.00 0.00
ATOM  698 CA  ASN A 564   -1.710 -5.941  1.569 1.00 0.00
ATOM  699 C   ASN A 564   -3.102 -6.582  1.520 1.00 0.00
ATOM  700 O   ASN A 564   -3.801 -6.536  0.512 1.00 0.00
ATOM  701 CB  ASN A 564   -0.592 -7.011  1.653 1.00 0.00
ATOM  702 CG  ASN A 564   -0.641 -8.077  0.538 1.00 0.00
ATOM  703 OD1 ASN A 564   -1.700 -8.457  0.065 1.00 0.00
ATOM  704 ND2 ASN A 564    0.545 -8.582  0.169 1.00 0.00
ATOM  705 HN  ASN A 564   -0.928 -5.159  3.402 1.00 0.00
ATOM  706 HA  ASN A 564   -1.582 -5.330  0.675 1.00 0.00
ATOM  707 1HB ASN A 564   -0.651 -7.542  2.602 1.00 0.00
ATOM  708 2HB ASN A 564    0.379 -6.522  1.619 1.00 0.00
ATOM  709 1HD2 ASN A 564   0.559 -9.377 -0.441 1.00 0.00
ATOM  710 2HD2 ASN A 564   1.444 -8.223  0.435 1.00 0.00
ATOM  711 N   MET A 565   -3.472 -7.139  2.692 1.00 0.00
ATOM  712 CA  MET A 565   -4.686 -7.899  2.761 1.00 0.00
ATOM  713 C   MET A 565   -5.855 -7.025  2.425 1.00 0.00
ATOM  714 O   MET A 565   -6.733 -7.428  1.664 1.00 0.00
ATOM  715 CB  MET A 565   -4.937 -8.481  4.163 1.00 0.00
ATOM  716 CG  MET A 565   -3.928 -9.557  4.569 1.00 0.00
ATOM  717 SD  MET A 565   -4.074 -11.110  3.635 1.00 0.00
ATOM  718 CE  MET A 565   -5.609 -11.633  4.455 1.00 0.00
ATOM  719 HN  MET A 565   -2.938 -6.992  3.525 1.00 0.00
ATOM  720 HA  MET A 565   -4.595 -8.703  2.030 1.00 0.00
ATOM  721 1HB MET A 565   -5.937 -8.912  4.188 1.00 0.00
ATOM  722 2HB MET A 565   -4.895 -7.671  4.890 1.00 0.00
ATOM  723 1HG MET A 565   -4.066 -9.787  5.625 1.00 0.00
ATOM  724 2HG MET A 565   -2.921 -9.170  4.419 1.00 0.00
ATOM  725 1HE MET A 565   -6.429 -10.989  4.136 1.00 0.00
ATOM  726 2HE MET A 565   -5.500 -11.548  5.536 1.00 0.00
ATOM  727 3HE MET A 565   -5.845 -12.660  4.178 1.00 0.00
ATOM  728 N   LEU A 566   -5.845 -5.812  3.021 1.00 0.00
ATOM  729 CA  LEU A 566   -6.856 -4.788  2.773 1.00 0.00
ATOM  730 C   LEU A 566   -7.043 -4.576  1.264 1.00 0.00
ATOM  731 O   LEU A 566   -8.154 -4.613  0.750 1.00 0.00
ATOM  732 CB  LEU A 566   -6.464 -3.475  3.487 1.00 0.00
ATOM  733 CG  LEU A 566   -6.893 -3.414  4.968 1.00 0.00
ATOM  734 CD1 LEU A 566   -5.988 -2.478  5.781 1.00 0.00
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ATOM   735 CD2 LEU A 566    -8.353 -2.956  5.095 1.00 0.00
ATOM   736 HN  LEU A 566    -5.087 -5.613  3.643 1.00 0.00
ATOM   737 HA  LEU A 566    -7.791 -5.160  3.176 1.00 0.00
ATOM   738 1HB LEU A 566    -6.893 -2.613  2.973 1.00 0.00
ATOM   739 2HB LEU A 566    -5.388 -3.342  3.410 1.00 0.00
ATOM   740 HG  LEU A 566    -6.798 -4.408  5.407 1.00 0.00
ATOM   741 1HD1 LEU A 566   -4.981 -2.879  5.866 1.00 0.00
ATOM   742 2HD1 LEU A 566   -6.363 -2.343  6.796 1.00 0.00
ATOM   743 3HD1 LEU A 566   -5.914 -1.497  5.316 1.00 0.00
ATOM   744 1HD2 LEU A 566   -8.650 -2.858  6.138 1.00 0.00
ATOM   745 2HD2 LEU A 566   -9.029 -3.662  4.622 1.00 0.00
ATOM   746 3HD2 LEU A 566   -8.503 -1.982  4.627 1.00 0.00
ATOM   747 N   GLY A 567    -5.891 -4.374  0.598 1.00 0.00
ATOM   748 CA  GLY A 567    -5.899 -4.129 -0.841 1.00 0.00
ATOM   749 C   GLY A 567    -6.516 -5.286 -1.627 1.00 0.00
ATOM   750 O   GLY A 567    -7.377 -5.103 -2.480 1.00 0.00
ATOM   751 HN  GLY A 567    -5.023 -4.395  1.103 1.00 0.00
ATOM   752 1HA GLY A 567    -4.867 -3.974 -1.156 1.00 0.00
ATOM   753 2HA GLY A 567    -6.481 -3.231 -1.031 1.00 0.00
ATOM   754 N   GLY A 568    -6.043 -6.488 -1.267 1.00 0.00
ATOM   755 CA  GLY A 568    -6.495 -7.693 -1.948 1.00 0.00
ATOM   756 C   GLY A 568    -8.001 -7.959 -1.776 1.00 0.00
ATOM   757 O   GLY A 568    -8.615 -8.640 -2.582 1.00 0.00
ATOM   758 HN  GLY A 568    -5.345 -6.546 -0.547 1.00 0.00
ATOM   759 1HA GLY A 568    -5.925 -8.524 -1.533 1.00 0.00
ATOM   760 2HA GLY A 568    -6.253 -7.593 -3.007 1.00 0.00
ATOM   761 N   ARG A 569    -8.568 -7.380 -0.701 1.00 0.00
ATOM   762 CA  ARG A 569    -9.988 -7.439 -0.493 1.00 0.00
ATOM   763 C   ARG A 569   -10.710 -6.424 -1.328 1.00 0.00
ATOM   764 O   ARG A 569   -11.707 -6.727 -1.980 1.00 0.00
ATOM   765 CB  ARG A 569   -10.338 -7.144  0.977 1.00 0.00
ATOM   766 CG  ARG A 569    -9.768 -8.193  1.934 1.00 0.00
ATOM   767 CD  ARG A 569    -9.594 -7.720  3.379 1.00 0.00
ATOM   768 NE  ARG A 569   -10.941 -7.532  3.984 1.00 0.00
ATOM   769 CZ  ARG A 569   -11.478 -6.280  4.060 1.00 0.00
ATOM   770 NH1 ARG A 569   -10.793 -5.217  3.548 1.00 0.00
ATOM   771 NH2 ARG A 569   -12.689 -6.097  4.662 1.00 0.00
ATOM   772 HN  ARG A 569    -7.980 -7.066  0.045 1.00 0.00
ATOM   773 HA  ARG A 569   -10.314 -8.441 -0.770 1.00 0.00
ATOM   774 1HB ARG A 569   -11.422 -7.116  1.085 1.00 0.00
ATOM   775 2HB ARG A 569    -9.943 -6.165  1.246 1.00 0.00
ATOM   776 1HG ARG A 569    -8.796 -8.508  1.557 1.00 0.00
ATOM   777 2HG ARG A 569   -10.432 -9.055  1.932 1.00 0.00
ATOM   778 1HD ARG A 569    -9.077 -6.762  3.419 1.00 0.00
ATOM   779 2HD ARG A 569    -9.064 -8.463  3.974 1.00 0.00
ATOM   780 HE  ARG A 569   -11.450 -8.319  4.333 1.00 0.00
ATOM   781 1HH1 ARG A 569   -9.901 -5.357  3.119 1.00 0.00
ATOM   782 2HH1 ARG A 569   -11.184 -4.298  3.602 1.00 0.00
ATOM   783 1HH2 ARG A 569   -12.893 -5.232  5.122 1.00 0.00
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ATOM  784 2HH2 ARG A 569   -13.372  -6.827   4.644  1.00  0.00
ATOM  785  N   GLN A 570   -10.148  -5.202  -1.264  1.00  0.00
ATOM  786  CA  GLN A 570   -10.705  -4.047  -1.949  1.00  0.00
ATOM  787  C   GLN A 570   -10.795  -4.290  -3.471  1.00  0.00
ATOM  788  O   GLN A 570   -11.690  -3.789  -4.138  1.00  0.00
ATOM  789  CB  GLN A 570    -9.800  -2.832  -1.665  1.00  0.00
ATOM  790  CG  GLN A 570    -9.791  -2.333  -0.204  1.00  0.00
ATOM  791  CD  GLN A 570   -10.411  -0.934  -0.079  1.00  0.00
ATOM  792  OE1 GLN A 570   -11.507  -0.680  -0.549  1.00  0.00
ATOM  793  NE2 GLN A 570    -9.663  -0.034   0.566  1.00  0.00
ATOM  794  HN  GLN A 570    -9.315  -5.093  -0.714  1.00  0.00
ATOM  795  HA  GLN A 570   -11.711  -3.886  -1.560  1.00  0.00
ATOM  796 1HB  GLN A 570   -10.072  -2.022  -2.342  1.00  0.00
ATOM  797 2HB  GLN A 570    -8.776  -3.100  -1.915  1.00  0.00
ATOM  798 1HG  GLN A 570    -8.767  -2.289   0.165  1.00  0.00
ATOM  799 2HG  GLN A 570   -10.334  -3.011   0.452  1.00  0.00
ATOM  800 1HE2 GLN A 570    -8.752  -0.195   0.949  1.00  0.00
ATOM  801 2HE2 GLN A 570   -10.037   0.888   0.666  1.00  0.00
ATOM  802  N   VAL A 571    -9.829  -5.086  -3.988  1.00  0.00
ATOM  803  CA  VAL A 571    -9.746  -5.296  -5.400  1.00  0.00
ATOM  804  C   VAL A 571   -10.979  -5.988  -5.885  1.00  0.00
ATOM  805  O   VAL A 571   -11.453  -5.695  -6.980  1.00  0.00
ATOM  806  CB  VAL A 571    -8.564  -6.113  -5.838  1.00  0.00
ATOM  807  CG1 VAL A 571    -8.809  -7.579  -5.465  1.00  0.00
ATOM  808  CG2 VAL A 571    -8.355  -5.896  -7.346  1.00  0.00
ATOM  809  HN  VAL A 571    -9.145  -5.485  -3.377  1.00  0.00
ATOM  810  HA  VAL A 571    -9.697  -4.306  -5.853  1.00  0.00
ATOM  811  HB  VAL A 571    -7.661  -5.751  -5.347  1.00  0.00
ATOM  812 1HG1 VAL A 571    -9.464  -8.058  -6.194  1.00  0.00
ATOM  813 2HG1 VAL A 571    -9.288  -7.645  -4.488  1.00  0.00
ATOM  814 3HG1 VAL A 571    -7.866  -8.126  -5.449  1.00  0.00
ATOM  815 1HG2 VAL A 571    -8.168  -4.845  -7.562  1.00  0.00
ATOM  816 2HG2 VAL A 571    -9.245  -6.200  -7.897  1.00  0.00
ATOM  817 3HG2 VAL A 571    -7.496  -6.470  -7.693  1.00  0.00
ATOM  818  N   ILE A 572   -11.533  -6.934  -5.099  1.00  0.00
ATOM  819  CA  ILE A 572   -12.701  -7.619  -5.569  1.00  0.00
ATOM  820  C   ILE A 572   -13.819  -6.633  -5.718  1.00  0.00
ATOM  821  O   ILE A 572   -14.523  -6.622  -6.725  1.00  0.00
ATOM  822  CB  ILE A 572   -13.177  -8.716  -4.653  1.00  0.00
ATOM  823  CG1 ILE A 572   -13.637  -8.160  -3.296  1.00  0.00
ATOM  824  CG2 ILE A 572   -12.047  -9.754  -4.539  1.00  0.00
ATOM  825  CD1 ILE A 572   -14.406  -9.173  -2.447  1.00  0.00
ATOM  826  HN  ILE A 572   -11.136  -7.152  -4.207  1.00  0.00
ATOM  827  HA  ILE A 572   -12.442  -8.035  -6.542  1.00  0.00
ATOM  828  HB  ILE A 572   -14.076  -9.181  -5.057  1.00  0.00
ATOM  829 1HG2 ILE A 572   -11.145  -9.299  -4.131  1.00  0.00
ATOM  830 2HG2 ILE A 572   -11.806 -10.157  -5.523  1.00  0.00
ATOM  831 3HG2 ILE A 572   -12.346 -10.564  -3.874  1.00  0.00
ATOM  832 1HG1 ILE A 572   -14.276  -7.296  -3.471  1.00  0.00
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ATOM 833 2HG1 ILE A 572 -12.761 -7.831 -2.738 1.00 0.00
ATOM 834 1HD1 ILE A 572 -13.787 -10.046 -2.234 1.00 0.00
ATOM 835 2HD1 ILE A 572 -15.295 -9.512 -2.978 1.00 0.00
ATOM 836 3HD1 ILE A 572 -14.695 -8.726 -1.496 1.00 0.00
ATOM 837 N ALA A 573 -13.995 -5.749 -4.721 1.00 0.00
ATOM 838 CA ALA A 573 -15.062 -4.793 -4.764 1.00 0.00
ATOM 839 C ALA A 573 -14.833 -3.877 -5.920 1.00 0.00
ATOM 840 O ALA A 573 -15.775 -3.457 -6.590 1.00 0.00
ATOM 841 CB ALA A 573 -15.137 -3.928 -3.494 1.00 0.00
ATOM 842 HN ALA A 573 -13.372 -5.759 -3.939 1.00 0.00
ATOM 843 HA ALA A 573 -15.985 -5.359 -4.888 1.00 0.00
ATOM 844 1HB ALA A 573 -14.292 -3.242 -3.444 1.00 0.00
ATOM 845 2HB ALA A 573 -15.110 -4.560 -2.606 1.00 0.00
ATOM 846 3HB ALA A 573 -16.052 -3.336 -3.495 1.00 0.00
ATOM 847 N ALA A 574 -13.554 -3.564 -6.190 1.00 0.00
ATOM 848 CA ALA A 574 -13.203 -2.632 -7.220 1.00 0.00
ATOM 849 C ALA A 574 -13.693 -3.097 -8.553 1.00 0.00
ATOM 850 O ALA A 574 -14.242 -2.312 -9.323 1.00 0.00
ATOM 851 CB ALA A 574 -11.683 -2.427 -7.337 1.00 0.00
ATOM 852 HN ALA A 574 -12.827 -3.994 -5.655 1.00 0.00
ATOM 853 HA ALA A 574 -13.691 -1.690 -6.971 1.00 0.00
ATOM 854 1HB ALA A 574 -11.184 -3.368 -7.569 1.00 0.00
ATOM 855 2HB ALA A 574 -11.280 -2.055 -6.395 1.00 0.00
ATOM 856 3HB ALA A 574 -11.459 -1.721 -8.137 1.00 0.00
ATOM 857 N VAL A 575 -13.530 -4.399 -8.853 1.00 0.00
ATOM 858 CA VAL A 575 -13.925 -4.888 -10.141 1.00 0.00
ATOM 859 C VAL A 575 -15.398 -4.687 -10.298 1.00 0.00
ATOM 860 O VAL A 575 -15.870 -4.340 -11.381 1.00 0.00
ATOM 861 CB VAL A 575 -13.632 -6.348 -10.347 1.00 0.00
ATOM 862 CG1 VAL A 575 -14.518 -7.183 -9.409 1.00 0.00
ATOM 863 CG2 VAL A 575 -13.839 -6.673 -11.835 1.00 0.00
ATOM 864 HN VAL A 575 -13.134 -5.023 -8.179 1.00 0.00
ATOM 865 HA VAL A 575 -13.384 -4.293 -10.877 1.00 0.00
ATOM 866 HB VAL A 575 -12.581 -6.547 -10.136 1.00 0.00
ATOM 867 1HG1 VAL A 575 -15.377 -7.584 -9.947 1.00 0.00
ATOM 868 2HG1 VAL A 575 -14.890 -6.565 -8.592 1.00 0.00
ATOM 869 3HG1 VAL A 575 -13.952 -8.023 -9.005 1.00 0.00
ATOM 870 1HG2 VAL A 575 -13.305 -5.960 -12.463 1.00 0.00
ATOM 871 2HG2 VAL A 575 -14.897 -6.619 -12.089 1.00 0.00
ATOM 872 3HG2 VAL A 575 -13.459 -7.670 -12.059 1.00 0.00
ATOM 873 N LYS A 576 -16.162 -4.895 -9.209 1.00 0.00
ATOM 874 CA LYS A 576 -17.590 -4.759 -9.248 1.00 0.00
ATOM 875 C LYS A 576 -17.917 -3.345 -9.608 1.00 0.00
ATOM 876 O LYS A 576 -18.759 -3.086 -10.468 1.00 0.00
ATOM 877 CB LYS A 576 -18.241 -4.998 -7.873 1.00 0.00
ATOM 878 CG LYS A 576 -17.958 -6.373 -7.268 1.00 0.00
ATOM 879 CD LYS A 576 -18.478 -7.544 -8.101 1.00 0.00
ATOM 880 CE LYS A 576 -18.182 -8.907 -7.472 1.00 0.00
ATOM 881 NZ LYS A 576 -18.714 -9.988 -8.331 1.00 0.00

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ATOM    882 HN  LYS A 576     -15.722  -5.152  -8.349  1.00  0.00
ATOM    883 HA  LYS A 576     -17.956  -5.490  -9.969  1.00  0.00
ATOM    884 1HB LYS A 576     -19.319  -4.882  -7.977  1.00  0.00
ATOM    885 2HB LYS A 576     -17.879  -4.236  -7.184  1.00  0.00
ATOM    886 1HG LYS A 576     -18.419  -6.419  -6.282  1.00  0.00
ATOM    887 2HG LYS A 576     -16.881  -6.484  -7.149  1.00  0.00
ATOM    888 1HD LYS A 576     -18.017  -7.506  -9.088  1.00  0.00
ATOM    889 2HD LYS A 576     -19.555  -7.439  -8.222  1.00  0.00
ATOM    890 1HE LYS A 576     -18.657  -8.984  -6.494  1.00  0.00
ATOM    891 2HE LYS A 576     -17.107  -9.052  -7.369  1.00  0.00
ATOM    892 1HZ LYS A 576     -18.266  -9.940  -9.267  1.00  0.00
ATOM    893 2HZ LYS A 576     -19.743  -9.875  -8.433  1.00  0.00
ATOM    894 3HZ LYS A 576     -18.509 -10.910  -7.895  1.00  0.00
ATOM    895  N  TRP A 577     -17.222  -2.390  -8.964  1.00  0.00
ATOM    896  CA TRP A 577     -17.460  -0.991  -9.166  1.00  0.00
ATOM    897  C  TRP A 577     -17.218  -0.636 -10.591  1.00  0.00
ATOM    898  O  TRP A 577     -17.991   0.096 -11.206  1.00  0.00
ATOM    899  CB TRP A 577     -16.491  -0.113  -8.355  1.00  0.00
ATOM    900  CG TRP A 577     -16.575   1.365  -8.665  1.00  0.00
ATOM    901  CD1 TRP A 577     -17.346   2.331  -8.087  1.00  0.00
ATOM    902  CD2 TRP A 577     -15.783   2.025  -9.667  1.00  0.00
ATOM    903  NE1 TRP A 577     -17.099   3.546  -8.679  1.00  0.00
ATOM    904  CE2 TRP A 577     -16.136   3.374  -9.651  1.00  0.00
ATOM    905  CE3 TRP A 577     -14.836   1.549 -10.529  1.00  0.00
ATOM    906  CZ2 TRP A 577     -15.548   4.269 -10.500  1.00  0.00
ATOM    907  CZ3 TRP A 577     -14.245   2.455 -11.383  1.00  0.00
ATOM    908  CH2 TRP A 577     -14.593   3.789 -11.370  1.00  0.00
ATOM    909  HN  TRP A 577     -16.511  -2.669  -8.319  1.00  0.00
ATOM    910  HA  TRP A 577     -18.489  -0.799  -8.860  1.00  0.00
ATOM    911 1HB TRP A 577     -15.471  -0.439  -8.555  1.00  0.00
ATOM    912 2HB TRP A 577     -16.703  -0.245  -7.294  1.00  0.00
ATOM    913  HE3 TRP A 577     -14.563   0.505 -10.542  1.00  0.00
ATOM    914  HD1 TRP A 577     -18.047   2.165  -7.283  1.00  0.00
ATOM    915  HE1 TRP A 577     -17.534   4.393  -8.450  1.00  0.00
ATOM    916  HZ2 TRP A 577     -15.821   5.314 -10.490  1.00  0.00
ATOM    917  HZ3 TRP A 577     -13.492   2.113 -12.077  1.00  0.00
ATOM    918  HH2 TRP A 577     -14.109   4.470 -12.054  1.00  0.00
ATOM    919  N  ALA A 578     -16.141  -1.186 -11.164  1.00  0.00
ATOM    920  CA ALA A 578     -15.751  -0.831 -12.495  1.00  0.00
ATOM    921  C  ALA A 578     -16.858  -1.134 -13.453  1.00  0.00
ATOM    922  O  ALA A 578     -17.130  -0.350 -14.361  1.00  0.00
ATOM    923  CB ALA A 578     -14.504  -1.599 -12.969  1.00  0.00
ATOM    924  HN ALA A 578     -15.601  -1.856 -10.654  1.00  0.00
ATOM    925  HA ALA A 578     -15.554   0.240 -12.488  1.00  0.00
ATOM    926 1HB ALA A 578     -14.737  -2.651 -13.130  1.00  0.00
ATOM    927 2HB ALA A 578     -13.717  -1.539 -12.217  1.00  0.00
ATOM    928 3HB ALA A 578     -14.143  -1.185 -13.910  1.00  0.00
ATOM    929  N  LYS A 579     -17.560  -2.259 -13.246  1.00  0.00
ATOM    930  CA LYS A 579     -18.569  -2.685 -14.173  1.00  0.00
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ATOM  931 C   LYS A 579   -19.602  -1.613 -14.317  1.00  0.00
ATOM  932 O   LYS A 579   -20.149  -1.402 -15.396  1.00  0.00
ATOM  933 CB  LYS A 579   -19.301  -3.950 -13.690  1.00  0.00
ATOM  934 CG  LYS A 579   -18.376  -5.153 -13.491  1.00  0.00
ATOM  935 CD  LYS A 579   -17.692  -5.639 -14.770  1.00  0.00
ATOM  936 CE  LYS A 579   -18.527  -6.650 -15.559  1.00  0.00
ATOM  937 NZ  LYS A 579   -17.774  -7.115 -16.747  1.00  0.00
ATOM  938 HN  LYS A 579   -17.377  -2.809 -12.431  1.00  0.00
ATOM  939 HA  LYS A 579   -18.066  -2.878 -15.120  1.00  0.00
ATOM  940 1HB LYS A 579   -20.064  -4.212 -14.421  1.00  0.00
ATOM  941 2HB LYS A 579   -19.795  -3.728 -12.745  1.00  0.00
ATOM  942 1HG LYS A 579   -18.961  -5.974 -13.079  1.00  0.00
ATOM  943 2HG LYS A 579   -17.608  -4.882 -12.769  1.00  0.00
ATOM  944 1HD LYS A 579   -16.742  -6.101 -14.505  1.00  0.00
ATOM  945 2HD LYS A 579   -17.489  -4.779 -15.407  1.00  0.00
ATOM  946 1HE LYS A 579   -19.454  -6.190 -15.903  1.00  0.00
ATOM  947 2HE LYS A 579   -18.756  -7.518 -14.941  1.00  0.00
ATOM  948 1HZ LYS A 579   -17.214  -7.954 -16.495  1.00  0.00
ATOM  949 2HZ LYS A 579   -17.139  -6.358 -17.072  1.00  0.00
ATOM  950 3HZ LYS A 579   -18.441  -7.358 -17.507  1.00  0.00
ATOM  951 N   ALA A 580   -19.912  -0.937 -13.203  1.00  0.00
ATOM  952 CA  ALA A 580   -20.909   0.087 -13.093  1.00  0.00
ATOM  953 C   ALA A 580   -20.599   1.416 -13.730  1.00  0.00
ATOM  954 O   ALA A 580   -21.517   2.183 -14.014  1.00  0.00
ATOM  955 CB  ALA A 580   -21.275   0.329 -11.631  1.00  0.00
ATOM  956 HN  ALA A 580   -19.401  -1.166 -12.376  1.00  0.00
ATOM  957 HA  ALA A 580   -21.779  -0.250 -13.656  1.00  0.00
ATOM  958 1HB ALA A 580   -20.701  -0.327 -10.976  1.00  0.00
ATOM  959 2HB ALA A 580   -22.333   0.125 -11.469  1.00  0.00
ATOM  960 3HB ALA A 580   -21.054   1.359 -11.353  1.00  0.00
ATOM  961 N   ILE A 581   -19.308   1.770 -13.915  1.00  0.00
ATOM  962 CA  ILE A 581   -19.009   3.067 -14.463  1.00  0.00
ATOM  963 C   ILE A 581   -19.485   3.141 -15.877  1.00  0.00
ATOM  964 O   ILE A 581   -19.052   2.378 -16.741  1.00  0.00
ATOM  965 CB  ILE A 581   -17.545   3.400 -14.445  1.00  0.00
ATOM  966 CG1 ILE A 581   -17.304   4.796 -15.038  1.00  0.00
ATOM  967 CG2 ILE A 581   -16.779   2.273 -15.149  1.00  0.00
ATOM  968 CD1 ILE A 581   -15.857   5.261 -14.898  1.00  0.00
ATOM  969 HN  ILE A 581   -18.571   1.139 -13.674  1.00  0.00
ATOM  970 HA  ILE A 581   -19.563   3.791 -13.865  1.00  0.00
ATOM  971 HB  ILE A 581   -17.198   3.501 -13.417  1.00  0.00
ATOM  972 1HG2 ILE A 581  -17.468   1.591 -15.648  1.00  0.00
ATOM  973 2HG2 ILE A 581  -16.203   1.699 -14.424  1.00  0.00
ATOM  974 3HG2 ILE A 581  -16.110   2.687 -15.903  1.00  0.00
ATOM  975 1HG1 ILE A 581  -17.954   5.510 -14.534  1.00  0.00
ATOM  976 2HG1 ILE A 581  -17.568   4.780 -16.095  1.00  0.00
ATOM  977 1HD1 ILE A 581  -15.168   4.438 -15.083  1.00  0.00
ATOM  978 2HD1 ILE A 581  -15.677   5.630 -13.888  1.00  0.00
ATOM  979 3HD1 ILE A 581  -15.643   6.049 -15.620  1.00  0.00
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ATOM   980 N   PRO A 582   -20.368   4.076 -16.116  1.00  0.00
ATOM   981 CA  PRO A 582   -20.989   4.240 -17.404  1.00  0.00
ATOM   982 C   PRO A 582   -19.969   4.258 -18.500  1.00  0.00
ATOM   983 O   PRO A 582   -19.001   5.010 -18.407  1.00  0.00
ATOM   984 CB  PRO A 582   -21.759   5.557 -17.322  1.00  0.00
ATOM   985 CG  PRO A 582   -20.958   6.369 -16.287  1.00  0.00
ATOM   986 CD  PRO A 582   -20.393   5.302 -15.335  1.00  0.00
ATOM   987 1HD PRO A 582   -19.386   5.561 -15.006  1.00  0.00
ATOM   988 2HD PRO A 582   -21.029   5.179 -14.458  1.00  0.00
ATOM   989 HA  PRO A 582   -21.661   3.406 -17.606  1.00  0.00
ATOM   990 1HB PRO A 582   -22.786   5.397 -16.993  1.00  0.00
ATOM   991 2HB PRO A 582   -21.785   6.062 -18.287  1.00  0.00
ATOM   992 1HG PRO A 582   -20.158   6.934 -16.764  1.00  0.00
ATOM   993 2HG PRO A 582   -21.601   7.070 -15.754  1.00  0.00
ATOM   994 N   GLY A 583   -20.176   3.417 -19.535  1.00  0.00
ATOM   995 CA  GLY A 583   -19.319   3.366 -20.683  1.00  0.00
ATOM   996 C   GLY A 583   -18.265   2.305 -20.568  1.00  0.00
ATOM   997 O   GLY A 583   -17.716   1.855 -21.571  1.00  0.00
ATOM   998 HN  GLY A 583   -20.964   2.802 -19.498  1.00  0.00
ATOM   999 1HA GLY A 583   -18.842   4.341 -20.773  1.00  0.00
ATOM  1000 2HA GLY A 583   -19.950   3.155 -21.547  1.00  0.00
ATOM  1001 N   PHE A 584   -17.960   1.858 -19.339  1.00  0.00
ATOM  1002 CA  PHE A 584   -16.904   0.905 -19.124  1.00  0.00
ATOM  1003 C   PHE A 584   -17.199  -0.427 -19.753  1.00  0.00
ATOM  1004 O   PHE A 584   -16.348  -1.026 -20.411  1.00  0.00
ATOM  1005 CB  PHE A 584   -16.664   0.684 -17.623  1.00  0.00
ATOM  1006 CG  PHE A 584   -15.471  -0.178 -17.407  1.00  0.00
ATOM  1007 CD1 PHE A 584   -14.204   0.322 -17.608  1.00  0.00
ATOM  1008 CD2 PHE A 584   -15.612  -1.384 -16.760  1.00  0.00
ATOM  1009 CE1 PHE A 584   -13.096  -0.406 -17.241  1.00  0.00
ATOM  1010 CE2 PHE A 584   -14.509  -2.100 -16.364  1.00  0.00
ATOM  1011 CZ  PHE A 584   -13.246  -1.619 -16.614  1.00  0.00
ATOM  1012 HN  PHE A 584   -18.479   2.197 -18.555  1.00  0.00
ATOM  1013 HA  PHE A 584   -16.008   1.303 -19.601  1.00  0.00
ATOM  1014 1HB PHE A 584   -17.533   0.202 -17.177  1.00  0.00
ATOM  1015 2HB PHE A 584   -16.501   1.643 -17.131  1.00  0.00
ATOM  1016 HD1 PHE A 584   -14.079   1.296 -18.058  1.00  0.00
ATOM  1017 HD2 PHE A 584   -16.600  -1.771 -16.561  1.00  0.00
ATOM  1018 HE1 PHE A 584   -12.107  -0.023 -17.446  1.00  0.00
ATOM  1019 HE2 PHE A 584   -14.635  -3.044 -15.854  1.00  0.00
ATOM  1020 HZ  PHE A 584   -12.378  -2.190 -16.320  1.00  0.00
ATOM  1021 N   ARG A 585   -18.450  -0.893 -19.595  1.00  0.00
ATOM  1022 CA  ARG A 585   -18.881  -2.187 -20.037  1.00  0.00
ATOM  1023 C   ARG A 585   -18.770  -2.297 -21.522  1.00  0.00
ATOM  1024 O   ARG A 585   -18.582  -3.387 -22.060  1.00  0.00
ATOM  1025 CB  ARG A 585   -20.341  -2.478 -19.653  1.00  0.00
ATOM  1026 CG  ARG A 585   -20.830  -3.866 -20.073  1.00  0.00
ATOM  1027 CD  ARG A 585   -22.284  -4.140 -19.683  1.00  0.00
ATOM  1028 NE  ARG A 585   -22.624  -5.515 -20.148  1.00  0.00
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ATOM  1029 CZ  ARG A 585   -23.782  -6.107 -19.736  1.00  0.00
ATOM  1030 NH1 ARG A 585   -24.095  -7.365 -20.161  1.00  0.00
ATOM  1031 NH2 ARG A 585   -24.629  -5.440 -18.897  1.00  0.00
ATOM  1032 HN  ARG A 585   -19.118  -0.302 -19.143  1.00  0.00
ATOM  1033 HA  ARG A 585   -18.217  -2.916 -19.573  1.00  0.00
ATOM  1034 1HB ARG A 585   -20.979  -1.730 -20.120  1.00  0.00
ATOM  1035 2HB ARG A 585   -20.441  -2.387 -18.572  1.00  0.00
ATOM  1036 1HG ARG A 585   -20.194  -4.617 -19.605  1.00  0.00
ATOM  1037 2HG ARG A 585   -20.732  -3.959 -21.154  1.00  0.00
ATOM  1038 1HD ARG A 585   -22.963  -3.442 -20.172  1.00  0.00
ATOM  1039 2HD ARG A 585   -22.418  -4.107 -18.603  1.00  0.00
ATOM  1040 HE  ARG A 585   -22.003  -6.004 -20.760  1.00  0.00
ATOM  1041 1HH1 ARG A 585  -23.475  -7.854 -20.775  1.00  0.00
ATOM  1042 2HH1 ARG A 585  -24.944  -7.798 -19.860  1.00  0.00
ATOM  1043 1HH2 ARG A 585  -24.480  -4.471 -18.703  1.00  0.00
ATOM  1044 2HH2 ARG A 585  -25.398  -5.922 -18.477  1.00  0.00
ATOM  1045 N   ASN A 586   -18.893  -1.162 -22.227  1.00  0.00
ATOM  1046 CA  ASN A 586   -18.871  -1.149 -23.658  1.00  0.00
ATOM  1047 C   ASN A 586   -17.577  -1.675 -24.203  1.00  0.00
ATOM  1048 O   ASN A 586   -17.544  -2.196 -25.315  1.00  0.00
ATOM  1049 CB  ASN A 586   -19.118   0.251 -24.236  1.00  0.00
ATOM  1050 CG  ASN A 586   -20.571   0.587 -23.938  1.00  0.00
ATOM  1051 OD1 ASN A 586   -21.465  -0.218 -24.195  1.00  0.00
ATOM  1052 ND2 ASN A 586   -20.815   1.795 -23.364  1.00  0.00
ATOM  1053 HN  ASN A 586   -19.004  -0.298 -21.736  1.00  0.00
ATOM  1054 HA  ASN A 586   -19.650  -1.836 -23.990  1.00  0.00
ATOM  1055 1HB ASN A 586   -18.950   0.263 -25.312  1.00  0.00
ATOM  1056 2HB ASN A 586   -18.466   0.987 -23.765  1.00  0.00
ATOM  1057 1HD2 ASN A 586  -20.132   2.522 -23.430  1.00  0.00
ATOM  1058 2HD2 ASN A 586  -21.669   1.973 -22.876  1.00  0.00
ATOM  1059 N   LEU A 587   -16.462  -1.528 -23.464  1.00  0.00
ATOM  1060 CA  LEU A 587   -15.216  -2.041 -23.971  1.00  0.00
ATOM  1061 C   LEU A 587   -15.207  -3.534 -23.839  1.00  0.00
ATOM  1062 O   LEU A 587   -15.985  -4.117 -23.087  1.00  0.00
ATOM  1063 CB  LEU A 587   -13.966  -1.549 -23.218  1.00  0.00
ATOM  1064 CG  LEU A 587   -13.683  -0.036 -23.312  1.00  0.00
ATOM  1065 CD1 LEU A 587   -14.647   0.804 -22.461  1.00  0.00
ATOM  1066 CD2 LEU A 587   -12.217   0.255 -22.978  1.00  0.00
ATOM  1067 HN  LEU A 587   -16.499  -1.069 -22.577  1.00  0.00
ATOM  1068 HA  LEU A 587   -15.162  -1.731 -25.014  1.00  0.00
ATOM  1069 1HB LEU A 587   -13.102  -2.081 -23.612  1.00  0.00
ATOM  1070 2HB LEU A 587   -14.080  -1.809 -22.167  1.00  0.00
ATOM  1071 HG  LEU A 587   -13.768   0.275 -24.352  1.00  0.00
ATOM  1072 1HD1 LEU A 587  -14.703   0.414 -21.445  1.00  0.00
ATOM  1073 2HD1 LEU A 587  -15.649   0.776 -22.889  1.00  0.00
ATOM  1074 3HD1 LEU A 587  -14.300   1.836 -22.407  1.00  0.00
ATOM  1075 1HD2 LEU A 587  -11.554  -0.262 -23.671  1.00  0.00
ATOM  1076 2HD2 LEU A 587  -11.985  -0.088 -21.970  1.00  0.00
ATOM  1077 3HD2 LEU A 587  -12.019   1.324 -23.056  1.00  0.00
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ATOM 1078 N HIS A 588 -14.324 -4.224 -24.583 1.00 0.00
ATOM 1079 CA HIS A 588 -14.302 -5.645 -24.394 1.00 0.00
ATOM 1080 C HIS A 588 -13.680 -5.962 -23.057 1.00 0.00
ATOM 1081 O HIS A 588 -13.397 -5.069 -22.263 1.00 0.00
ATOM 1082 CB HIS A 588 -13.564 -6.456 -25.471 1.00 0.00
ATOM 1083 CG HIS A 588 -14.329 -6.632 -26.751 1.00 0.00
ATOM 1084 ND1 HIS A 588 -14.228 -5.801 -27.843 1.00 0.00
ATOM 1085 CD2 HIS A 588 -15.196 -7.619 -27.114 1.00 0.00
ATOM 1086 CE1 HIS A 588 -15.033 -6.320 -28.805 1.00 0.00
ATOM 1087 NE2 HIS A 588 -15.641 -7.422 -28.409 1.00 0.00
ATOM 1088 HN HIS A 588 -13.715 -3.769 -25.232 1.00 0.00
ATOM 1089 HA HIS A 588 -15.346 -5.955 -24.360 1.00 0.00
ATOM 1090 1HB HIS A 588 -13.344 -7.446 -25.075 1.00 0.00
ATOM 1091 2HB HIS A 588 -12.627 -5.953 -25.708 1.00 0.00
ATOM 1092 HD2 HIS A 588 -15.494 -8.439 -26.479 1.00 0.00
ATOM 1093 HD1 HIS A 588 -13.681 -4.992 -27.913 1.00 0.00
ATOM 1094 HE1 HIS A 588 -15.160 -5.881 -29.783 1.00 0.00
ATOM 1095 N LEU A 589 -13.524 -7.268 -22.754 1.00 0.00
ATOM 1096 CA LEU A 589 -12.907 -7.782 -21.549 1.00 0.00
ATOM 1097 C LEU A 589 -11.421 -7.545 -21.600 1.00 0.00
ATOM 1098 O LEU A 589 -10.690 -7.638 -20.621 1.00 0.00
ATOM 1099 CB LEU A 589 -13.182 -9.270 -21.281 1.00 0.00
ATOM 1100 CG LEU A 589 -14.650 -9.519 -20.885 1.00 0.00
ATOM 1101 CD1 LEU A 589 -15.603 -9.313 -22.073 1.00 0.00
ATOM 1102 CD2 LEU A 589 -14.825 -10.869 -20.181 1.00 0.00
ATOM 1103 HN LEU A 589 -13.862 -7.935 -23.416 1.00 0.00
ATOM 1104 HA LEU A 589 -13.296 -7.182 -20.728 1.00 0.00
ATOM 1105 1HB LEU A 589 -12.532 -9.615 -20.478 1.00 0.00
ATOM 1106 2HB LEU A 589 -12.952 -9.844 -22.178 1.00 0.00
ATOM 1107 HG LEU A 589 -14.925 -8.835 -20.083 1.00 0.00
ATOM 1108 1HD1 LEU A 589 -15.171 -9.716 -22.989 1.00 0.00
ATOM 1109 2HD1 LEU A 589 -15.789 -8.250 -22.227 1.00 0.00
ATOM 1110 3HD1 LEU A 589 -16.547 -9.827 -21.892 1.00 0.00
ATOM 1111 1HD2 LEU A 589 -14.225 -10.909 -19.272 1.00 0.00
ATOM 1112 2HD2 LEU A 589 -14.502 -11.679 -20.834 1.00 0.00
ATOM 1113 3HD2 LEU A 589 -15.868 -11.016 -19.902 1.00 0.00
ATOM 1114 N ASP A 590 -11.031 -7.149 -22.805 1.00 0.00
ATOM 1115 CA ASP A 590 -9.924 -6.818 -23.641 1.00 0.00
ATOM 1116 C ASP A 590 -10.032 -5.373 -23.370 1.00 0.00
ATOM 1117 O ASP A 590 -11.115 -4.836 -23.268 1.00 0.00
ATOM 1118 CB ASP A 590 -10.004 -7.103 -25.178 1.00 0.00
ATOM 1119 CG ASP A 590 -10.722 -6.130 -26.144 1.00 0.00
ATOM 1120 OD1 ASP A 590 -10.727 -6.510 -27.345 1.00 0.00
ATOM 1121 OD2 ASP A 590 -11.240 -5.041 -25.780 1.00 0.00
ATOM 1122 HN ASP A 590 -11.837 -7.036 -23.342 1.00 0.00
ATOM 1123 HA ASP A 590 -9.087 -7.380 -23.229 1.00 0.00
ATOM 1124 1HB ASP A 590 -10.503 -8.061 -25.301 1.00 0.00
ATOM 1125 2HB ASP A 590 -8.982 -7.178 -25.542 1.00 0.00
ATOM 1126 N ASP A 591 -8.993 -4.639 -23.046 1.00 0.00

ATOM 1127 CA ASP A 591 -8.947 -3.488 -22.220 1.00 0.00
ATOM 1128 C ASP A 591 -9.839 -3.337 -21.017 1.00 0.00
ATOM 1129 O ASP A 591 -9.322 -2.693 -20.111 1.00 0.00
ATOM 1130 CB ASP A 591 -9.244 -2.289 -23.151 1.00 0.00
ATOM 1131 CG ASP A 591 -9.012 -0.909 -22.554 1.00 0.00
ATOM 1132 OD1 ASP A 591 -8.376 -0.782 -21.477 1.00 0.00
ATOM 1133 OD2 ASP A 591 -9.478 0.062 -23.206 1.00 0.00
ATOM 1134 HN ASP A 591 -8.121 -4.930 -23.433 1.00 0.00
ATOM 1135 HA ASP A 591 -7.953 -3.420 -21.779 1.00 0.00
ATOM 1136 1HB ASP A 591 -10.289 -2.337 -23.455 1.00 0.00
ATOM 1137 2HB ASP A 591 -8.611 -2.370 -24.034 1.00 0.00
ATOM 1138 N GLN A 592 -11.100 -3.786 -20.880 1.00 0.00
ATOM 1139 CA GLN A 592 -11.706 -3.638 -19.564 1.00 0.00
ATOM 1140 C GLN A 592 -10.809 -4.237 -18.494 1.00 0.00
ATOM 1141 O GLN A 592 -10.526 -3.611 -17.468 1.00 0.00
ATOM 1142 CB GLN A 592 -13.062 -4.362 -19.519 1.00 0.00
ATOM 1143 CG GLN A 592 -13.773 -4.302 -18.176 1.00 0.00
ATOM 1144 CD GLN A 592 -15.098 -5.034 -18.326 1.00 0.00
ATOM 1145 OE1 GLN A 592 -15.704 -5.451 -17.341 1.00 0.00
ATOM 1146 NE2 GLN A 592 -15.565 -5.192 -19.595 1.00 0.00
ATOM 1147 HN GLN A 592 -11.595 -4.199 -21.643 1.00 0.00
ATOM 1148 HA GLN A 592 -11.832 -2.572 -19.381 1.00 0.00
ATOM 1149 1HB GLN A 592 -12.902 -5.408 -19.776 1.00 0.00
ATOM 1150 2HB GLN A 592 -13.713 -3.919 -20.272 1.00 0.00
ATOM 1151 1HG GLN A 592 -13.961 -3.268 -17.886 1.00 0.00
ATOM 1152 2HG GLN A 592 -13.177 -4.786 -17.402 1.00 0.00
ATOM 1153 1HE2 GLN A 592 -15.039 -4.833 -20.365 1.00 0.00
ATOM 1154 2HE2 GLN A 592 -16.429 -5.663 -19.774 1.00 0.00
ATOM 1155 N MET A 593 -10.260 -5.437 -18.742 1.00 0.00
ATOM 1156 CA MET A 593 -9.370 -6.015 -17.780 1.00 0.00
ATOM 1157 C MET A 593 -8.169 -5.123 -17.698 1.00 0.00
ATOM 1158 O MET A 593 -7.646 -4.868 -16.610 1.00 0.00
ATOM 1159 CB MET A 593 -8.929 -7.431 -18.199 1.00 0.00
ATOM 1160 CG MET A 593 -8.478 -8.331 -17.047 1.00 0.00
ATOM 1161 SD MET A 593 -6.901 -7.880 -16.276 1.00 0.00
ATOM 1162 CE MET A 593 -6.846 -9.316 -15.164 1.00 0.00
ATOM 1163 HN MET A 593 -10.471 -5.922 -19.591 1.00 0.00
ATOM 1164 HA MET A 593 -9.905 -6.049 -16.831 1.00 0.00
ATOM 1165 1HB MET A 593 -8.104 -7.338 -18.905 1.00 0.00
ATOM 1166 2HB MET A 593 -9.762 -7.914 -18.707 1.00 0.00
ATOM 1167 1HG MET A 593 -8.383 -9.350 -17.420 1.00 0.00
ATOM 1168 2HG MET A 593 -9.242 -8.309 -16.271 1.00 0.00
ATOM 1169 1HE MET A 593 -6.846 -10.232 -15.754 1.00 0.00
ATOM 1170 2HE MET A 593 -7.723 -9.318 -14.517 1.00 0.00
ATOM 1171 3HE MET A 593 -5.935 -9.286 -14.566 1.00 0.00
ATOM 1172 N THR A 594 -7.699 -4.597 -18.851 1.00 0.00
ATOM 1173 CA THR A 594 -6.500 -3.820 -18.739 1.00 0.00
ATOM 1174 C THR A 594 -6.684 -2.533 -17.985 1.00 0.00
ATOM 1175 O THR A 594 -5.791 -2.161 -17.226 1.00 0.00

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ATOM  1176  CB  THR A 594     -5.721  -3.609 -20.009  1.00  0.00
ATOM  1177  OG1 THR A 594     -4.434  -3.097 -19.695  1.00  0.00
ATOM  1178  CG2 THR A 594     -6.449  -2.635 -20.928  1.00  0.00
ATOM  1179  HN  THR A 594     -8.159  -4.741 -19.727  1.00  0.00
ATOM  1180  HA  THR A 594     -5.875  -4.345 -18.016  1.00  0.00
ATOM  1181  HB  THR A 594     -5.596  -4.552 -20.541  1.00  0.00
ATOM  1182  HG1 THR A 594     -4.553  -2.470 -18.995  1.00  0.00
ATOM  1183 1HG2 THR A 594     -5.913  -1.688 -20.989  1.00  0.00
ATOM  1184 2HG2 THR A 594     -7.449  -2.432 -20.545  1.00  0.00
ATOM  1185 3HG2 THR A 594     -6.519  -3.048 -21.935  1.00  0.00
ATOM  1186  N   LEU A 595     -7.840  -1.833 -18.125  1.00  0.00
ATOM  1187  CA  LEU A 595     -7.992  -0.587 -17.402  1.00  0.00
ATOM  1188  C   LEU A 595     -7.869  -0.929 -15.955  1.00  0.00
ATOM  1189  O   LEU A 595     -7.238  -0.225 -15.165  1.00  0.00
ATOM  1190  CB  LEU A 595     -9.378   0.113 -17.468  1.00  0.00
ATOM  1191  CG  LEU A 595     -9.880   0.767 -18.781  1.00  0.00
ATOM  1192  CD1 LEU A 595     -8.871   1.762 -19.367  1.00  0.00
ATOM  1193  CD2 LEU A 595    -10.458  -0.238 -19.780  1.00  0.00
ATOM  1194  HN  LEU A 595     -8.572  -2.172 -18.715  1.00  0.00
ATOM  1195  HA  LEU A 595     -7.237   0.081 -17.815  1.00  0.00
ATOM  1196 1HB  LEU A 595     -9.370   0.895 -16.713  1.00  0.00
ATOM  1197 2HB  LEU A 595    -10.118  -0.633 -17.189  1.00  0.00
ATOM  1198  HG  LEU A 595    -10.816   1.288 -18.582  1.00  0.00
ATOM  1199 1HD1 LEU A 595     -7.996   1.240 -19.756  1.00  0.00
ATOM  1200 2HD1 LEU A 595     -8.534   2.455 -18.596  1.00  0.00
ATOM  1201 3HD1 LEU A 595     -9.323   2.318 -20.188  1.00  0.00
ATOM  1202 1HD2 LEU A 595    -11.538  -0.117 -19.866  1.00  0.00
ATOM  1203 2HD2 LEU A 595    -10.259  -1.257 -19.447  1.00  0.00
ATOM  1204 3HD2 LEU A 595    -10.022  -0.082 -20.766  1.00  0.00
ATOM  1205  N   LEU A 596     -8.477  -2.053 -15.561  1.00  0.00
ATOM  1206  CA  LEU A 596     -8.431  -2.348 -14.173  1.00  0.00
ATOM  1207  C   LEU A 596     -7.005  -2.577 -13.776  1.00  0.00
ATOM  1208  O   LEU A 596     -6.529  -2.006 -12.796  1.00  0.00
ATOM  1209  CB  LEU A 596     -9.288  -3.570 -13.814  1.00  0.00
ATOM  1210  CG  LEU A 596     -9.576  -3.691 -12.312  1.00  0.00
ATOM  1211  CD1 LEU A 596    -10.386  -2.487 -11.801  1.00  0.00
ATOM  1212  CD2 LEU A 596    -10.268  -5.021 -11.996  1.00  0.00
ATOM  1213  HN  LEU A 596     -8.941  -2.654 -16.211  1.00  0.00
ATOM  1214  HA  LEU A 596     -8.795  -1.465 -13.649  1.00  0.00
ATOM  1215 1HB  LEU A 596     -8.772  -4.470 -14.146  1.00  0.00
ATOM  1216 2HB  LEU A 596    -10.235  -3.502 -14.348  1.00  0.00
ATOM  1217  HG  LEU A 596     -8.634  -3.749 -11.768  1.00  0.00
ATOM  1218 1HD1 LEU A 596    -11.255  -2.310 -12.434  1.00  0.00
ATOM  1219 2HD1 LEU A 596     -9.771  -1.587 -11.813  1.00  0.00
ATOM  1220 3HD1 LEU A 596    -10.740  -2.674 -10.787  1.00  0.00
ATOM  1221 1HD2 LEU A 596     -9.639  -5.862 -12.290  1.00  0.00
ATOM  1222 2HD2 LEU A 596    -11.208  -5.096 -12.542  1.00  0.00
ATOM  1223 3HD2 LEU A 596    -10.459  -5.102 -10.926  1.00  0.00
ATOM  1224  N   GLN A 597     -6.254  -3.356 -14.577  1.00  0.00
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ATOM  1225 CA  GLN A 597     -4.895  -3.650 -14.216  1.00  0.00
ATOM  1226 C   GLN A 597     -4.138  -2.371 -14.131  1.00  0.00
ATOM  1227 O   GLN A 597     -3.312  -2.175 -13.242  1.00  0.00
ATOM  1228 CB  GLN A 597     -4.169  -4.488 -15.273  1.00  0.00
ATOM  1229 CG  GLN A 597     -4.725  -5.897 -15.424  1.00  0.00
ATOM  1230 CD  GLN A 597     -3.981  -6.553 -16.577  1.00  0.00
ATOM  1231 OE1 GLN A 597     -3.425  -7.638 -16.436  1.00  0.00
ATOM  1232 NE2 GLN A 597     -3.972  -5.874 -17.757  1.00  0.00
ATOM  1233 HN  GLN A 597     -6.641  -3.728 -15.421  1.00  0.00
ATOM  1234 HA  GLN A 597     -4.932  -4.189 -13.270  1.00  0.00
ATOM  1235 1HB GLN A 597     -3.117  -4.556 -15.001  1.00  0.00
ATOM  1236 2HB GLN A 597     -4.243  -3.979 -16.233  1.00  0.00
ATOM  1237 1HG GLN A 597     -5.791  -5.870 -15.647  1.00  0.00
ATOM  1238 2HG GLN A 597     -4.566  -6.474 -14.513  1.00  0.00
ATOM  1239 1HE2 GLN A 597    -4.441  -4.994 -17.826  1.00  0.00
ATOM  1240 2HE2 GLN A 597    -3.505  -6.240 -18.561  1.00  0.00
ATOM  1241 N   TYR A 598     -4.409  -1.463 -15.078  1.00  0.00
ATOM  1242 CA  TYR A 598     -3.683  -0.231 -15.173  1.00  0.00
ATOM  1243 C   TYR A 598     -3.830   0.698 -14.007  1.00  0.00
ATOM  1244 O   TYR A 598     -2.830   1.205 -13.499  1.00  0.00
ATOM  1245 CB  TYR A 598     -4.094   0.568 -16.422  1.00  0.00
ATOM  1246 CG  TYR A 598     -3.326   1.843 -16.414  1.00  0.00
ATOM  1247 CD1 TYR A 598     -2.013   1.869 -16.821  1.00  0.00
ATOM  1248 CD2 TYR A 598     -3.932   3.021 -16.038  1.00  0.00
ATOM  1249 CE1 TYR A 598     -1.307   3.047 -16.831  1.00  0.00
ATOM  1250 CE2 TYR A 598     -3.231   4.204 -16.048  1.00  0.00
ATOM  1251 CZ  TYR A 598     -1.914   4.216 -16.440  1.00  0.00
ATOM  1252 OH  TYR A 598     -1.187   5.426 -16.448  1.00  0.00
ATOM  1253 HN  TYR A 598     -5.138  -1.650 -15.736  1.00  0.00
ATOM  1254 HA  TYR A 598     -2.624  -0.488 -15.217  1.00  0.00
ATOM  1255 1HB TYR A 598     -5.162   0.784 -16.403  1.00  0.00
ATOM  1256 2HB TYR A 598     -3.864   0.008 -17.328  1.00  0.00
ATOM  1257 HD1 TYR A 598     -1.532   0.954 -17.137  1.00  0.00
ATOM  1258 HE1 TYR A 598     -0.274   3.055 -17.146  1.00  0.00
ATOM  1259 HD2 TYR A 598     -4.968   3.015 -15.733  1.00  0.00
ATOM  1260 HE2 TYR A 598     -3.715   5.122 -15.749  1.00  0.00
ATOM  1261 HH  TYR A 598     -1.413   5.935 -15.680  1.00  0.00
ATOM  1262 N   SER A 599     -5.066   0.937 -13.524  1.00  0.00
ATOM  1263 CA  SER A 599     -5.201   1.987 -12.548  1.00  0.00
ATOM  1264 C   SER A 599     -5.623   1.487 -11.203  1.00  0.00
ATOM  1265 O   SER A 599     -6.170   2.237 -10.397  1.00  0.00
ATOM  1266 CB  SER A 599     -6.228   3.049 -13.002  1.00  0.00
ATOM  1267 OG  SER A 599     -6.261   4.154 -12.109  1.00  0.00
ATOM  1268 HN  SER A 599     -5.856   0.407 -13.831  1.00  0.00
ATOM  1269 HA  SER A 599     -4.216   2.438 -12.425  1.00  0.00
ATOM  1270 1HB SER A 599     -7.227   2.613 -13.032  1.00  0.00
ATOM  1271 2HB SER A 599     -5.964   3.424 -13.991  1.00  0.00
ATOM  1272 HG  SER A 599     -7.009   4.682 -12.355  1.00  0.00
ATOM  1273 N   TRP A 600     -5.374   0.197 -10.930  1.00  0.00
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ATOM  1274  CA  TRP A 600     -5.750  -0.339  -9.618  1.00  0.00
ATOM  1275  C   TRP A 600     -5.235   0.537  -8.454  1.00  0.00
ATOM  1276  O   TRP A 600     -5.982   0.998  -7.602  1.00  0.00
ATOM  1277  CB  TRP A 600     -5.158  -1.745  -9.508  1.00  0.00
ATOM  1278  CG  TRP A 600     -5.055  -2.226  -8.069  1.00  0.00
ATOM  1279  CD1 TRP A 600     -3.885  -2.666  -7.450  1.00  0.00
ATOM  1280  CD2 TRP A 600     -6.086  -2.286  -7.065  1.00  0.00
ATOM  1281  NE1 TRP A 600     -4.138  -2.989  -6.162  1.00  0.00
ATOM  1282  CE2 TRP A 600     -5.478  -2.771  -5.881  1.00  0.00
ATOM  1283  CE3 TRP A 600     -7.415  -1.962  -7.073  1.00  0.00
ATOM  1284  CZ2 TRP A 600     -6.220  -2.924  -4.744  1.00  0.00
ATOM  1285  CZ3 TRP A 600     -8.169  -2.109  -5.914  1.00  0.00
ATOM  1286  CH2 TRP A 600     -7.572  -2.594  -4.754  1.00  0.00
ATOM  1287  HN  TRP A 600     -5.041  -0.407 -11.658  1.00  0.00
ATOM  1288  HA  TRP A 600     -6.840  -0.362  -9.586  1.00  0.00
ATOM  1289 1HB  TRP A 600     -4.152  -1.676  -9.917  1.00  0.00
ATOM  1290 2HB  TRP A 600     -5.714  -2.461 -10.115  1.00  0.00
ATOM  1291  HE3 TRP A 600     -7.881  -1.589  -7.972  1.00  0.00
ATOM  1292  HD1 TRP A 600     -2.918  -2.729  -7.926  1.00  0.00
ATOM  1293  HE1 TRP A 600     -3.470  -3.318  -5.525  1.00  0.00
ATOM  1294  HZ2 TRP A 600     -5.762  -3.299  -3.842  1.00  0.00
ATOM  1295  HZ3 TRP A 600     -9.212  -1.838  -5.907  1.00  0.00
ATOM  1296  HH2 TRP A 600     -8.161  -2.715  -3.864  1.00  0.00
ATOM  1297  N   MET A 601     -3.903   0.714  -8.453  1.00  0.00
ATOM  1298  CA  MET A 601     -3.290   1.376  -7.306  1.00  0.00
ATOM  1299  C   MET A 601     -3.711   2.849  -7.232  1.00  0.00
ATOM  1300  O   MET A 601     -3.783   3.435  -6.160  1.00  0.00
ATOM  1301  CB  MET A 601     -1.761   1.224  -7.356  1.00  0.00
ATOM  1302  CG  MET A 601     -1.317  -0.233  -7.166  1.00  0.00
ATOM  1303  SD  MET A 601     -1.813  -0.871  -5.552  1.00  0.00
ATOM  1304  CE  MET A 601     -0.700  -2.284  -5.450  1.00  0.00
ATOM  1305  HN  MET A 601     -3.367   0.312  -9.194  1.00  0.00
ATOM  1306  HA  MET A 601     -3.678   0.887  -6.410  1.00  0.00
ATOM  1307 1HB  MET A 601     -1.305   1.830  -6.572  1.00  0.00
ATOM  1308 2HB  MET A 601     -1.377   1.612  -8.300  1.00  0.00
ATOM  1309 1HG  MET A 601     -0.235  -0.297  -7.234  1.00  0.00
ATOM  1310 2HG  MET A 601     -1.700  -0.874  -7.957  1.00  0.00
ATOM  1311 1HE  MET A 601     -1.012  -3.065  -6.143  1.00  0.00
ATOM  1312 2HE  MET A 601     -0.682  -2.677  -4.433  1.00  0.00
ATOM  1313 3HE  MET A 601      0.315  -1.986  -5.713  1.00  0.00
ATOM  1314  N   PHE A 602     -4.012   3.399  -8.430  1.00  0.00
ATOM  1315  CA  PHE A 602     -4.329   4.792  -8.552  1.00  0.00
ATOM  1316  C   PHE A 602     -5.642   4.922  -7.841  1.00  0.00
ATOM  1317  O   PHE A 602     -5.808   5.741  -6.936  1.00  0.00
ATOM  1318  CB  PHE A 602     -4.600   5.152 -10.026  1.00  0.00
ATOM  1319  CG  PHE A 602     -4.341   6.595 -10.299  1.00  0.00
ATOM  1320  CD1 PHE A 602     -3.197   6.950 -10.976  1.00  0.00
ATOM  1321  CD2 PHE A 602     -5.191   7.584  -9.864  1.00  0.00
ATOM  1322  CE1 PHE A 602     -2.935   8.262 -11.292  1.00  0.00
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ATOM  1323 CE2 PHE A 602     -4.909   8.902 -10.141  1.00  0.00
ATOM  1324  CZ PHE A 602     -3.804   9.242 -10.885  1.00  0.00
ATOM  1325  HN PHE A 602     -3.876   2.850  -9.254  1.00  0.00
ATOM  1326  HA PHE A 602     -3.478   5.353  -8.169  1.00  0.00
ATOM  1327 1HB PHE A 602     -5.640   4.934 -10.269  1.00  0.00
ATOM  1328 2HB PHE A 602     -3.955   4.556 -10.671  1.00  0.00
ATOM  1329 HD1 PHE A 602     -2.492   6.184 -11.265  1.00  0.00
ATOM  1330 HD2 PHE A 602     -6.079   7.328  -9.306  1.00  0.00
ATOM  1331 HE1 PHE A 602     -2.051   8.519 -11.857  1.00  0.00
ATOM  1332 HE2 PHE A 602     -5.562   9.677  -9.769  1.00  0.00
ATOM  1333  HZ PHE A 602     -3.622  10.274 -11.148  1.00  0.00
ATOM  1334  N  LEU A 603     -6.582   4.031  -8.209  1.00  0.00
ATOM  1335  CA LEU A 603     -7.919   3.980  -7.692  1.00  0.00
ATOM  1336  C  LEU A 603     -7.888   3.784  -6.209  1.00  0.00
ATOM  1337  O  LEU A 603     -8.534   4.518  -5.462  1.00  0.00
ATOM  1338  CB LEU A 603     -8.662   2.763  -8.271  1.00  0.00
ATOM  1339  CG LEU A 603    -10.109   2.593  -7.789  1.00  0.00
ATOM  1340 CD1 LEU A 603    -11.000   3.712  -8.331  1.00  0.00
ATOM  1341 CD2 LEU A 603    -10.648   1.191  -8.117  1.00  0.00
ATOM  1342  HN LEU A 603     -6.327   3.352  -8.896  1.00  0.00
ATOM  1343  HA LEU A 603     -8.414   4.907  -7.979  1.00  0.00
ATOM  1344 1HB LEU A 603     -8.106   1.865  -8.005  1.00  0.00
ATOM  1345 2HB LEU A 603     -8.671   2.852  -9.356  1.00  0.00
ATOM  1346  HG LEU A 603    -10.132   2.607  -6.700  1.00  0.00
ATOM  1347 1HD1 LEU A 603    -10.542   4.183  -9.200  1.00  0.00
ATOM  1348 2HD1 LEU A 603    -11.146   4.478  -7.570  1.00  0.00
ATOM  1349 3HD1 LEU A 603    -11.966   3.310  -8.635  1.00  0.00
ATOM  1350 1HD2 LEU A 603    -10.043   0.423  -7.635  1.00  0.00
ATOM  1351 2HD2 LEU A 603    -10.618   1.018  -9.193  1.00  0.00
ATOM  1352 3HD2 LEU A 603    -11.672   1.088  -7.759  1.00  0.00
ATOM  1353  N  MET A 604     -7.108   2.801  -5.735  1.00  0.00
ATOM  1354  CA MET A 604     -7.162   2.563  -4.295  1.00  0.00
ATOM  1355  C  MET A 604     -6.553   3.736  -3.494  1.00  0.00
ATOM  1356  O  MET A 604     -6.989   4.068  -2.394  1.00  0.00
ATOM  1357  CB MET A 604     -6.551   1.197  -3.954  1.00  0.00
ATOM  1358  CG MET A 604     -7.377   0.461  -2.891  1.00  0.00
ATOM  1359  SD MET A 604     -9.047   0.097  -3.483  1.00  0.00
ATOM  1360  CE MET A 604    -10.010   1.373  -2.647  1.00  0.00
ATOM  1361  HN MET A 604     -6.591   2.225  -6.370  1.00  0.00
ATOM  1362  HA MET A 604     -8.222   2.547  -4.050  1.00  0.00
ATOM  1363 1HB MET A 604     -5.513   1.302  -3.633  1.00  0.00
ATOM  1364 2HB MET A 604     -6.522   0.572  -4.849  1.00  0.00
ATOM  1365 1HG MET A 604     -7.413   1.016  -1.954  1.00  0.00
ATOM  1366 2HG MET A 604     -6.900  -0.491  -2.669  1.00  0.00
ATOM  1367 1HE MET A 604    -10.288   2.160  -3.348  1.00  0.00
ATOM  1368 2HE MET A 604     -9.473   1.797  -1.800  1.00  0.00
ATOM  1369 3HE MET A 604    -10.936   0.941  -2.272  1.00  0.00
ATOM  1370  N  ALA A 605     -5.545   4.363  -4.137  1.00  0.00
ATOM  1371  CA ALA A 605     -4.874   5.506  -3.532  1.00  0.00
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ATOM  1372  C   ALA A 605    -5.827   6.702  -3.362  1.00  0.00
ATOM  1373  O   ALA A 605    -5.878   7.310  -2.299  1.00  0.00
ATOM  1374  CB  ALA A 605    -3.646   5.903  -4.361  1.00  0.00
ATOM  1375  HN  ALA A 605    -5.229   4.030  -5.030  1.00  0.00
ATOM  1376  HA  ALA A 605    -4.552   5.187  -2.539  1.00  0.00
ATOM  1377 1HB  ALA A 605    -3.118   6.743  -3.908  1.00  0.00
ATOM  1378 2HB  ALA A 605    -3.918   6.189  -5.378  1.00  0.00
ATOM  1379 3HB  ALA A 605    -2.940   5.075  -4.429  1.00  0.00
ATOM  1380  N   PHE A 606    -6.591   7.014  -4.438  1.00  0.00
ATOM  1381  CA  PHE A 606    -7.447   8.165  -4.365  1.00  0.00
ATOM  1382  C   PHE A 606    -8.499   7.924  -3.332  1.00  0.00
ATOM  1383  O   PHE A 606    -8.914   8.843  -2.626  1.00  0.00
ATOM  1384  CB  PHE A 606    -8.128   8.482  -5.709  1.00  0.00
ATOM  1385  CG  PHE A 606    -8.764   9.826  -5.599  1.00  0.00
ATOM  1386  CD1 PHE A 606    -7.983  10.937  -5.380  1.00  0.00
ATOM  1387  CD2 PHE A 606   -10.075  10.011  -5.972  1.00  0.00
ATOM  1388  CE1 PHE A 606    -8.527  12.200  -5.390  1.00  0.00
ATOM  1389  CE2 PHE A 606   -10.612  11.275  -6.033  1.00  0.00
ATOM  1390  CZ  PHE A 606    -9.853  12.370  -5.702  1.00  0.00
ATOM  1391  HN  PHE A 606    -6.547   6.469  -5.275  1.00  0.00
ATOM  1392  HA  PHE A 606    -6.822   9.002  -4.055  1.00  0.00
ATOM  1393 1HB  PHE A 606    -8.890   7.736  -5.934  1.00  0.00
ATOM  1394 2HB  PHE A 606    -7.395   8.490  -6.515  1.00  0.00
ATOM  1395  HD1 PHE A 606    -6.926  10.816  -5.196  1.00  0.00
ATOM  1396  HD2 PHE A 606   -10.687   9.156  -6.219  1.00  0.00
ATOM  1397  HE1 PHE A 606    -7.912  13.056  -5.154  1.00  0.00
ATOM  1398  HE2 PHE A 606   -11.638  11.408  -6.342  1.00  0.00
ATOM  1399  HZ  PHE A 606   -10.295  13.356  -5.687  1.00  0.00
ATOM  1400  N   ALA A 607    -8.951   6.658  -3.251  1.00  0.00
ATOM  1401  CA  ALA A 607    -9.986   6.362  -2.267  1.00  0.00
ATOM  1402  C   ALA A 607    -9.485   6.561  -0.843  1.00  0.00
ATOM  1403  O   ALA A 607   -10.155   7.114   0.022  1.00  0.00
ATOM  1404  CB  ALA A 607   -10.490   4.929  -2.480  1.00  0.00
ATOM  1405  HN  ALA A 607    -8.636   5.964  -3.904  1.00  0.00
ATOM  1406  HA  ALA A 607   -10.759   7.108  -2.388  1.00  0.00
ATOM  1407 1HB  ALA A 607    -9.697   4.201  -2.307  1.00  0.00
ATOM  1408 2HB  ALA A 607   -10.839   4.790  -3.503  1.00  0.00
ATOM  1409 3HB  ALA A 607   -11.318   4.698  -1.809  1.00  0.00
ATOM  1410  N   LEU A 608    -8.251   6.069  -0.661  1.00  0.00
ATOM  1411  CA  LEU A 608    -7.589   6.185   0.626  1.00  0.00
ATOM  1412  C   LEU A 608    -7.499   7.666   1.051  1.00  0.00
ATOM  1413  O   LEU A 608    -7.854   8.037   2.161  1.00  0.00
ATOM  1414  CB  LEU A 608    -6.231   5.473   0.480  1.00  0.00
ATOM  1415  CG  LEU A 608    -5.341   5.404   1.730  1.00  0.00
ATOM  1416  CD1 LEU A 608    -4.488   6.666   1.889  1.00  0.00
ATOM  1417  CD2 LEU A 608    -6.131   5.062   3.000  1.00  0.00
ATOM  1418  HN  LEU A 608    -7.785   5.630  -1.434  1.00  0.00
ATOM  1419  HA  LEU A 608    -8.219   5.663   1.348  1.00  0.00
ATOM  1420 1HB  LEU A 608    -5.662   5.906  -0.342  1.00  0.00
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ATOM  1421 2HB  LEU A 608    -6.446  4.453  0.166 1.00 0.00
ATOM  1422  HG  LEU A 608    -4.638  4.586  1.562 1.00 0.00
ATOM  1423 1HD1 LEU A 608    -3.936  6.889  0.977 1.00 0.00
ATOM  1424 2HD1 LEU A 608    -3.758  6.534  2.684 1.00 0.00
ATOM  1425 3HD1 LEU A 608    -5.087  7.542  2.119 1.00 0.00
ATOM  1426 1HD2 LEU A 608    -5.464  4.811  3.825 1.00 0.00
ATOM  1427 2HD2 LEU A 608    -6.776  4.201  2.829 1.00 0.00
ATOM  1428 3HD2 LEU A 608    -6.760  5.891  3.325 1.00 0.00
ATOM  1429  N   GLY A 609    -7.042  8.497  0.093 1.00 0.00
ATOM  1430  CA  GLY A 609    -6.823  9.887  0.364 1.00 0.00
ATOM  1431  C   GLY A 609    -8.130 10.530  0.702 1.00 0.00
ATOM  1432  O   GLY A 609    -8.225 11.332  1.631 1.00 0.00
ATOM  1433  HN  GLY A 609    -6.813  8.122 -0.806 1.00 0.00
ATOM  1434 1HA  GLY A 609    -6.401 10.344 -0.530 1.00 0.00
ATOM  1435 2HA  GLY A 609    -6.138  9.963  1.208 1.00 0.00
ATOM  1436  N   TRP A 610    -9.180 10.177 -0.058 1.00 0.00
ATOM  1437  CA  TRP A 610   -10.495 10.719  0.121 1.00 0.00
ATOM  1438  C   TRP A 610   -11.037 10.406  1.478 1.00 0.00
ATOM  1439  O   TRP A 610   -11.582 11.277  2.154 1.00 0.00
ATOM  1440  CB  TRP A 610   -11.473 10.139 -0.913 1.00 0.00
ATOM  1441  CG  TRP A 610   -12.929 10.398 -0.623 1.00 0.00
ATOM  1442  CD1 TRP A 610   -13.862  9.539 -0.122 1.00 0.00
ATOM  1443  CD2 TRP A 610   -13.576 11.671 -0.753 1.00 0.00
ATOM  1444  NE1 TRP A 610   -15.063 10.187  0.033 1.00 0.00
ATOM  1445  CE2 TRP A 610   -14.899 11.503 -0.345 1.00 0.00
ATOM  1446  CE3 TRP A 610   -13.106 12.882 -1.173 1.00 0.00
ATOM  1447  CZ2 TRP A 610   -15.777 12.548 -0.356 1.00 0.00
ATOM  1448  CZ3 TRP A 610   -13.993 13.934 -1.180 1.00 0.00
ATOM  1449  CH2 TRP A 610   -15.303 13.769 -0.781 1.00 0.00
ATOM  1450  HN  TRP A 610    -9.037  9.503 -0.783 1.00 0.00
ATOM  1451  HA  TRP A 610   -10.415 11.800  0.008 1.00 0.00
ATOM  1452 1HB  TRP A 610   -11.331  9.060 -0.961 1.00 0.00
ATOM  1453 2HB  TRP A 610   -11.246 10.569 -1.887 1.00 0.00
ATOM  1454  HE3 TRP A 610   -12.080 13.008 -1.487 1.00 0.00
ATOM  1455  HD1 TRP A 610   -13.682  8.502  0.119 1.00 0.00
ATOM  1456  HE1 TRP A 610   -15.894  9.783  0.357 1.00 0.00
ATOM  1457  HZ2 TRP A 610   -16.803 12.422 -0.044 1.00 0.00
ATOM  1458  HZ3 TRP A 610   -13.657 14.907 -1.504 1.00 0.00
ATOM  1459  HH2 TRP A 610   -15.971 14.617 -0.802 1.00 0.00
ATOM  1460  N   ARG A 611   -10.908  9.137  1.904 1.00 0.00
ATOM  1461  CA  ARG A 611   -11.485  8.823  3.212 1.00 0.00
ATOM  1462  C   ARG A 611   -10.630  9.382  4.363 1.00 0.00
ATOM  1463  O   ARG A 611   -11.108  9.620  5.463 1.00 0.00
ATOM  1464  CB  ARG A 611   -11.704  7.323  3.367 1.00 0.00
ATOM  1465  CG  ARG A 611   -12.850  6.806  2.484 1.00 0.00
ATOM  1466  CD  ARG A 611   -13.346  5.416  2.901 1.00 0.00
ATOM  1467  NE  ARG A 611   -12.276  4.442  2.750 1.00 0.00
ATOM  1468  CZ  ARG A 611   -11.360  4.161  3.704 1.00 0.00
ATOM  1469 NH1 ARG A 611   -11.429  4.663  4.939 1.00 0.00
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ATOM  1470 NH2 ARG A 611   -10.349  3.373  3.370 1.00 0.00
ATOM  1471 HN  ARG A 611   -10.461  8.449  1.327 1.00 0.00
ATOM  1472 HA  ARG A 611   -12.458  9.315  3.274 1.00 0.00
ATOM  1473 1HB ARG A 611   -11.960  7.134  4.408 1.00 0.00
ATOM  1474 2HB ARG A 611   -10.775  6.791  3.162 1.00 0.00
ATOM  1475 1HG ARG A 611   -12.533  6.795  1.440 1.00 0.00
ATOM  1476 2HG ARG A 611   -13.693  7.495  2.541 1.00 0.00
ATOM  1477 1HD ARG A 611   -14.154  5.084  2.248 1.00 0.00
ATOM  1478 2HD ARG A 611   -13.724  5.389  3.923 1.00 0.00
ATOM  1479 HE  ARG A 611   -12.203  4.016  1.848 1.00 0.00
ATOM  1480 1HH1 ARG A 611  -12.239  5.161  5.293 1.00 0.00
ATOM  1481 2HH1 ARG A 611  -10.631  4.578  5.546 1.00 0.00
ATOM  1482 1HH2 ARG A 611   -9.738  2.982  4.066 1.00 0.00
ATOM  1483 2HH2 ARG A 611  -10.158  3.134  2.412 1.00 0.00
ATOM  1484 N   SER A 612    -9.356  9.624  4.043 1.00 0.00
ATOM  1485 CA  SER A 612    -8.434 10.203  4.984 1.00 0.00
ATOM  1486 C   SER A 612    -8.651 11.664  5.221 1.00 0.00
ATOM  1487 O   SER A 612    -8.081 12.237  6.147 1.00 0.00
ATOM  1488 CB  SER A 612    -6.965 10.024  4.572 1.00 0.00
ATOM  1489 OG  SER A 612    -6.605  8.656  4.662 1.00 0.00
ATOM  1490 HN  SER A 612    -9.005  9.410  3.133 1.00 0.00
ATOM  1491 HA  SER A 612    -8.617  9.712  5.940 1.00 0.00
ATOM  1492 1HB SER A 612    -6.313 10.595  5.233 1.00 0.00
ATOM  1493 2HB SER A 612    -6.817 10.351  3.543 1.00 0.00
ATOM  1494 HG  SER A 612    -5.753  8.571  4.254 1.00 0.00
ATOM  1495 N   TYR A 613    -9.470 12.302  4.372 1.00 0.00
ATOM  1496 CA  TYR A 613    -9.629 13.727  4.326 1.00 0.00
ATOM  1497 C   TYR A 613    -9.847 14.349  5.675 1.00 0.00
ATOM  1498 O   TYR A 613    -9.040 15.171  6.102 1.00 0.00
ATOM  1499 CB  TYR A 613   -10.852 14.052  3.449 1.00 0.00
ATOM  1500 CG  TYR A 613   -10.984 15.506  3.166 1.00 0.00
ATOM  1501 CD1 TYR A 613   -11.417 16.382  4.134 1.00 0.00
ATOM  1502 CD2 TYR A 613   -10.952 15.928  1.857 1.00 0.00
ATOM  1503 CE1 TYR A 613   -11.756 17.674  3.804 1.00 0.00
ATOM  1504 CE2 TYR A 613   -11.302 17.211  1.518 1.00 0.00
ATOM  1505 CZ  TYR A 613   -11.707 18.087  2.494 1.00 0.00
ATOM  1506 OH  TYR A 613   -12.108 19.393  2.145 1.00 0.00
ATOM  1507 HN  TYR A 613   -10.002 11.750  3.732 1.00 0.00
ATOM  1508 HA  TYR A 613    -8.718 14.150  3.903 1.00 0.00
ATOM  1509 1HB TYR A 613   -11.757 13.718  3.955 1.00 0.00
ATOM  1510 2HB TYR A 613   -10.763 13.525  2.499 1.00 0.00
ATOM  1511 HD1 TYR A 613   -11.492 16.053  5.160 1.00 0.00
ATOM  1512 HE1 TYR A 613   -12.060 18.366  4.576 1.00 0.00
ATOM  1513 HD2 TYR A 613   -10.647 15.238  1.084 1.00 0.00
ATOM  1514 HE2 TYR A 613   -11.260 17.530  0.487 1.00 0.00
ATOM  1515 HH  TYR A 613   -11.566 20.023  2.601 1.00 0.00
ATOM  1516 N   ARG A 614   -10.901 13.979  6.422 1.00 0.00
ATOM  1517 CA  ARG A 614   -11.083 14.637  7.689 1.00 0.00
ATOM  1518 C   ARG A 614   -10.061 14.304  8.732 1.00 0.00
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ATOM 1519 O ARG A 614 -9.739 15.139 9.577 1.00 0.00
ATOM 1520 CB ARG A 614 -12.507 14.538 8.277 1.00 0.00
ATOM 1521 CG ARG A 614 -13.137 13.148 8.278 1.00 0.00
ATOM 1522 CD ARG A 614 -12.266 12.021 8.819 1.00 0.00
ATOM 1523 NE ARG A 614 -13.095 10.787 8.732 1.00 0.00
ATOM 1524 CZ ARG A 614 -13.441 10.285 7.509 1.00 0.00
ATOM 1525 NH1 ARG A 614 -13.181 11.003 6.378 1.00 0.00
ATOM 1526 NH2 ARG A 614 -14.083 9.085 7.418 1.00 0.00
ATOM 1527 HN ARG A 614 -11.535 13.273 6.108 1.00 0.00
ATOM 1528 HA ARG A 614 -10.827 15.683 7.525 1.00 0.00
ATOM 1529 1HB ARG A 614 -13.154 15.201 7.705 1.00 0.00
ATOM 1530 2HB ARG A 614 -12.472 14.894 9.305 1.00 0.00
ATOM 1531 1HG ARG A 614 -13.411 12.900 7.255 1.00 0.00
ATOM 1532 2HG ARG A 614 -14.045 13.190 8.878 1.00 0.00
ATOM 1533 1HD ARG A 614 -11.998 12.183 9.862 1.00 0.00
ATOM 1534 2HD ARG A 614 -11.371 11.878 8.215 1.00 0.00
ATOM 1535 HE ARG A 614 -13.400 10.327 9.566 1.00 0.00
ATOM 1536 1HH1 ARG A 614 -12.608 11.822 6.425 1.00 0.00
ATOM 1537 2HH1 ARG A 614 -13.563 10.711 5.501 1.00 0.00
ATOM 1538 1HH2 ARG A 614 -14.302 8.571 8.247 1.00 0.00
ATOM 1539 2HH2 ARG A 614 -14.335 8.719 6.522 1.00 0.00
ATOM 1540 N GLN A 615 -9.518 13.078 8.712 1.00 0.00
ATOM 1541 CA GLN A 615 -8.577 12.675 9.719 1.00 0.00
ATOM 1542 C GLN A 615 -7.221 13.187 9.341 1.00 0.00
ATOM 1543 O GLN A 615 -6.452 12.503 8.664 1.00 0.00
ATOM 1544 CB GLN A 615 -8.505 11.148 9.800 1.00 0.00
ATOM 1545 CG GLN A 615 -9.842 10.488 10.155 1.00 0.00
ATOM 1546 CD GLN A 615 -10.217 10.878 11.579 1.00 0.00
ATOM 1547 OE1 GLN A 615 -9.475 11.575 12.269 1.00 0.00
ATOM 1548 NE2 GLN A 615 -11.411 10.413 12.035 1.00 0.00
ATOM 1549 HN GLN A 615 -9.771 12.437 7.987 1.00 0.00
ATOM 1550 HA GLN A 615 -8.916 13.095 10.666 1.00 0.00
ATOM 1551 1HB GLN A 615 -7.768 10.872 10.553 1.00 0.00
ATOM 1552 2HB GLN A 615 -8.171 10.763 8.837 1.00 0.00
ATOM 1553 1HG GLN A 615 -9.759 9.403 10.093 1.00 0.00
ATOM 1554 2HG GLN A 615 -10.624 10.826 9.475 1.00 0.00
ATOM 1555 1HE2 GLN A 615 -11.913 9.731 11.502 1.00 0.00
ATOM 1556 2HE2 GLN A 615 -11.800 10.740 12.895 1.00 0.00
ATOM 1557 N SER A 616 -6.865 14.393 9.825 1.00 0.00
ATOM 1558 CA SER A 616 -5.661 15.027 9.371 1.00 0.00
ATOM 1559 C SER A 616 -4.431 14.879 10.213 1.00 0.00
ATOM 1560 O SER A 616 -4.477 14.649 11.421 1.00 0.00
ATOM 1561 CB SER A 616 -5.840 16.541 9.163 1.00 0.00
ATOM 1562 OG SER A 616 -4.622 17.122 8.721 1.00 0.00
ATOM 1563 HN SER A 616 -7.443 14.848 10.504 1.00 0.00
ATOM 1564 HA SER A 616 -5.388 14.547 8.432 1.00 0.00
ATOM 1565 1HB SER A 616 -6.127 17.020 10.099 1.00 0.00
ATOM 1566 2HB SER A 616 -6.603 16.731 8.407 1.00 0.00
ATOM 1567 HG SER A 616 -4.480 16.816 7.835 1.00 0.00

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ATOM  1568 N   SER A 617   -3.286 14.953  9.504 1.00 0.00
ATOM  1569 CA  SER A 617   -1.945 15.132  9.987 1.00 0.00
ATOM  1570 C   SER A 617   -1.302 14.020 10.728 1.00 0.00
ATOM  1571 O   SER A 617   -0.091 13.825 10.625 1.00 0.00
ATOM  1572 CB  SER A 617   -1.804 16.386 10.867 1.00 0.00
ATOM  1573 OG  SER A 617   -2.536 16.222 12.072 1.00 0.00
ATOM  1574 HN  SER A 617   -3.383 14.873  8.515 1.00 0.00
ATOM  1575 HA  SER A 617   -1.303 15.212  9.110 1.00 0.00
ATOM  1576 1HB SER A 617   -2.195 17.260 10.346 1.00 0.00
ATOM  1577 2HB SER A 617   -0.757 16.553 11.123 1.00 0.00
ATOM  1578 HG  SER A 617   -2.282 15.383 12.433 1.00 0.00
ATOM  1579 N   ALA A 618   -2.055 13.181 11.440 1.00 0.00
ATOM  1580 CA  ALA A 618   -1.297 12.170 12.109 1.00 0.00
ATOM  1581 C   ALA A 618   -1.203 11.075 11.117 1.00 0.00
ATOM  1582 O   ALA A 618   -1.451  9.937 11.510 1.00 0.00
ATOM  1583 CB  ALA A 618   -2.014 11.587 13.336 1.00 0.00
ATOM  1584 HN  ALA A 618   -3.048 13.253 11.500 1.00 0.00
ATOM  1585 HA  ALA A 618   -0.359 12.634 12.411 1.00 0.00
ATOM  1586 1HB ALA A 618   -2.962 11.133 13.049 1.00 0.00
ATOM  1587 2HB ALA A 618   -2.222 12.375 14.060 1.00 0.00
ATOM  1588 3HB ALA A 618   -1.398 10.816 13.800 1.00 0.00
ATOM  1589 N   ASN A 619   -0.796 11.421  9.859 1.00 0.00
ATOM  1590 CA  ASN A 619   -0.825 10.611  8.670 1.00 0.00
ATOM  1591 C   ASN A 619   -2.027  9.830  8.892 1.00 0.00
ATOM  1592 O   ASN A 619   -1.981  8.604  8.928 1.00 0.00
ATOM  1593 CB  ASN A 619    0.358  9.664  8.464 1.00 0.00
ATOM  1594 CG  ASN A 619    0.176  8.729  7.272 1.00 0.00
ATOM  1595 OD1 ASN A 619    0.496  7.545  7.372 1.00 0.00
ATOM  1596 ND2 ASN A 619   -0.308  9.261  6.121 1.00 0.00
ATOM  1597 HN  ASN A 619   -0.437 12.346  9.753 1.00 0.00
ATOM  1598 HA  ASN A 619   -0.872 11.312  7.837 1.00 0.00
ATOM  1599 1HB ASN A 619    0.487  9.051  9.355 1.00 0.00
ATOM  1600 2HB ASN A 619    1.262 10.248  8.298 1.00 0.00
ATOM  1601 1HD2 ASN A 619   -0.165  8.782  5.255 1.00 0.00
ATOM  1602 2HD2 ASN A 619   -0.808 10.126  6.121 1.00 0.00
ATOM  1603 N   LEU A 620   -3.132 10.545  9.137 1.00 0.00
ATOM  1604 CA  LEU A 620   -4.225  9.747  9.520 1.00 0.00
ATOM  1605 C   LEU A 620   -4.730  9.261  8.225 1.00 0.00
ATOM  1606 O   LEU A 620   -5.412  9.965  7.478 1.00 0.00
ATOM  1607 CB  LEU A 620   -5.288 10.498 10.341 1.00 0.00
ATOM  1608 CG  LEU A 620   -6.190  9.548 11.155 1.00 0.00
ATOM  1609 CD1 LEU A 620   -7.024 10.322 12.191 1.00 0.00
ATOM  1610 CD2 LEU A 620   -7.029  8.637 10.242 1.00 0.00
ATOM  1611 HN  LEU A 620   -3.174 11.538  9.056 1.00 0.00
ATOM  1612 HA  LEU A 620   -3.815  8.927 10.108 1.00 0.00
ATOM  1613 1HB LEU A 620   -5.910 11.082  9.664 1.00 0.00
ATOM  1614 2HB LEU A 620   -4.789 11.183 11.024 1.00 0.00
ATOM  1615 HG  LEU A 620   -5.570  8.814 11.667 1.00 0.00
ATOM  1616 1HD1 LEU A 620   -6.943 11.397 12.025 1.00 0.00
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ATOM  1617 2HD1 LEU A 620    -6.666  10.109  13.198  1.00  0.00
ATOM  1618 3HD1 LEU A 620    -8.075  10.047  12.110  1.00  0.00
ATOM  1619 1HD2 LEU A 620    -6.433   7.798   9.883  1.00  0.00
ATOM  1620 2HD2 LEU A 620    -7.383   9.195   9.376  1.00  0.00
ATOM  1621 3HD2 LEU A 620    -7.880   8.235  10.792  1.00  0.00
ATOM  1622  N  LEU A 621     -4.250   8.020   7.935  1.00  0.00
ATOM  1623  CA LEU A 621     -4.711   7.307   6.773  1.00  0.00
ATOM  1624  C  LEU A 621     -5.670   6.299   7.278  1.00  0.00
ATOM  1625  O  LEU A 621     -5.333   5.304   7.915  1.00  0.00
ATOM  1626  CB LEU A 621     -3.721   6.649   5.792  1.00  0.00
ATOM  1627  CG LEU A 621     -2.520   7.497   5.409  1.00  0.00
ATOM  1628  CD1 LEU A 621     -1.471   6.654   4.663  1.00  0.00
ATOM  1629  CD2 LEU A 621     -2.900   8.754   4.603  1.00  0.00
ATOM  1630  HN  LEU A 621     -3.596   7.614   8.584  1.00  0.00
ATOM  1631  HA  LEU A 621     -5.268   8.045   6.264  1.00  0.00
ATOM  1632 1HB  LEU A 621     -4.261   6.377   4.887  1.00  0.00
ATOM  1633 2HB  LEU A 621     -3.363   5.699   6.173  1.00  0.00
ATOM  1634  HG LEU A 621     -2.110   7.785   6.370  1.00  0.00
ATOM  1635 1HD1 LEU A 621     -1.902   6.153   3.797  1.00  0.00
ATOM  1636 2HD1 LEU A 621     -1.059   5.885   5.317  1.00  0.00
ATOM  1637 3HD1 LEU A 621     -0.638   7.255   4.304  1.00  0.00
ATOM  1638 1HD2 LEU A 621     -3.553   9.411   5.177  1.00  0.00
ATOM  1639 2HD2 LEU A 621     -3.386   8.494   3.666  1.00  0.00
ATOM  1640 3HD2 LEU A 621     -2.029   9.340   4.318  1.00  0.00
ATOM  1641  N  CYS A 622     -6.921   6.628   6.985  1.00  0.00
ATOM  1642  CA CYS A 622     -7.895   5.726   7.488  1.00  0.00
ATOM  1643  C  CYS A 622     -7.990   4.641   6.469  1.00  0.00
ATOM  1644  O  CYS A 622     -8.809   4.706   5.555  1.00  0.00
ATOM  1645  CB CYS A 622     -9.280   6.384   7.620  1.00  0.00
ATOM  1646  SG CYS A 622    -10.556   5.264   8.264  1.00  0.00
ATOM  1647  HN CYS A 622     -7.194   7.414   6.431  1.00  0.00
ATOM  1648  HA CYS A 622     -7.541   5.391   8.463  1.00  0.00
ATOM  1649 1HB CYS A 622     -9.601   6.735   6.640  1.00  0.00
ATOM  1650 2HB CYS A 622     -9.206   7.236   8.294  1.00  0.00
ATOM  1651  HG CYS A 622    -10.037   4.510   9.236  1.00  0.00
ATOM  1652  N  PHE A 623     -7.120   3.616   6.603  1.00  0.00
ATOM  1653  CA PHE A 623     -7.232   2.532   5.627  1.00  0.00
ATOM  1654  C  PHE A 623     -8.592   1.854   5.778  1.00  0.00
ATOM  1655  O  PHE A 623     -9.217   1.491   4.790  1.00  0.00
ATOM  1656  CB PHE A 623     -6.106   1.494   5.696  1.00  0.00
ATOM  1657  CG PHE A 623     -4.839   1.984   5.052  1.00  0.00
ATOM  1658  CD1 PHE A 623     -3.876   2.685   5.771  1.00  0.00
ATOM  1659  CD2 PHE A 623     -4.619   1.727   3.704  1.00  0.00
ATOM  1660  CE1 PHE A 623     -2.708   3.107   5.147  1.00  0.00
ATOM  1661  CE2 PHE A 623     -3.457   2.152   3.080  1.00  0.00
ATOM  1662  CZ  PHE A 623     -2.497   2.843   3.801  1.00  0.00
ATOM  1663  HN  PHE A 623     -6.464   3.646   7.361  1.00  0.00
ATOM  1664  HA  PHE A 623     -7.218   2.992   4.638  1.00  0.00
ATOM  1665 1HB  PHE A 623     -6.416   0.606   5.143  1.00  0.00
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ATOM  1666 2HB  PHE A 623    -5.923   1.144   6.704  1.00  0.00
ATOM  1667  HD1 PHE A 623    -4.032   2.911   6.817  1.00  0.00
ATOM  1668  HD2 PHE A 623    -5.362   1.190   3.135  1.00  0.00
ATOM  1669  HE1 PHE A 623    -1.954   3.639   5.703  1.00  0.00
ATOM  1670  HE2 PHE A 623    -3.306   1.942   2.035  1.00  0.00
ATOM  1671  HZ  PHE A 623    -1.590   3.174   3.318  1.00  0.00
ATOM  1672  N   ALA A 624    -9.041   1.779   7.044  1.00  0.00
ATOM  1673  CA  ALA A 624   -10.350   1.267   7.317  1.00  0.00
ATOM  1674  C   ALA A 624   -10.855   2.038   8.493  1.00  0.00
ATOM  1675  O   ALA A 624   -10.065   2.613   9.241  1.00  0.00
ATOM  1676  CB  ALA A 624   -10.355  -0.217   7.721  1.00  0.00
ATOM  1677  HN  ALA A 624    -8.434   1.998   7.809  1.00  0.00
ATOM  1678  HA  ALA A 624   -10.933   1.407   6.407  1.00  0.00
ATOM  1679 1HB  ALA A 624   -10.609  -0.329   8.775  1.00  0.00
ATOM  1680 2HB  ALA A 624    -9.368  -0.653   7.564  1.00  0.00
ATOM  1681 3HB  ALA A 624   -11.094  -0.764   7.136  1.00  0.00
ATOM  1682  N   PRO A 625   -12.151   2.098   8.664  1.00  0.00
ATOM  1683  CA  PRO A 625   -12.727   2.784   9.789  1.00  0.00
ATOM  1684  C   PRO A 625   -12.116   2.154  10.996  1.00  0.00
ATOM  1685  O   PRO A 625   -11.963   2.805  12.029  1.00  0.00
ATOM  1686  CB  PRO A 625   -14.224   2.503   9.706  1.00  0.00
ATOM  1687  CG  PRO A 625   -14.283   1.125   9.020  1.00  0.00
ATOM  1688  CD  PRO A 625   -13.055   1.114   8.094  1.00  0.00
ATOM  1689 1HD  PRO A 625   -12.583   0.132   8.076  1.00  0.00
ATOM  1690 2HD  PRO A 625   -13.327   1.393   7.076  1.00  0.00
ATOM  1691  HA  PRO A 625   -12.524   3.853   9.724  1.00  0.00
ATOM  1692 1HB  PRO A 625   -14.739   3.261   9.117  1.00  0.00
ATOM  1693 2HB  PRO A 625   -14.679   2.473  10.696  1.00  0.00
ATOM  1694 1HG  PRO A 625   -14.230   0.320   9.753  1.00  0.00
ATOM  1695 2HG  PRO A 625   -15.205   1.009   8.452  1.00  0.00
ATOM  1696  N   ASP A 626   -11.833   0.854  10.863  1.00  0.00
ATOM  1697  CA  ASP A 626   -11.223  -0.014  11.814  1.00  0.00
ATOM  1698  C   ASP A 626    -9.743   0.240  11.957  1.00  0.00
ATOM  1699  O   ASP A 626    -9.180   0.039  13.029  1.00  0.00
ATOM  1700  CB  ASP A 626   -11.465  -1.471  11.380  1.00  0.00
ATOM  1701  CG  ASP A 626   -10.953  -2.418  12.437  1.00  0.00
ATOM  1702  OD1 ASP A 626    -9.716  -2.411  12.662  1.00  0.00
ATOM  1703  OD2 ASP A 626   -11.780  -3.159  13.032  1.00  0.00
ATOM  1704  HN  ASP A 626   -12.081   0.441   9.989  1.00  0.00
ATOM  1705  HA  ASP A 626   -11.677   0.186  12.785  1.00  0.00
ATOM  1706 1HB  ASP A 626   -10.944  -1.674  10.445  1.00  0.00
ATOM  1707 2HB  ASP A 626   -12.532  -1.647  11.239  1.00  0.00
ATOM  1708  N   LEU A 627    -9.066   0.665  10.865  1.00  0.00
ATOM  1709  CA  LEU A 627    -7.633   0.818  10.880  1.00  0.00
ATOM  1710  C   LEU A 627    -7.271   2.255  10.627  1.00  0.00
ATOM  1711  O   LEU A 627    -7.550   2.793   9.558  1.00  0.00
ATOM  1712  CB  LEU A 627    -7.009  -0.060   9.768  1.00  0.00
ATOM  1713  CG  LEU A 627    -5.475  -0.052   9.587  1.00  0.00
ATOM  1714  CD1 LEU A 627    -4.957   1.295   9.077  1.00  0.00
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ATOM 1715 CD2 LEU A 627 -4.745 -0.561 10.841 1.00 0.00
ATOM 1716 HN LEU A 627 -9.573 0.878 10.029 1.00 0.00
ATOM 1717 HA LEU A 627 -7.280 0.508 11.864 1.00 0.00
ATOM 1718 1HB LEU A 627 -7.448 0.254 8.824 1.00 0.00
ATOM 1719 2HB LEU A 627 -7.306 -1.088 9.963 1.00 0.00
ATOM 1720 HG LEU A 627 -5.197 -0.831 8.878 1.00 0.00
ATOM 1721 1HD1 LEU A 627 -4.551 1.887 9.897 1.00 0.00
ATOM 1722 2HD1 LEU A 627 -5.768 1.862 8.621 1.00 0.00
ATOM 1723 3HD1 LEU A 627 -4.163 1.140 8.347 1.00 0.00
ATOM 1724 1HD2 LEU A 627 -5.167 -1.509 11.174 1.00 0.00
ATOM 1725 2HD2 LEU A 627 -4.846 0.158 11.653 1.00 0.00
ATOM 1726 3HD2 LEU A 627 -3.689 -0.721 10.622 1.00 0.00
ATOM 1727 N ILE A 628 -6.627 2.909 11.619 1.00 0.00
ATOM 1728 CA ILE A 628 -6.196 4.272 11.489 1.00 0.00
ATOM 1729 C ILE A 628 -4.708 4.248 11.691 1.00 0.00
ATOM 1730 O ILE A 628 -4.206 3.906 12.759 1.00 0.00
ATOM 1731 CB ILE A 628 -6.840 5.162 12.519 1.00 0.00
ATOM 1732 CG1 ILE A 628 -6.414 6.624 12.342 1.00 0.00
ATOM 1733 CG2 ILE A 628 -6.587 4.587 13.923 1.00 0.00
ATOM 1734 CD1 ILE A 628 -7.235 7.570 13.214 1.00 0.00
ATOM 1735 HN ILE A 628 -6.445 2.426 12.474 1.00 0.00
ATOM 1736 HA ILE A 628 -6.467 4.596 10.485 1.00 0.00
ATOM 1737 HB ILE A 628 -7.912 5.225 12.334 1.00 0.00
ATOM 1738 1HG2 ILE A 628 -5.586 4.844 14.270 1.00 0.00
ATOM 1739 2HG2 ILE A 628 -6.669 3.500 13.904 1.00 0.00
ATOM 1740 3HG2 ILE A 628 -7.305 4.997 14.633 1.00 0.00
ATOM 1741 1HG1 ILE A 628 -6.534 6.906 11.297 1.00 0.00
ATOM 1742 2HG1 ILE A 628 -5.361 6.722 12.604 1.00 0.00
ATOM 1743 1HD1 ILE A 628 -7.708 7.028 14.033 1.00 0.00
ATOM 1744 2HD1 ILE A 628 -8.022 8.039 12.622 1.00 0.00
ATOM 1745 3HD1 ILE A 628 -6.593 8.338 13.644 1.00 0.00
ATOM 1746 N ILE A 629 -3.950 4.627 10.651 1.00 0.00
ATOM 1747 CA ILE A 629 -2.526 4.519 10.716 1.00 0.00
ATOM 1748 C ILE A 629 -2.067 5.921 10.908 1.00 0.00
ATOM 1749 O ILE A 629 -2.791 6.847 10.547 1.00 0.00
ATOM 1750 CB ILE A 629 -2.017 3.951 9.416 1.00 0.00
ATOM 1751 CG1 ILE A 629 -0.621 3.322 9.516 1.00 0.00
ATOM 1752 CG2 ILE A 629 -2.118 5.071 8.367 1.00 0.00
ATOM 1753 CD1 ILE A 629 0.507 4.329 9.632 1.00 0.00
ATOM 1754 HN ILE A 629 -4.384 4.987 9.826 1.00 0.00
ATOM 1755 HA ILE A 629 -2.282 3.862 11.551 1.00 0.00
ATOM 1756 HB ILE A 629 -2.617 3.092 9.115 1.00 0.00
ATOM 1757 1HG2 ILE A 629 -1.666 5.990 8.740 1.00 0.00
ATOM 1758 2HG2 ILE A 629 -3.164 5.279 8.139 1.00 0.00
ATOM 1759 3HG2 ILE A 629 -1.594 4.783 7.456 1.00 0.00
ATOM 1760 1HG1 ILE A 629 -0.451 2.712 8.629 1.00 0.00
ATOM 1761 2HG1 ILE A 629 -0.596 2.671 10.389 1.00 0.00
ATOM 1762 1HD1 ILE A 629 0.483 4.823 10.604 1.00 0.00
ATOM 1763 2HD1 ILE A 629 0.409 5.095 8.862 1.00 0.00

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ATOM  1764 3HD1 ILE A 629     1.470  3.829  9.532 1.00 0.00
ATOM  1765  N  ASN A 630     -0.885  6.114 11.532 1.00 0.00
ATOM  1766  CA  ASN A 630    -0.400  7.444 11.749 1.00 0.00
ATOM  1767  C  ASN A 630     0.924  7.601 11.071 1.00 0.00
ATOM  1768  O  ASN A 630     1.551  6.630 10.661 1.00 0.00
ATOM  1769  CB  ASN A 630    -0.253  7.854 13.235 1.00 0.00
ATOM  1770  CG  ASN A 630     0.838  7.047 13.930 1.00 0.00
ATOM  1771  OD1 ASN A 630     1.458  6.163 13.344 1.00 0.00
ATOM  1772  ND2 ASN A 630     1.082  7.357 15.231 1.00 0.00
ATOM  1773  HN  ASN A 630    -0.349  5.328 11.841 1.00 0.00
ATOM  1774  HA  ASN A 630    -1.110  8.108 11.256 1.00 0.00
ATOM  1775 1HB  ASN A 630    -1.194  7.683 13.759 1.00 0.00
ATOM  1776 2HB  ASN A 630     0.006  8.910 13.302 1.00 0.00
ATOM  1777 1HD2 ASN A 630     1.675  6.766 15.779 1.00 0.00
ATOM  1778 2HD2 ASN A 630     0.680  8.168 15.655 1.00 0.00
ATOM  1779  N  GLU A 631     1.406  8.849 10.956 1.00 0.00
ATOM  1780  CA  GLU A 631    2.599  9.081 10.196 1.00 0.00
ATOM  1781  C  GLU A 631     3.753  8.273 10.685 1.00 0.00
ATOM  1782  O  GLU A 631     4.423  7.610  9.898 1.00 0.00
ATOM  1783  CB  GLU A 631    2.986 10.570 10.200 1.00 0.00
ATOM  1784  CG  GLU A 631    4.040 10.927  9.155 1.00 0.00
ATOM  1785  CD  GLU A 631    3.969 12.424  8.908 1.00 0.00
ATOM  1786  OE1 GLU A 631    4.594 12.887  7.918 1.00 0.00
ATOM  1787  OE2 GLU A 631    3.280 13.124  9.698 1.00 0.00
ATOM  1788  HN  GLU A 631     0.934  9.612 11.398 1.00 0.00
ATOM  1789  HA  GLU A 631     2.402  8.742  9.179 1.00 0.00
ATOM  1790 1HB  GLU A 631     3.370 10.829 11.185 1.00 0.00
ATOM  1791 2HB  GLU A 631     2.093 11.164 10.013 1.00 0.00
ATOM  1792 1HG  GLU A 631     3.847 10.399  8.221 1.00 0.00
ATOM  1793 2HG  GLU A 631     5.036 10.667  9.511 1.00 0.00
ATOM  1794  N  GLN A 632     3.989  8.256 12.002 1.00 0.00
ATOM  1795  CA  GLN A 632    5.122  7.551 12.527 1.00 0.00
ATOM  1796  C  GLN A 632     5.005  6.083 12.267 1.00 0.00
ATOM  1797  O  GLN A 632     6.003  5.400 12.040 1.00 0.00
ATOM  1798  CB  GLN A 632    5.289  7.747 14.043 1.00 0.00
ATOM  1799  CG  GLN A 632    5.656  9.183 14.423 1.00 0.00
ATOM  1800  CD  GLN A 632    5.770  9.271 15.938 1.00 0.00
ATOM  1801  OE1 GLN A 632    5.297 10.231 16.543 1.00 0.00
ATOM  1802  NE2 GLN A 632    6.417  8.255 16.568 1.00 0.00
ATOM  1803  HN  GLN A 632     3.371  8.738 12.623 1.00 0.00
ATOM  1804  HA  GLN A 632     5.998  7.930 12.000 1.00 0.00
ATOM  1805 1HB  GLN A 632     6.071  7.077 14.400 1.00 0.00
ATOM  1806 2HB  GLN A 632     4.357  7.478 14.538 1.00 0.00
ATOM  1807 1HG  GLN A 632     4.886  9.875 14.081 1.00 0.00
ATOM  1808 2HG  GLN A 632     6.610  9.463 13.975 1.00 0.00
ATOM  1809 1HE2 GLN A 632     6.919  7.578 16.030 1.00 0.00
ATOM  1810 2HE2 GLN A 632     6.402  8.170 17.564 1.00 0.00
ATOM  1811  N  ARG A 633     3.764  5.568 12.261 1.00 0.00
ATOM  1812  CA  ARG A 633    3.523  4.160 12.139 1.00 0.00
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ATOM  1813  C   ARG A 633      4.131   3.680  10.869  1.00  0.00
ATOM  1814  O   ARG A 633      4.547   2.529  10.774  1.00  0.00
ATOM  1815  CB  ARG A 633      2.030   3.797  12.093  1.00  0.00
ATOM  1816  CG  ARG A 633      1.725   2.310  12.292  1.00  0.00
ATOM  1817  CD  ARG A 633      1.890   1.851  13.742  1.00  0.00
ATOM  1818  NE  ARG A 633      1.264   2.893  14.605  1.00  0.00
ATOM  1819  CZ  ARG A 633     -0.083   2.891  14.828  1.00  0.00
ATOM  1820  NH1 ARG A 633     -0.871   1.932  14.259  1.00  0.00
ATOM  1821  NH2 ARG A 633     -0.645   3.856  15.614  1.00  0.00
ATOM  1822  HN  ARG A 633      2.984   6.188  12.345  1.00  0.00
ATOM  1823  HA  ARG A 633      3.994   3.689  13.001  1.00  0.00
ATOM  1824 1HB  ARG A 633      1.631   4.103  11.127  1.00  0.00
ATOM  1825 2HB  ARG A 633      1.515   4.361  12.870  1.00  0.00
ATOM  1826 1HG  ARG A 633      2.393   1.727  11.660  1.00  0.00
ATOM  1827 2HG  ARG A 633      0.700   2.117  11.977  1.00  0.00
ATOM  1828 1HD  ARG A 633      2.941   1.769  14.017  1.00  0.00
ATOM  1829 2HD  ARG A 633      1.376   0.907  13.922  1.00  0.00
ATOM  1830  HE  ARG A 633      1.835   3.598  15.025  1.00  0.00
ATOM  1831 1HH1 ARG A 633     -0.461   1.228  13.678  1.00  0.00
ATOM  1832 2HH1 ARG A 633     -1.857   1.932  14.423  1.00  0.00
ATOM  1833 1HH2 ARG A 633     -0.070   4.562  16.027  1.00  0.00
ATOM  1834 2HH2 ARG A 633     -1.631   3.855  15.778  1.00  0.00
ATOM  1835  N   MET A 634      4.194   4.586   9.871  1.00  0.00
ATOM  1836  CA  MET A 634      4.756   4.246   8.570  1.00  0.00
ATOM  1837  C   MET A 634      6.239   3.832   8.629  1.00  0.00
ATOM  1838  O   MET A 634      6.849   3.485   7.623  1.00  0.00
ATOM  1839  CB  MET A 634      4.684   5.489   7.677  1.00  0.00
ATOM  1840  CG  MET A 634      5.822   6.509   7.893  1.00  0.00
ATOM  1841  SD  MET A 634      5.311   8.055   7.121  1.00  0.00
ATOM  1842  CE  MET A 634      6.623   9.183   7.556  1.00  0.00
ATOM  1843  HN  MET A 634      3.844   5.517  10.017  1.00  0.00
ATOM  1844  HA  MET A 634      4.138   3.444   8.169  1.00  0.00
ATOM  1845 1HB  MET A 634      3.717   5.974   7.823  1.00  0.00
ATOM  1846 2HB  MET A 634      4.706   5.183   6.635  1.00  0.00
ATOM  1847 1HG  MET A 634      6.771   6.152   7.508  1.00  0.00
ATOM  1848 2HG  MET A 634      6.077   6.655   8.938  1.00  0.00
ATOM  1849 1HE  MET A 634      7.173   9.429   6.652  1.00  0.00
ATOM  1850 2HE  MET A 634      7.254   8.773   8.343  1.00  0.00
ATOM  1851 3HE  MET A 634      6.206  10.122   7.903  1.00  0.00
ATOM  1852  N   THR A 635      6.805   3.946   9.834  1.00  0.00
ATOM  1853  CA  THR A 635      8.166   3.585  10.197  1.00  0.00
ATOM  1854  C   THR A 635      8.562   2.126  10.015  1.00  0.00
ATOM  1855  O   THR A 635      9.434   1.608  10.711  1.00  0.00
ATOM  1856  CB  THR A 635      8.480   3.949  11.621  1.00  0.00
ATOM  1857  OG1 THR A 635      9.877   3.870  11.867  1.00  0.00
ATOM  1858  CG2 THR A 635      7.724   2.979  12.544  1.00  0.00
ATOM  1859  HN  THR A 635      6.292   4.442  10.530  1.00  0.00
ATOM  1860  HA  THR A 635      8.828   4.118   9.515  1.00  0.00
ATOM  1861  HB  THR A 635      8.158   4.970  11.827  1.00  0.00
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ATOM  1862 HG1 THR A 635    10.134  2.975 11.694 1.00 0.00
ATOM  1863 1HG2 THR A 635    8.151  1.978 12.483 1.00 0.00
ATOM  1864 2HG2 THR A 635    6.677  2.918 12.248 1.00 0.00
ATOM  1865 3HG2 THR A 635    7.794  3.313 13.579 1.00 0.00
ATOM  1866 N  LEU A 636     7.821  1.446  9.104 1.00 0.00
ATOM  1867 CA LEU A 636     8.154  0.172  8.494 1.00 0.00
ATOM  1868 C  LEU A 636     8.817  0.534  7.166 1.00 0.00
ATOM  1869 O  LEU A 636     8.410  0.111  6.097 1.00 0.00
ATOM  1870 CB LEU A 636     6.897 -0.722  8.320 1.00 0.00
ATOM  1871 CG LEU A 636     5.812 -0.400  7.243 1.00 0.00
ATOM  1872 CD1 LEU A 636    5.590  1.062  6.929 1.00 0.00
ATOM  1873 CD2 LEU A 636    5.875 -1.271  5.970 1.00 0.00
ATOM  1874 HN LEU A 636     7.059  1.888  8.645 1.00 0.00
ATOM  1875 HA LEU A 636     8.869 -0.331  9.147 1.00 0.00
ATOM  1876 1HB LEU A 636    6.408 -0.765  9.294 1.00 0.00
ATOM  1877 2HB LEU A 636    7.246 -1.734  8.137 1.00 0.00
ATOM  1878 HG LEU A 636     4.857 -0.636  7.692 1.00 0.00
ATOM  1879 1HD1 LEU A 636   5.311  1.582  7.839 1.00 0.00
ATOM  1880 2HD1 LEU A 636   4.765  1.181  6.233 1.00 0.00
ATOM  1881 3HD1 LEU A 636   6.470  1.511  6.482 1.00 0.00
ATOM  1882 1HD2 LEU A 636   6.080 -2.315  6.206 1.00 0.00
ATOM  1883 2HD2 LEU A 636   6.622 -0.946  5.252 1.00 0.00
ATOM  1884 3HD2 LEU A 636   4.921 -1.241  5.443 1.00 0.00
ATOM  1885 N  PRO A 637     9.812  1.437  7.273 1.00 0.00
ATOM  1886 CA PRO A 637    10.350  2.125  6.111 1.00 0.00
ATOM  1887 C  PRO A 637    10.363  1.662  4.692 1.00 0.00
ATOM  1888 O  PRO A 637    10.335  0.477  4.364 1.00 0.00
ATOM  1889 CB PRO A 637    11.736  2.648  6.492 1.00 0.00
ATOM  1890 CG PRO A 637    12.187  1.711  7.606 1.00 0.00
ATOM  1891 CD PRO A 637    10.867  1.322  8.280 1.00 0.00
ATOM  1892 1HD PRO A 637   10.912  0.298  8.651 1.00 0.00
ATOM  1893 2HD PRO A 637   10.651  1.989  9.115 1.00 0.00
ATOM  1894 HA PRO A 637     9.692  2.949  5.834 1.00 0.00
ATOM  1895 1HB PRO A 637   11.685  3.679  6.841 1.00 0.00
ATOM  1896 2HB PRO A 637   12.419  2.609  5.643 1.00 0.00
ATOM  1897 1HG PRO A 637   12.702  0.837  7.207 1.00 0.00
ATOM  1898 2HG PRO A 637   12.857  2.214  8.303 1.00 0.00
ATOM  1899 N  CYS A 638    10.449  2.743  3.865 1.00 0.00
ATOM  1900 CA CYS A 638    10.294  2.855  2.427 1.00 0.00
ATOM  1901 C  CYS A 638     8.818  3.110  2.059 1.00 0.00
ATOM  1902 O  CYS A 638     8.523  3.510  0.936 1.00 0.00
ATOM  1903 CB CYS A 638    10.982  1.745  1.628 1.00 0.00
ATOM  1904 SG CYS A 638    10.969  2.069 -0.161 1.00 0.00
ATOM  1905 HN CYS A 638    10.630  3.611  4.327 1.00 0.00
ATOM  1906 HA CYS A 638    10.814  3.783  2.192 1.00 0.00
ATOM  1907 1HB CYS A 638   10.524  0.785  1.832 1.00 0.00
ATOM  1908 2HB CYS A 638   12.019  1.656  1.951 1.00 0.00
ATOM  1909 HG CYS A 638    11.560  1.050 -0.793 1.00 0.00
ATOM  1910 N  MET A 639     7.943  2.913  3.080 1.00 0.00
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ATOM  1911 CA  MET A 639      6.573  3.419  3.022 1.00 0.00
ATOM  1912 C   MET A 639      6.516  4.893  3.449 1.00 0.00
ATOM  1913 O   MET A 639      5.612  5.614  3.065 1.00 0.00
ATOM  1914 CB  MET A 639      5.630  2.616  3.935 1.00 0.00
ATOM  1915 CG  MET A 639      4.149  2.912  3.646 1.00 0.00
ATOM  1916 SD  MET A 639      3.022  1.729  4.408 1.00 0.00
ATOM  1917 CE  MET A 639      2.363  2.759  5.733 1.00 0.00
ATOM  1918 HN  MET A 639      8.222  2.383  3.879 1.00 0.00
ATOM  1919 HA  MET A 639      6.243  3.341  1.983 1.00 0.00
ATOM  1920 1HB MET A 639      5.842  2.853  4.976 1.00 0.00
ATOM  1921 2HB MET A 639      5.812  1.549  3.817 1.00 0.00
ATOM  1922 1HG MET A 639      3.991  2.853  2.574 1.00 0.00
ATOM  1923 2HG MET A 639      3.875  3.928  3.931 1.00 0.00
ATOM  1924 1HE MET A 639      2.035  2.132  6.563 1.00 0.00
ATOM  1925 2HE MET A 639      1.522  3.354  5.376 1.00 0.00
ATOM  1926 3HE MET A 639      3.133  3.427  6.113 1.00 0.00
ATOM  1927 N   TYR A 640      7.505  5.290  4.280 1.00 0.00
ATOM  1928 CA  TYR A 640      7.618  6.639  4.842 1.00 0.00
ATOM  1929 C   TYR A 640      7.155  7.706  3.865 1.00 0.00
ATOM  1930 O   TYR A 640      6.223  8.472  4.087 1.00 0.00
ATOM  1931 CB  TYR A 640      9.112  6.859  5.261 1.00 0.00
ATOM  1932 CG  TYR A 640      9.494  8.274  5.672 1.00 0.00
ATOM  1933 CD1 TYR A 640      9.735  9.264  4.719 1.00 0.00
ATOM  1934 CD2 TYR A 640      9.594  8.630  7.016 1.00 0.00
ATOM  1935 CE1 TYR A 640      9.961 10.583  5.086 1.00 0.00
ATOM  1936 CE2 TYR A 640      9.828  9.953  7.392 1.00 0.00
ATOM  1937 CZ  TYR A 640      9.977 10.941  6.424 1.00 0.00
ATOM  1938 OH  TYR A 640     10.117 12.278  6.766 1.00 0.00
ATOM  1939 HN  TYR A 640      8.092  4.572  4.641 1.00 0.00
ATOM  1940 HA  TYR A 640      6.931  6.686  5.661 1.00 0.00
ATOM  1941 1HB TYR A 640      9.768  6.572  4.439 1.00 0.00
ATOM  1942 2HB TYR A 640      9.355  6.179  6.079 1.00 0.00
ATOM  1943 HD1 TYR A 640      9.757  9.027  3.668 1.00 0.00
ATOM  1944 HE1 TYR A 640     10.124 11.326  4.321 1.00 0.00
ATOM  1945 HD2 TYR A 640      9.464  7.879  7.782 1.00 0.00
ATOM  1946 HE2 TYR A 640      9.866 10.198  8.444 1.00 0.00
ATOM  1947 HH  TYR A 640     10.860 12.349  7.362 1.00 0.00
ATOM  1948 N   ASP A 641      7.900  7.689  2.756 1.00 0.00
ATOM  1949 CA  ASP A 641      7.691  8.725  1.788 1.00 0.00
ATOM  1950 C   ASP A 641      6.322  8.607  1.202 1.00 0.00
ATOM  1951 O   ASP A 641      5.659  9.612  0.950 1.00 0.00
ATOM  1952 CB  ASP A 641      8.725  8.718  0.644 1.00 0.00
ATOM  1953 CG  ASP A 641      8.628  7.412 -0.130 1.00 0.00
ATOM  1954 OD1 ASP A 641      8.232  6.383  0.482 1.00 0.00
ATOM  1955 OD2 ASP A 641      8.951  7.425 -1.348 1.00 0.00
ATOM  1956 HN  ASP A 641      8.594  6.986  2.603 1.00 0.00
ATOM  1957 HA  ASP A 641      7.744  9.669  2.330 1.00 0.00
ATOM  1958 1HB ASP A 641      9.732  8.812  1.049 1.00 0.00
ATOM  1959 2HB ASP A 641      8.535  9.546 -0.038 1.00 0.00
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ATOM  1960 N   GLN A 642     5.820  7.376  0.975 1.00 0.00
ATOM  1961 CA  GLN A 642     4.539  7.246  0.288 1.00 0.00
ATOM  1962 C   GLN A 642     3.405  7.741  1.196 1.00 0.00
ATOM  1963 O   GLN A 642     2.481  8.398  0.744 1.00 0.00
ATOM  1964 CB  GLN A 642     4.351  5.846 -0.336 1.00 0.00
ATOM  1965 CG  GLN A 642     3.695  4.769  0.544 1.00 0.00
ATOM  1966 CD  GLN A 642     2.169  4.926  0.592 1.00 0.00
ATOM  1967 OE1 GLN A 642     1.499  4.941 -0.429 1.00 0.00
ATOM  1968 NE2 GLN A 642     1.658  5.033  1.823 1.00 0.00
ATOM  1969 HN  GLN A 642     6.396  6.590  1.211 1.00 0.00
ATOM  1970 HA  GLN A 642     4.591  7.947 -0.548 1.00 0.00
ATOM  1971 1HB GLN A 642     5.329  5.487 -0.658 1.00 0.00
ATOM  1972 2HB GLN A 642     3.771  5.944 -1.256 1.00 0.00
ATOM  1973 1HG GLN A 642     4.104  4.785  1.547 1.00 0.00
ATOM  1974 2HG GLN A 642     3.903  3.782  0.131 1.00 0.00
ATOM  1975 1HE2 GLN A 642    2.223  5.000  2.645 1.00 0.00
ATOM  1976 2HE2 GLN A 642    0.669  5.157  1.891 1.00 0.00
ATOM  1977 N   CYS A 643     3.555  7.450  2.506 1.00 0.00
ATOM  1978 CA  CYS A 643     2.631  8.001  3.484 1.00 0.00
ATOM  1979 C   CYS A 643     2.626  9.534  3.413 1.00 0.00
ATOM  1980 O   CYS A 643     1.580 10.157  3.530 1.00 0.00
ATOM  1981 CB  CYS A 643     3.045  7.537  4.885 1.00 0.00
ATOM  1982 SG  CYS A 643     2.794  8.786  6.171 1.00 0.00
ATOM  1983 HN  CYS A 643     4.332  6.879  2.775 1.00 0.00
ATOM  1984 HA  CYS A 643     1.634  7.633  3.235 1.00 0.00
ATOM  1985 1HB CYS A 643     4.097  7.254  4.889 1.00 0.00
ATOM  1986 2HB CYS A 643     2.489  6.639  5.154 1.00 0.00
ATOM  1987 HG  CYS A 643     2.847  8.193  7.368 1.00 0.00
ATOM  1988 N   LYS A 644     3.835 10.104  3.196 1.00 0.00
ATOM  1989 CA  LYS A 644     3.964 11.530  3.171 1.00 0.00
ATOM  1990 C   LYS A 644     3.198 12.069  2.014 1.00 0.00
ATOM  1991 O   LYS A 644     2.389 12.983  2.164 1.00 0.00
ATOM  1992 CB  LYS A 644     5.421 11.993  2.987 1.00 0.00
ATOM  1993 CG  LYS A 644     6.299 11.902  4.238 1.00 0.00
ATOM  1994 CD  LYS A 644     5.885 12.868  5.350 1.00 0.00
ATOM  1995 CE  LYS A 644     6.921 12.991  6.470 1.00 0.00
ATOM  1996 NZ  LYS A 644     8.145 13.645  5.957 1.00 0.00
ATOM  1997 HN  LYS A 644     4.648  9.527  3.117 1.00 0.00
ATOM  1998 HA  LYS A 644     3.570 11.896  4.118 1.00 0.00
ATOM  1999 1HB LYS A 644     5.409 13.030  2.655 1.00 0.00
ATOM  2000 2HB LYS A 644     5.876 11.387  2.206 1.00 0.00
ATOM  2001 1HG LYS A 644     7.330 12.114  3.957 1.00 0.00
ATOM  2002 2HG LYS A 644     6.251 10.884  4.624 1.00 0.00
ATOM  2003 1HD LYS A 644     4.945 12.525  5.780 1.00 0.00
ATOM  2004 2HD LYS A 644     5.722 13.853  4.914 1.00 0.00
ATOM  2005 1HE LYS A 644     7.194 12.005  6.844 1.00 0.00
ATOM  2006 2HE LYS A 644     6.528 13.597  7.286 1.00 0.00
ATOM  2007 1HZ LYS A 644     7.909 14.595  5.604 1.00 0.00
ATOM  2008 2HZ LYS A 644     8.544 13.077  5.183 1.00 0.00
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ATOM  2009 3HZ LYS A 644     8.843 13.725  6.724 1.00 0.00
ATOM  2010 N  HIS A 645      3.413 11.483  0.825 1.00 0.00
ATOM  2011 CA HIS A 645      2.750 11.978 -0.342 1.00 0.00
ATOM  2012 C  HIS A 645      1.281 11.777 -0.183 1.00 0.00
ATOM  2013 O  HIS A 645      0.485 12.612 -0.611 1.00 0.00
ATOM  2014 CB HIS A 645      3.245 11.314 -1.636 1.00 0.00
ATOM  2015 CG HIS A 645      4.645 11.751 -1.963 1.00 0.00
ATOM  2016 ND1 HIS A 645     5.461 11.146 -2.893 1.00 0.00
ATOM  2017 CD2 HIS A 645     5.363 12.796 -1.465 1.00 0.00
ATOM  2018 CE1 HIS A 645     6.623 11.848 -2.909 1.00 0.00
ATOM  2019 NE2 HIS A 645     6.610 12.858 -2.059 1.00 0.00
ATOM  2020 HN HIS A 645      4.035 10.704  0.756 1.00 0.00
ATOM  2021 HA HIS A 645      2.938 13.051 -0.376 1.00 0.00
ATOM  2022 1HB HIS A 645     2.590 11.588 -2.463 1.00 0.00
ATOM  2023 2HB HIS A 645     3.234 10.231 -1.521 1.00 0.00
ATOM  2024 HD2 HIS A 645     5.007 13.481 -0.711 1.00 0.00
ATOM  2025 HD1 HIS A 645     5.244 10.361 -3.438 1.00 0.00
ATOM  2026 HE1 HIS A 645     7.462 11.607 -3.544 1.00 0.00
ATOM  2027 N  MET A 646      0.886 10.654  0.460 1.00 0.00
ATOM  2028 CA MET A 646     -0.539 10.371  0.669 1.00 0.00
ATOM  2029 C  MET A 646     -1.199 11.378  1.633 1.00 0.00
ATOM  2030 O  MET A 646     -2.362 11.742  1.495 1.00 0.00
ATOM  2031 CB MET A 646     -0.755  8.943  1.199 1.00 0.00
ATOM  2032 CG MET A 646     -0.620  7.867  0.116 1.00 0.00
ATOM  2033 SD MET A 646     -1.146  6.270  0.769 1.00 0.00
ATOM  2034 CE MET A 646     -2.105  5.669 -0.634 1.00 0.00
ATOM  2035 HN MET A 646      1.576  9.999  0.768 1.00 0.00
ATOM  2036 HA MET A 646     -1.022 10.471 -0.303 1.00 0.00
ATOM  2037 1HB MET A 646    -1.763  8.859  1.610 1.00 0.00
ATOM  2038 2HB MET A 646    -0.075  8.738  2.027 1.00 0.00
ATOM  2039 1HG MET A 646     0.406  7.791 -0.241 1.00 0.00
ATOM  2040 2HG MET A 646    -1.243  8.141 -0.735 1.00 0.00
ATOM  2041 1HE MET A 646    -2.864  4.977 -0.275 1.00 0.00
ATOM  2042 2HE MET A 646    -1.459  5.169 -1.356 1.00 0.00
ATOM  2043 3HE MET A 646    -2.632  6.484 -1.129 1.00 0.00
ATOM  2044 N  LEU A 647     -0.416 11.831  2.622 1.00 0.00
ATOM  2045 CA LEU A 647     -0.963 12.840  3.484 1.00 0.00
ATOM  2046 C  LEU A 647     -1.102 14.128  2.759 1.00 0.00
ATOM  2047 O  LEU A 647     -2.124 14.808  2.872 1.00 0.00
ATOM  2048 CB LEU A 647     -0.078 13.164  4.691 1.00 0.00
ATOM  2049 CG LEU A 647     -0.153 12.091  5.768 1.00 0.00
ATOM  2050 CD1 LEU A 647     0.730 12.449  6.975 1.00 0.00
ATOM  2051 CD2 LEU A 647    -1.626 11.821  6.118 1.00 0.00
ATOM  2052 HN LEU A 647      0.457 11.394  2.840 1.00 0.00
ATOM  2053 HA LEU A 647     -1.929 12.466  3.822 1.00 0.00
ATOM  2054 1HB LEU A 647    -0.393 14.116  5.117 1.00 0.00
ATOM  2055 2HB LEU A 647     0.955 13.262  4.359 1.00 0.00
ATOM  2056 HG LEU A 647      0.175 11.139  5.351 1.00 0.00
ATOM  2057 1HD1 LEU A 647    0.117 12.701  7.840 1.00 0.00
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ATOM  2058 2HD1 LEU A 647     1.354  13.312   6.741  1.00  0.00
ATOM  2059 3HD1 LEU A 647     1.361  11.602   7.244  1.00  0.00
ATOM  2060 1HD2 LEU A 647    -2.243  11.826   5.219  1.00  0.00
ATOM  2061 2HD2 LEU A 647    -2.002  12.594   6.788  1.00  0.00
ATOM  2062 3HD2 LEU A 647    -1.728  10.844   6.591  1.00  0.00
ATOM  2063  N  TYR A 648    -0.080  14.492   1.971  1.00  0.00
ATOM  2064  CA TYR A 648    -0.102  15.769   1.332  1.00  0.00
ATOM  2065  C  TYR A 648    -1.285  15.860   0.425  1.00  0.00
ATOM  2066  O  TYR A 648    -1.946  16.896   0.366  1.00  0.00
ATOM  2067  CB TYR A 648     1.167  16.042   0.507  1.00  0.00
ATOM  2068  CG TYR A 648     1.014  17.399  -0.087  1.00  0.00
ATOM  2069  CD1 TYR A 648     0.389  17.572  -1.299  1.00  0.00
ATOM  2070  CD2 TYR A 648     1.439  18.507   0.610  1.00  0.00
ATOM  2071  CE1 TYR A 648     0.206  18.831  -1.817  1.00  0.00
ATOM  2072  CE2 TYR A 648     1.257  19.769   0.098  1.00  0.00
ATOM  2073  CZ  TYR A 648     0.640  19.932  -1.118  1.00  0.00
ATOM  2074  OH  TYR A 648     0.444  21.226  -1.644  1.00  0.00
ATOM  2075  HN  TYR A 648     0.692  13.872   1.832  1.00  0.00
ATOM  2076  HA  TYR A 648    -0.202  16.513   2.123  1.00  0.00
ATOM  2077 1HB  TYR A 648     1.277  15.303  -0.286  1.00  0.00
ATOM  2078 2HB  TYR A 648     2.053  16.014   1.141  1.00  0.00
ATOM  2079  HD1 TYR A 648     0.038  16.711  -1.849  1.00  0.00
ATOM  2080  HE1 TYR A 648    -0.278  18.956  -2.774  1.00  0.00
ATOM  2081  HD2 TYR A 648     1.921  18.383   1.569  1.00  0.00
ATOM  2082  HE2 TYR A 648     1.599  20.631   0.652  1.00  0.00
ATOM  2083  HH  TYR A 648    -0.245  21.202  -2.295  1.00  0.00
ATOM  2084  N  VAL A 649    -1.593  14.783  -0.320  1.00  0.00
ATOM  2085  CA VAL A 649    -2.721  14.865  -1.204  1.00  0.00
ATOM  2086  C  VAL A 649    -3.964  14.983  -0.384  1.00  0.00
ATOM  2087  O  VAL A 649    -4.867  15.755  -0.707  1.00  0.00
ATOM  2088  CB VAL A 649    -2.861  13.681  -2.118  1.00  0.00
ATOM  2089  CG1 VAL A 649    -3.212  12.435  -1.292  1.00  0.00
ATOM  2090  CG2 VAL A 649    -3.907  14.026  -3.193  1.00  0.00
ATOM  2091  HN  VAL A 649    -1.049  13.946  -0.260  1.00  0.00
ATOM  2092  HA  VAL A 649    -2.586  15.773  -1.791  1.00  0.00
ATOM  2093  HB  VAL A 649    -1.927  13.516  -2.655  1.00  0.00
ATOM  2094 1HG1 VAL A 649    -4.048  12.639  -0.623  1.00  0.00
ATOM  2095 2HG1 VAL A 649    -2.359  12.135  -0.683  1.00  0.00
ATOM  2096 3HG1 VAL A 649    -3.499  11.615  -1.950  1.00  0.00
ATOM  2097 1HG2 VAL A 649    -3.686  14.991  -3.650  1.00  0.00
ATOM  2098 2HG2 VAL A 649    -4.900  14.084  -2.747  1.00  0.00
ATOM  2099 3HG2 VAL A 649    -3.902  13.272  -3.979  1.00  0.00
ATOM  2100  N  SER A 650    -4.023  14.232   0.732  1.00  0.00
ATOM  2101  CA SER A 650    -5.193  14.243   1.556  1.00  0.00
ATOM  2102  C  SER A 650    -5.420  15.645   2.021  1.00  0.00
ATOM  2103  O  SER A 650    -6.549  16.135   2.029  1.00  0.00
ATOM  2104  CB SER A 650    -5.044  13.361   2.807  1.00  0.00
ATOM  2105  OG SER A 650    -6.232  13.412   3.584  1.00  0.00
ATOM  2106  HN SER A 650    -3.241  13.662   0.986  1.00  0.00
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ATOM  2107 HA  SER A 650     -6.015  13.884   0.938  1.00  0.00
ATOM  2108 1HB SER A 650     -4.217  13.714   3.423  1.00  0.00
ATOM  2109 2HB SER A 650     -4.869  12.324   2.520  1.00  0.00
ATOM  2110 HG  SER A 650     -6.530  14.312   3.566  1.00  0.00
ATOM  2111 N   SER A 651     -4.335  16.334   2.416  1.00  0.00
ATOM  2112 CA  SER A 651     -4.456  17.677   2.903  1.00  0.00
ATOM  2113 C   SER A 651     -4.931  18.597   1.820  1.00  0.00
ATOM  2114 O   SER A 651     -5.771  19.464   2.059  1.00  0.00
ATOM  2115 CB  SER A 651     -3.139  18.242   3.471  1.00  0.00
ATOM  2116 OG  SER A 651     -2.170  18.402   2.446  1.00  0.00
ATOM  2117 HN  SER A 651     -3.434  15.904   2.369  1.00  0.00
ATOM  2118 HA  SER A 651     -5.219  17.657   3.680  1.00  0.00
ATOM  2119 1HB SER A 651     -2.732  17.561   4.218  1.00  0.00
ATOM  2120 2HB SER A 651     -3.315  19.218   3.924  1.00  0.00
ATOM  2121 HG  SER A 651     -2.577  18.115   1.639  1.00  0.00
ATOM  2122 N   GLU A 652     -4.421  18.421   0.586  1.00  0.00
ATOM  2123 CA  GLU A 652     -4.800  19.296  -0.486  1.00  0.00
ATOM  2124 C   GLU A 652     -6.268  19.145  -0.716  1.00  0.00
ATOM  2125 O   GLU A 652     -6.970  20.122  -0.969  1.00  0.00
ATOM  2126 CB  GLU A 652     -4.057  18.993  -1.797  1.00  0.00
ATOM  2127 CG  GLU A 652     -4.250  20.074  -2.862  1.00  0.00
ATOM  2128 CD  GLU A 652     -3.249  19.813  -3.976  1.00  0.00
ATOM  2129 OE1 GLU A 652     -2.042  19.647  -3.657  1.00  0.00
ATOM  2130 OE2 GLU A 652     -3.677  19.773  -5.160  1.00  0.00
ATOM  2131 HN  GLU A 652     -3.774  17.677   0.417  1.00  0.00
ATOM  2132 HA  GLU A 652     -4.576  20.310  -0.154  1.00  0.00
ATOM  2133 1HB GLU A 652     -4.416  18.044  -2.192  1.00  0.00
ATOM  2134 2HB GLU A 652     -2.994  18.897  -1.584  1.00  0.00
ATOM  2135 1HG GLU A 652     -4.072  21.063  -2.441  1.00  0.00
ATOM  2136 2HG GLU A 652     -5.261  20.036  -3.268  1.00  0.00
ATOM  2137 N   LEU A 653     -6.779  17.906  -0.610  1.00  0.00
ATOM  2138 CA  LEU A 653     -8.176  17.673  -0.822  1.00  0.00
ATOM  2139 C   LEU A 653     -8.916  18.459   0.215  1.00  0.00
ATOM  2140 O   LEU A 653     -9.976  19.020  -0.063  1.00  0.00
ATOM  2141 CB  LEU A 653     -8.555  16.191  -0.658  1.00  0.00
ATOM  2142 CG  LEU A 653     -7.855  15.278  -1.684  1.00  0.00
ATOM  2143 CD1 LEU A 653     -8.258  13.807  -1.496  1.00  0.00
ATOM  2144 CD2 LEU A 653     -8.074  15.782  -3.118  1.00  0.00
ATOM  2145 HN  LEU A 653     -6.177  17.141  -0.381  1.00  0.00
ATOM  2146 HA  LEU A 653     -8.401  18.010  -1.834  1.00  0.00
ATOM  2147 1HB LEU A 653     -9.633  16.088  -0.772  1.00  0.00
ATOM  2148 2HB LEU A 653     -8.284  15.867   0.346  1.00  0.00
ATOM  2149 HG  LEU A 653     -6.775  15.372  -1.571  1.00  0.00
ATOM  2150 1HD1 LEU A 653    -9.334  13.684  -1.619  1.00  0.00
ATOM  2151 2HD1 LEU A 653    -7.994  13.469  -0.494  1.00  0.00
ATOM  2152 3HD1 LEU A 653    -7.760  13.182  -2.237  1.00  0.00
ATOM  2153 1HD2 LEU A 653    -7.394  16.603  -3.347  1.00  0.00
ATOM  2154 2HD2 LEU A 653    -9.094  16.147  -3.238  1.00  0.00
ATOM  2155 3HD2 LEU A 653    -7.885  14.980  -3.832  1.00  0.00
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ATOM  2156 N   HIS A 654    -8.355  18.527   1.440  1.00  0.00
ATOM  2157 CA  HIS A 654    -8.965  19.245   2.528  1.00  0.00
ATOM  2158 C   HIS A 654    -9.167  20.664   2.111  1.00  0.00
ATOM  2159 O   HIS A 654   -10.270  21.201   2.179  1.00  0.00
ATOM  2160 CB  HIS A 654    -8.019  19.455   3.728  1.00  0.00
ATOM  2161 CG  HIS A 654    -7.730  18.335   4.681  1.00  0.00
ATOM  2162 ND1 HIS A 654    -8.058  18.419   6.018  1.00  0.00
ATOM  2163 CD2 HIS A 654    -6.904  17.262   4.569  1.00  0.00
ATOM  2164 CE1 HIS A 654    -7.416  17.402   6.643  1.00  0.00
ATOM  2165 NE2 HIS A 654    -6.709  16.666   5.803  1.00  0.00
ATOM  2166 HN  HIS A 654    -7.485  18.062   1.597  1.00  0.00
ATOM  2167 HA  HIS A 654    -9.834  18.662   2.835  1.00  0.00
ATOM  2168 1HB HIS A 654    -8.436  20.261   4.326  1.00  0.00
ATOM  2169 2HB HIS A 654    -7.058  19.766   3.327  1.00  0.00
ATOM  2170 HD2 HIS A 654    -6.461  16.921   3.645  1.00  0.00
ATOM  2171 HD1 HIS A 654    -8.643  19.085   6.435  1.00  0.00
ATOM  2172 HE1 HIS A 654    -7.476  17.215   7.704  1.00  0.00
ATOM  2173 N   ARG A 655    -8.078  21.301   1.645  1.00  0.00
ATOM  2174 CA  ARG A 655    -8.117  22.702   1.345  1.00  0.00
ATOM  2175 C   ARG A 655    -9.090  23.001   0.254  1.00  0.00
ATOM  2176 O   ARG A 655    -9.843  23.970   0.334  1.00  0.00
ATOM  2177 CB  ARG A 655    -6.736  23.261   0.961  1.00  0.00
ATOM  2178 CG  ARG A 655    -5.822  23.434   2.179  1.00  0.00
ATOM  2179 CD  ARG A 655    -5.468  22.124   2.888  1.00  0.00
ATOM  2180 NE  ARG A 655    -4.054  21.795   2.558  1.00  0.00
ATOM  2181 CZ  ARG A 655    -3.045  22.307   3.323  1.00  0.00
ATOM  2182 NH1 ARG A 655    -3.338  23.121   4.379  1.00  0.00
ATOM  2183 NH2 ARG A 655    -1.746  22.004   3.036  1.00  0.00
ATOM  2184 HN  ARG A 655    -7.230  20.790   1.506  1.00  0.00
ATOM  2185 HA  ARG A 655    -8.490  23.203   2.238  1.00  0.00
ATOM  2186 1HB ARG A 655    -6.866  24.226   0.473  1.00  0.00
ATOM  2187 2HB ARG A 655    -6.261  22.582   0.253  1.00  0.00
ATOM  2188 1HG ARG A 655    -6.317  24.092   2.892  1.00  0.00
ATOM  2189 2HG ARG A 655    -4.899  23.913   1.854  1.00  0.00
ATOM  2190 1HD ARG A 655    -6.094  21.304   2.539  1.00  0.00
ATOM  2191 2HD ARG A 655    -5.545  22.228   3.970  1.00  0.00
ATOM  2192 HE  ARG A 655    -3.843  21.202   1.781  1.00  0.00
ATOM  2193 1HH1 ARG A 655    -4.290  23.341   4.591  1.00  0.00
ATOM  2194 2HH1 ARG A 655    -2.601  23.497   4.940  1.00  0.00
ATOM  2195 1HH2 ARG A 655    -1.531  21.406   2.264  1.00  0.00
ATOM  2196 2HH2 ARG A 655    -1.009  22.380   3.598  1.00  0.00
ATOM  2197 N   LEU A 656    -9.103  22.163  -0.792  1.00  0.00
ATOM  2198 CA  LEU A 656   -10.001  22.337  -1.896  1.00  0.00
ATOM  2199 C   LEU A 656   -11.407  22.100  -1.453  1.00  0.00
ATOM  2200 O   LEU A 656   -12.349  22.583  -2.080  1.00  0.00
ATOM  2201 CB  LEU A 656    -9.700  21.407  -3.087  1.00  0.00
ATOM  2202 CG  LEU A 656    -8.472  21.835  -3.918  1.00  0.00
ATOM  2203 CD1 LEU A 656    -7.183  21.850  -3.084  1.00  0.00
ATOM  2204 CD2 LEU A 656    -8.342  20.980  -5.189  1.00  0.00
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ATOM  2205 HN  LEU A 656    -8.466  21.392  -0.802  1.00  0.00
ATOM  2206 HA  LEU A 656    -9.912  23.378  -2.205  1.00  0.00
ATOM  2207 1HB LEU A 656   -10.572  21.386  -3.740  1.00  0.00
ATOM  2208 2HB LEU A 656    -9.531  20.400  -2.709  1.00  0.00
ATOM  2209 HG  LEU A 656    -8.646  22.832  -4.322  1.00  0.00
ATOM  2210 1HD1 LEU A 656   -6.878  20.835  -2.827  1.00  0.00
ATOM  2211 2HD1 LEU A 656   -7.341  22.399  -2.156  1.00  0.00
ATOM  2212 3HD1 LEU A 656   -6.374  22.311  -3.650  1.00  0.00
ATOM  2213 1HD2 LEU A 656   -9.227  21.085  -5.816  1.00  0.00
ATOM  2214 2HD2 LEU A 656   -8.238  19.928  -4.926  1.00  0.00
ATOM  2215 3HD2 LEU A 656   -7.477  21.300  -5.771  1.00  0.00
ATOM  2216 N   GLN A 657   -11.597  21.333  -0.364  1.00  0.00
ATOM  2217 CA  GLN A 657   -12.934  21.062   0.071  1.00  0.00
ATOM  2218 C   GLN A 657   -13.598  20.292  -1.019  1.00  0.00
ATOM  2219 O   GLN A 657   -14.683  20.641  -1.479  1.00  0.00
ATOM  2220 CB  GLN A 657   -13.761  22.338   0.306  1.00  0.00
ATOM  2221 CG  GLN A 657   -13.224  23.227   1.431  1.00  0.00
ATOM  2222 CD  GLN A 657   -14.135  24.442   1.541  1.00  0.00
ATOM  2223 OE1 GLN A 657   -13.875  25.359   2.318  1.00  0.00
ATOM  2224 NE2 GLN A 657   -15.231  24.454   0.738  1.00  0.00
ATOM  2225 HN  GLN A 657   -10.815  20.957   0.134  1.00  0.00
ATOM  2226 HA  GLN A 657   -12.851  20.493   0.997  1.00  0.00
ATOM  2227 1HB GLN A 657   -14.783  22.051   0.549  1.00  0.00
ATOM  2228 2HB GLN A 657   -13.777  22.917  -0.616  1.00  0.00
ATOM  2229 1HG GLN A 657   -12.209  23.556   1.208  1.00  0.00
ATOM  2230 2HG GLN A 657   -13.224  22.688   2.378  1.00  0.00
ATOM  2231 1HE2 GLN A 657  -15.938  25.149   0.875  1.00  0.00
ATOM  2232 2HE2 GLN A 657  -15.347  23.780   0.009  1.00  0.00
ATOM  2233 N   VAL A 658   -12.935  19.205  -1.457  1.00  0.00
ATOM  2234 CA  VAL A 658   -13.459  18.405  -2.523  1.00  0.00
ATOM  2235 C   VAL A 658   -14.729  17.748  -2.099  1.00  0.00
ATOM  2236 O   VAL A 658   -14.827  17.196  -1.003  1.00  0.00
ATOM  2237 CB  VAL A 658   -12.516  17.329  -2.978  1.00  0.00
ATOM  2238 CG1 VAL A 658   -11.249  17.994  -3.543  1.00  0.00
ATOM  2239 CG2 VAL A 658   -12.249  16.381  -1.797  1.00  0.00
ATOM  2240 HN  VAL A 658   -12.065  18.954  -1.033  1.00  0.00
ATOM  2241 HA  VAL A 658   -13.671  19.087  -3.346  1.00  0.00
ATOM  2242 HB  VAL A 658   -12.991  16.718  -3.746  1.00  0.00
ATOM  2243 1HG1 VAL A 658  -10.668  18.456  -2.745  1.00  0.00
ATOM  2244 2HG1 VAL A 658  -11.519  18.772  -4.257  1.00  0.00
ATOM  2245 3HG1 VAL A 658  -10.620  17.250  -4.032  1.00  0.00
ATOM  2246 1HG2 VAL A 658  -13.032  16.474  -1.044  1.00  0.00
ATOM  2247 2HG2 VAL A 658  -11.298  16.627  -1.325  1.00  0.00
ATOM  2248 3HG2 VAL A 658  -12.232  15.347  -2.140  1.00  0.00
ATOM  2249 N   SER A 659   -15.746  17.803  -2.984  1.00  0.00
ATOM  2250 CA  SER A 659   -17.023  17.228  -2.686  1.00  0.00
ATOM  2251 C   SER A 659   -17.056  15.801  -3.130  1.00  0.00
ATOM  2252 O   SER A 659   -16.241  15.359  -3.938  1.00  0.00
ATOM  2253 CB  SER A 659   -18.205  17.959  -3.344  1.00  0.00
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ATOM  2254 OG  SER A 659   -18.194  17.764  -4.749  1.00  0.00
ATOM  2255 HN  SER A 659   -15.604  18.255  -3.864  1.00  0.00
ATOM  2256 HA  SER A 659   -17.128  17.258  -1.601  1.00  0.00
ATOM  2257 1HB SER A 659   -18.140  19.029  -3.150  1.00  0.00
ATOM  2258 2HB SER A 659   -19.148  17.574  -2.956  1.00  0.00
ATOM  2259 HG  SER A 659   -18.584  18.538  -5.134  1.00  0.00
ATOM  2260 N   TYR A 660   -18.026  15.044  -2.584  1.00  0.00
ATOM  2261 CA  TYR A 660   -18.187  13.647  -2.862  1.00  0.00
ATOM  2262 C   TYR A 660   -18.532  13.452  -4.305  1.00  0.00
ATOM  2263 O   TYR A 660   -18.025  12.539  -4.953  1.00  0.00
ATOM  2264 CB  TYR A 660   -19.292  13.024  -1.984  1.00  0.00
ATOM  2265 CG  TYR A 660   -19.424  11.571  -2.291  1.00  0.00
ATOM  2266 CD1 TYR A 660   -20.300  11.128  -3.255  1.00  0.00
ATOM  2267 CD2 TYR A 660   -18.694  10.647  -1.579  1.00  0.00
ATOM  2268 CE1 TYR A 660   -20.449   9.782  -3.499  1.00  0.00
ATOM  2269 CE2 TYR A 660   -18.824   9.301  -1.832  1.00  0.00
ATOM  2270 CZ  TYR A 660   -19.704   8.867  -2.793  1.00  0.00
ATOM  2271 OH  TYR A 660   -19.835   7.489  -3.061  1.00  0.00
ATOM  2272 HN  TYR A 660   -18.666  15.479  -1.952  1.00  0.00
ATOM  2273 HA  TYR A 660   -17.228  13.169  -2.663  1.00  0.00
ATOM  2274 1HB TYR A 660   -20.245  13.517  -2.179  1.00  0.00
ATOM  2275 2HB TYR A 660   -19.043  13.144  -0.930  1.00  0.00
ATOM  2276 HD1 TYR A 660   -20.875  11.842  -3.826  1.00  0.00
ATOM  2277 HE1 TYR A 660   -21.152   9.443  -4.245  1.00  0.00
ATOM  2278 HD2 TYR A 660   -18.011  10.982  -0.812  1.00  0.00
ATOM  2279 HE2 TYR A 660   -18.235   8.587  -1.275  1.00  0.00
ATOM  2280 HH  TYR A 660   -19.330   7.267  -3.832  1.00  0.00
ATOM  2281 N   GLU A 661   -19.398  14.316  -4.864  1.00  0.00
ATOM  2282 CA  GLU A 661   -19.761  14.171  -6.244  1.00  0.00
ATOM  2283 C   GLU A 661   -18.536  14.346  -7.089  1.00  0.00
ATOM  2284 O   GLU A 661   -18.372  13.667  -8.103  1.00  0.00
ATOM  2285 CB  GLU A 661   -20.863  15.156  -6.680  1.00  0.00
ATOM  2286 CG  GLU A 661   -20.651  16.585  -6.182  1.00  0.00
ATOM  2287 CD  GLU A 661   -21.158  16.652  -4.749  1.00  0.00
ATOM  2288 OE1 GLU A 661   -20.840  17.652  -4.055  1.00  0.00
ATOM  2289 OE2 GLU A 661   -21.873  15.702  -4.330  1.00  0.00
ATOM  2290 HN  GLU A 661   -19.787  15.057  -4.317  1.00  0.00
ATOM  2291 HA  GLU A 661   -20.104  13.145  -6.370  1.00  0.00
ATOM  2292 1HB GLU A 661   -21.819  14.796  -6.303  1.00  0.00
ATOM  2293 2HB GLU A 661   -20.906  15.170  -7.768  1.00  0.00
ATOM  2294 1HG GLU A 661   -21.206  17.293  -6.797  1.00  0.00
ATOM  2295 2HG GLU A 661   -19.593  16.848  -6.204  1.00  0.00
ATOM  2296 N   GLU A 662   -17.646  15.274  -6.688  1.00  0.00
ATOM  2297 CA  GLU A 662   -16.412  15.526  -7.380  1.00  0.00
ATOM  2298 C   GLU A 662   -15.564  14.293  -7.315  1.00  0.00
ATOM  2299 O   GLU A 662   -15.021  13.830  -8.319  1.00  0.00
ATOM  2300 CB  GLU A 662   -15.568  16.594  -6.662  1.00  0.00
ATOM  2301 CG  GLU A 662   -16.170  17.997  -6.642  1.00  0.00
ATOM  2302 CD  GLU A 662   -15.293  18.914  -7.473  1.00  0.00
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ATOM  2303 OE1 GLU A 662   -14.265  18.432  -8.015  1.00  0.00
ATOM  2304 OE2 GLU A 662   -15.631  20.123  -7.555  1.00  0.00
ATOM  2305  HN GLU A 662   -17.854  15.812  -5.871  1.00  0.00
ATOM  2306  HA GLU A 662   -16.672  15.859  -8.385  1.00  0.00
ATOM  2307 1HB GLU A 662   -14.597  16.646  -7.151  1.00  0.00
ATOM  2308 2HB GLU A 662   -15.418  16.273  -5.633  1.00  0.00
ATOM  2309 1HG GLU A 662   -16.217  18.376  -5.621  1.00  0.00
ATOM  2310 2HG GLU A 662   -17.175  17.985  -7.064  1.00  0.00
ATOM  2311  N  TYR A 663   -15.466  13.711  -6.105  1.00  0.00
ATOM  2312  CA TYR A 663   -14.615  12.585  -5.853  1.00  0.00
ATOM  2313  C  TYR A 663   -14.948  11.458  -6.774  1.00  0.00
ATOM  2314  O  TYR A 663   -14.074  10.896  -7.433  1.00  0.00
ATOM  2315  CB TYR A 663   -14.789  12.093  -4.404  1.00  0.00
ATOM  2316  CG TYR A 663   -14.191  10.738  -4.252  1.00  0.00
ATOM  2317  CD1 TYR A 663   -12.830  10.563  -4.239  1.00  0.00
ATOM  2318  CD2 TYR A 663   -15.000   9.658  -3.983  1.00  0.00
ATOM  2319  CE1 TYR A 663   -12.281   9.319  -4.041  1.00  0.00
ATOM  2320  CE2 TYR A 663   -14.459   8.414  -3.759  1.00  0.00
ATOM  2321  CZ  TYR A 663   -13.098   8.241  -3.803  1.00  0.00
ATOM  2322  OH  TYR A 663   -12.537   6.964  -3.581  1.00  0.00
ATOM  2323  HN TYR A 663   -16.010  14.080  -5.352  1.00  0.00
ATOM  2324  HA TYR A 663   -13.589  12.909  -6.029  1.00  0.00
ATOM  2325 1HB TYR A 663   -15.849  12.044  -4.152  1.00  0.00
ATOM  2326 2HB TYR A 663   -14.295  12.779  -3.716  1.00  0.00
ATOM  2327  HD1 TYR A 663   -12.182  11.414  -4.386  1.00  0.00
ATOM  2328  HE1 TYR A 663   -11.209   9.189  -4.073  1.00  0.00
ATOM  2329  HD2 TYR A 663   -16.071   9.788  -3.947  1.00  0.00
ATOM  2330  HE2 TYR A 663   -15.105   7.574  -3.550  1.00  0.00
ATOM  2331  HH  TYR A 663   -12.965   6.330  -4.140  1.00  0.00
ATOM  2332  N  LEU A 664   -16.242  11.130  -6.887  1.00  0.00
ATOM  2333  CA LEU A 664   -16.646  10.024  -7.700  1.00  0.00
ATOM  2334  C  LEU A 664   -16.277  10.231  -9.134  1.00  0.00
ATOM  2335  O  LEU A 664   -15.938   9.278  -9.834  1.00  0.00
ATOM  2336  CB LEU A 664   -18.150   9.737  -7.595  1.00  0.00
ATOM  2337  CG LEU A 664   -18.516   9.035  -6.274  1.00  0.00
ATOM  2338  CD1 LEU A 664   -18.042   7.572  -6.264  1.00  0.00
ATOM  2339  CD2 LEU A 664   -17.958   9.802  -5.070  1.00  0.00
ATOM  2340  HN LEU A 664   -16.932  11.663  -6.397  1.00  0.00
ATOM  2341  HA LEU A 664   -16.074   9.160  -7.363  1.00  0.00
ATOM  2342 1HB LEU A 664   -18.452   9.105  -8.430  1.00  0.00
ATOM  2343 2HB LEU A 664   -18.697  10.677  -7.662  1.00  0.00
ATOM  2344  HG LEU A 664   -19.597   9.063  -6.140  1.00  0.00
ATOM  2345 1HD1 LEU A 664   -17.391   7.372  -7.115  1.00  0.00
ATOM  2346 2HD1 LEU A 664   -18.897   6.899  -6.329  1.00  0.00
ATOM  2347 3HD1 LEU A 664   -17.481   7.364  -5.353  1.00  0.00
ATOM  2348 1HD2 LEU A 664   -18.594  10.652  -4.826  1.00  0.00
ATOM  2349 2HD2 LEU A 664   -16.961  10.181  -5.295  1.00  0.00
ATOM  2350 3HD2 LEU A 664   -17.914   9.152  -4.196  1.00  0.00
ATOM  2351  N  CYS A 665   -16.360  11.477  -9.628  1.00  0.00
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ATOM  2352 CA  CYS A 665   -16.026  11.718 -11.002  1.00  0.00
ATOM  2353 C   CYS A 665   -14.559  11.530 -11.271  1.00  0.00
ATOM  2354 O   CYS A 665   -14.176  10.917 -12.267  1.00  0.00
ATOM  2355 CB  CYS A 665   -16.440  13.121 -11.457  1.00  0.00
ATOM  2356 SG  CYS A 665   -18.245  13.318 -11.386  1.00  0.00
ATOM  2357 HN  CYS A 665   -16.652  12.231  -9.041  1.00  0.00
ATOM  2358 HA  CYS A 665   -16.545  10.961 -11.590  1.00  0.00
ATOM  2359 1HB CYS A 665   -16.109  13.289 -12.482  1.00  0.00
ATOM  2360 2HB CYS A 665   -15.979  13.869 -10.812  1.00  0.00
ATOM  2361 HG  CYS A 665   -18.563  14.157 -10.398  1.00  0.00
ATOM  2362 N   MET A 666   -13.682  12.032 -10.379  1.00  0.00
ATOM  2363 CA  MET A 666   -12.269  11.910 -10.626  1.00  0.00
ATOM  2364 C   MET A 666   -11.910  10.462 -10.680  1.00  0.00
ATOM  2365 O   MET A 666   -11.143  10.027 -11.537  1.00  0.00
ATOM  2366 CB  MET A 666   -11.385  12.529  -9.528  1.00  0.00
ATOM  2367 CG  MET A 666    -9.890  12.371  -9.834  1.00  0.00
ATOM  2368 SD  MET A 666    -8.751  12.899  -8.518  1.00  0.00
ATOM  2369 CE  MET A 666    -8.679  14.648  -8.996  1.00  0.00
ATOM  2370 HN  MET A 666   -14.012  12.485  -9.551  1.00  0.00
ATOM  2371 HA  MET A 666   -12.080  12.407 -11.577  1.00  0.00
ATOM  2372 1HB MET A 666   -11.607  12.046  -8.577  1.00  0.00
ATOM  2373 2HB MET A 666   -11.620  13.589  -9.437  1.00  0.00
ATOM  2374 1HG MET A 666    -9.656  12.955 -10.723  1.00  0.00
ATOM  2375 2HG MET A 666    -9.689  11.320 -10.038  1.00  0.00
ATOM  2376 1HE MET A 666    -9.197  15.250  -8.250  1.00  0.00
ATOM  2377 2HE MET A 666    -9.169  14.789  -9.959  1.00  0.00
ATOM  2378 3HE MET A 666    -7.641  14.975  -9.048  1.00  0.00
ATOM  2379 N   LYS A 667   -12.496   9.665  -9.774  1.00  0.00
ATOM  2380 CA  LYS A 667   -12.171   8.276  -9.706  1.00  0.00
ATOM  2381 C   LYS A 667   -12.427   7.639 -11.042  1.00  0.00
ATOM  2382 O   LYS A 667   -11.599   6.877 -11.541  1.00  0.00
ATOM  2383 CB  LYS A 667   -13.029   7.561  -8.645  1.00  0.00
ATOM  2384 CG  LYS A 667   -12.738   6.070  -8.521  1.00  0.00
ATOM  2385 CD  LYS A 667   -13.243   5.424  -7.228  1.00  0.00
ATOM  2386 CE  LYS A 667   -14.595   5.945  -6.740  1.00  0.00
ATOM  2387 NZ  LYS A 667   -15.045   5.151  -5.575  1.00  0.00
ATOM  2388 HN  LYS A 667   -13.166  10.049  -9.139  1.00  0.00
ATOM  2389 HA  LYS A 667   -11.113   8.205  -9.454  1.00  0.00
ATOM  2390 1HB LYS A 667   -14.079   7.690  -8.903  1.00  0.00
ATOM  2391 2HB LYS A 667   -12.852   8.032  -7.680  1.00  0.00
ATOM  2392 1HG LYS A 667   -11.660   5.925  -8.579  1.00  0.00
ATOM  2393 2HG LYS A 667   -13.200   5.559  -9.364  1.00  0.00
ATOM  2394 1HD LYS A 667   -12.505   5.596  -6.446  1.00  0.00
ATOM  2395 2HD LYS A 667   -13.326   4.350  -7.390  1.00  0.00
ATOM  2396 1HE LYS A 667   -15.345   5.853  -7.526  1.00  0.00
ATOM  2397 2HE LYS A 667   -14.513   6.987  -6.432  1.00  0.00
ATOM  2398 1HZ LYS A 667   -14.346   5.234  -4.809  1.00  0.00
ATOM  2399 2HZ LYS A 667   -15.139   4.153  -5.851  1.00  0.00
ATOM  2400 3HZ LYS A 667   -15.964   5.508  -5.246  1.00  0.00
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ATOM  2401 N   THR A 668   -13.575  7.951 -11.671  1.00  0.00
ATOM  2402 CA  THR A 668   -13.899  7.362 -12.940  1.00  0.00
ATOM  2403 C   THR A 668   -12.923  7.822 -13.968  1.00  0.00
ATOM  2404 O   THR A 668   -12.511  7.056 -14.838  1.00  0.00
ATOM  2405 CB  THR A 668   -15.262  7.745 -13.429  1.00  0.00
ATOM  2406 OG1 THR A 668   -15.314  9.130 -13.734  1.00  0.00
ATOM  2407 CG2 THR A 668   -16.267  7.419 -12.316  1.00  0.00
ATOM  2408 HN  THR A 668   -14.208  8.600 -11.250  1.00  0.00
ATOM  2409 HA  THR A 668   -13.840  6.282 -12.807  1.00  0.00
ATOM  2410 HB  THR A 668   -15.506  7.190 -14.335  1.00  0.00
ATOM  2411 HG1 THR A 668   -14.822  9.577 -13.058  1.00  0.00
ATOM  2412 1HG2 THR A 668   -16.142  8.099 -11.473  1.00  0.00
ATOM  2413 2HG2 THR A 668   -16.112  6.403 -11.955  1.00  0.00
ATOM  2414 3HG2 THR A 668   -17.286  7.526 -12.686  1.00  0.00
ATOM  2415 N   LEU A 669   -12.528  9.103 -13.882  1.00  0.00
ATOM  2416 CA  LEU A 669   -11.627  9.672 -14.836  1.00  0.00
ATOM  2417 C   LEU A 669   -10.377  8.854 -14.779  1.00  0.00
ATOM  2418 O   LEU A 669    -9.848  8.427 -15.801  1.00  0.00
ATOM  2419 CB  LEU A 669   -11.252 11.117 -14.451  1.00  0.00
ATOM  2420 CG  LEU A 669   -10.406 11.869 -15.492  1.00  0.00
ATOM  2421 CD1 LEU A 669   -11.238 12.181 -16.744  1.00  0.00
ATOM  2422 CD2 LEU A 669    -9.759 13.126 -14.890  1.00  0.00
ATOM  2423 HN  LEU A 669   -12.873  9.671 -13.134  1.00  0.00
ATOM  2424 HA  LEU A 669   -12.129  9.653 -15.803  1.00  0.00
ATOM  2425 1HB LEU A 669   -10.697 11.089 -13.514  1.00  0.00
ATOM  2426 2HB LEU A 669   -12.172 11.677 -14.288  1.00  0.00
ATOM  2427 HG  LEU A 669    -9.547 11.259 -15.769  1.00  0.00
ATOM  2428 1HD1 LEU A 669   -12.097 12.801 -16.491  1.00  0.00
ATOM  2429 2HD1 LEU A 669   -11.609 11.258 -17.189  1.00  0.00
ATOM  2430 3HD1 LEU A 669   -10.634 12.722 -17.472  1.00  0.00
ATOM  2431 1HD2 LEU A 669    -9.564 12.988 -13.827  1.00  0.00
ATOM  2432 2HD2 LEU A 669   -10.424 13.982 -15.003  1.00  0.00
ATOM  2433 3HD2 LEU A 669    -8.809 13.333 -15.383  1.00  0.00
ATOM  2434 N   LEU A 670    -9.878  8.557 -13.571  1.00  0.00
ATOM  2435 CA  LEU A 670    -8.653  7.820 -13.524  1.00  0.00
ATOM  2436 C   LEU A 670    -8.775  6.453 -14.115  1.00  0.00
ATOM  2437 O   LEU A 670    -7.844  5.969 -14.757  1.00  0.00
ATOM  2438 CB  LEU A 670    -8.036  7.728 -12.123  1.00  0.00
ATOM  2439 CG  LEU A 670    -7.389  9.061 -11.706  1.00  0.00
ATOM  2440 CD1 LEU A 670    -6.275  9.444 -12.693  1.00  0.00
ATOM  2441 CD2 LEU A 670    -8.411 10.188 -11.504  1.00  0.00
ATOM  2442 HN  LEU A 670   -10.346  8.841 -12.735  1.00  0.00
ATOM  2443 HA  LEU A 670    -7.963  8.326 -14.199  1.00  0.00
ATOM  2444 1HB LEU A 670    -7.280  6.943 -12.114  1.00  0.00
ATOM  2445 2HB LEU A 670    -8.812  7.464 -11.405  1.00  0.00
ATOM  2446 HG  LEU A 670    -6.972  8.967 -10.703  1.00  0.00
ATOM  2447 1HD1 LEU A 670    -6.696  9.727 -13.658  1.00  0.00
ATOM  2448 2HD1 LEU A 670    -5.606  8.599 -12.852  1.00  0.00
ATOM  2449 3HD1 LEU A 670    -5.709 10.293 -12.311  1.00  0.00
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ATOM 2450 1HD2 LEU A 670 -9.306 9.812 -11.010 1.00 0.00
ATOM 2451 2HD2 LEU A 670 -8.707 10.604 -12.467 1.00 0.00
ATOM 2452 3HD2 LEU A 670 -7.986 10.974 -10.880 1.00 0.00
ATOM 2453 N LEU A 671 -9.926 5.787 -13.931 1.00 0.00
ATOM 2454 CA LEU A 671 -10.044 4.459 -14.453 1.00 0.00
ATOM 2455 C LEU A 671 -9.944 4.433 -15.955 1.00 0.00
ATOM 2456 O LEU A 671 -9.366 3.509 -16.522 1.00 0.00
ATOM 2457 CB LEU A 671 -11.309 3.731 -13.950 1.00 0.00
ATOM 2458 CG LEU A 671 -11.475 2.292 -14.479 1.00 0.00
ATOM 2459 CD1 LEU A 671 -12.424 1.474 -13.594 1.00 0.00
ATOM 2460 CD2 LEU A 671 -11.975 2.298 -15.931 1.00 0.00
ATOM 2461 HN LEU A 671 -10.685 6.211 -13.438 1.00 0.00
ATOM 2462 HA LEU A 671 -9.151 3.919 -14.139 1.00 0.00
ATOM 2463 1HB LEU A 671 -12.181 4.311 -14.250 1.00 0.00
ATOM 2464 2HB LEU A 671 -11.277 3.697 -12.862 1.00 0.00
ATOM 2465 HG LEU A 671 -10.501 1.805 -14.507 1.00 0.00
ATOM 2466 1HD1 LEU A 671 -13.450 1.827 -13.700 1.00 0.00
ATOM 2467 2HD1 LEU A 671 -12.140 1.571 -12.547 1.00 0.00
ATOM 2468 3HD1 LEU A 671 -12.398 0.424 -13.885 1.00 0.00
ATOM 2469 1HD2 LEU A 671 -12.110 3.319 -16.288 1.00 0.00
ATOM 2470 2HD2 LEU A 671 -12.936 1.787 -16.000 1.00 0.00
ATOM 2471 3HD2 LEU A 671 -11.251 1.806 -16.580 1.00 0.00
ATOM 2472 N LEU A 672 -10.499 5.448 -16.647 1.00 0.00
ATOM 2473 CA LEU A 672 -10.544 5.514 -18.089 1.00 0.00
ATOM 2474 C LEU A 672 -9.324 5.736 -18.977 1.00 0.00
ATOM 2475 O LEU A 672 -9.312 5.224 -20.093 1.00 0.00
ATOM 2476 CB LEU A 672 -11.620 6.488 -18.600 1.00 0.00
ATOM 2477 CG LEU A 672 -13.033 5.882 -18.591 1.00 0.00
ATOM 2478 CD1 LEU A 672 -13.210 4.877 -19.740 1.00 0.00
ATOM 2479 CD2 LEU A 672 -13.351 5.236 -17.239 1.00 0.00
ATOM 2480 HN LEU A 672 -10.904 6.201 -16.129 1.00 0.00
ATOM 2481 HA LEU A 672 -10.751 4.505 -18.444 1.00 0.00
ATOM 2482 1HB LEU A 672 -11.371 6.786 -19.618 1.00 0.00
ATOM 2483 2HB LEU A 672 -11.615 7.379 -17.972 1.00 0.00
ATOM 2484 HG LEU A 672 -13.769 6.679 -18.692 1.00 0.00
ATOM 2485 1HD1 LEU A 672 -12.388 4.161 -19.756 1.00 0.00
ATOM 2486 2HD1 LEU A 672 -13.222 5.398 -20.697 1.00 0.00
ATOM 2487 3HD1 LEU A 672 -14.139 4.321 -19.614 1.00 0.00
ATOM 2488 1HD2 LEU A 672 -12.588 5.489 -16.503 1.00 0.00
ATOM 2489 2HD2 LEU A 672 -13.379 4.151 -17.337 1.00 0.00
ATOM 2490 3HD2 LEU A 672 -14.310 5.596 -16.867 1.00 0.00
ATOM 2491 N SER A 673 -8.272 6.488 -18.577 1.00 0.00
ATOM 2492 CA SER A 673 -7.270 6.880 -19.559 1.00 0.00
ATOM 2493 C SER A 673 -6.215 5.842 -19.924 1.00 0.00
ATOM 2494 O SER A 673 -5.320 5.609 -19.119 1.00 0.00
ATOM 2495 CB SER A 673 -6.473 8.135 -19.153 1.00 0.00
ATOM 2496 OG SER A 673 -7.309 9.282 -19.137 1.00 0.00
ATOM 2497 HN SER A 673 -8.185 6.770 -17.621 1.00 0.00
ATOM 2498 HA SER A 673 -7.805 7.063 -20.491 1.00 0.00

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ATOM  2499 1HB  SER A 673     -5.667   8.315 -19.866  1.00  0.00
ATOM  2500 2HB  SER A 673     -6.055   8.007 -18.155  1.00  0.00
ATOM  2501  HG  SER A 673     -8.075   9.053 -18.627  1.00  0.00
ATOM  2502  N   SER A 674     -6.229   5.234 -21.156  1.00  0.00
ATOM  2503  CA  SER A 674     -5.225   4.221 -21.490  1.00  0.00
ATOM  2504  C   SER A 674     -5.519   3.470 -22.793  1.00  0.00
ATOM  2505  O   SER A 674     -6.620   3.564 -23.322  1.00  0.00
ATOM  2506  CB  SER A 674     -5.151   3.147 -20.380  1.00  0.00
ATOM  2507  OG  SER A 674     -4.245   2.107 -20.714  1.00  0.00
ATOM  2508  HN  SER A 674     -6.927   5.485 -21.827  1.00  0.00
ATOM  2509  HA  SER A 674     -4.270   4.734 -21.594  1.00  0.00
ATOM  2510 1HB  SER A 674     -6.133   2.699 -20.231  1.00  0.00
ATOM  2511 2HB  SER A 674     -4.811   3.599 -19.448  1.00  0.00
ATOM  2512  HG  SER A 674     -4.370   1.421 -20.072  1.00  0.00
ATOM  2513  N   VAL A 675     -4.521   2.672 -23.293  1.00  0.00
ATOM  2514  CA  VAL A 675     -4.423   1.847 -24.498  1.00  0.00
ATOM  2515  C   VAL A 675     -5.492   0.778 -24.497  1.00  0.00
ATOM  2516  O   VAL A 675     -6.542   1.113 -23.963  1.00  0.00
ATOM  2517  CB  VAL A 675     -3.003   1.312 -24.570  1.00  0.00
ATOM  2518  CG1 VAL A 675     -2.839   0.093 -23.643  1.00  0.00
ATOM  2519  CG2 VAL A 675     -2.509   1.219 -26.026  1.00  0.00
ATOM  2520  HN  VAL A 675     -3.705   2.649 -22.725  1.00  0.00
ATOM  2521  HA  VAL A 675     -4.654   2.476 -25.357  1.00  0.00
ATOM  2522  HB  VAL A 675     -2.304   2.093 -24.273  1.00  0.00
ATOM  2523 1HG1 VAL A 675     -3.780  -0.449 -23.550  1.00  0.00
ATOM  2524 2HG1 VAL A 675     -2.536   0.416 -22.647  1.00  0.00
ATOM  2525 3HG1 VAL A 675     -2.095  -0.591 -24.049  1.00  0.00
ATOM  2526 1HG2 VAL A 675     -1.874   2.069 -26.273  1.00  0.00
ATOM  2527 2HG2 VAL A 675     -3.357   1.221 -26.712  1.00  0.00
ATOM  2528 3HG2 VAL A 675     -1.925   0.310 -26.168  1.00  0.00
ATOM  2529  N   PRO A 676     -5.477  -0.434 -25.043  1.00  0.00
ATOM  2530  CA  PRO A 676     -4.453  -1.012 -25.884  1.00  0.00
ATOM  2531  C   PRO A 676     -4.796  -0.749 -27.315  1.00  0.00
ATOM  2532  O   PRO A 676     -5.914  -0.312 -27.586  1.00  0.00
ATOM  2533  CB  PRO A 676     -4.440  -2.512 -25.580  1.00  0.00
ATOM  2534  CG  PRO A 676     -5.840  -2.792 -25.019  1.00  0.00
ATOM  2535  CD  PRO A 676     -6.217  -1.471 -24.338  1.00  0.00
ATOM  2536 1HD  PRO A 676     -7.288  -1.284 -24.415  1.00  0.00
ATOM  2537 2HD  PRO A 676     -5.937  -1.481 -23.285  1.00  0.00
ATOM  2538  HA  PRO A 676     -3.487  -0.562 -25.656  1.00  0.00
ATOM  2539 1HB  PRO A 676     -3.668  -2.759 -24.852  1.00  0.00
ATOM  2540 2HB  PRO A 676     -4.255  -3.094 -26.483  1.00  0.00
ATOM  2541 1HG  PRO A 676     -6.543  -3.044 -25.813  1.00  0.00
ATOM  2542 2HG  PRO A 676     -5.823  -3.615 -24.304  1.00  0.00
ATOM  2543  N   LYS A 677     -3.859  -1.003 -28.252  1.00  0.00
ATOM  2544  CA  LYS A 677     -4.201  -0.796 -29.627  1.00  0.00
ATOM  2545  C   LYS A 677     -4.195  -2.100 -30.367  1.00  0.00
ATOM  2546  O   LYS A 677     -3.171  -2.541 -30.886  1.00  0.00
ATOM  2547  CB  LYS A 677     -3.275   0.192 -30.374  1.00  0.00
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ATOM 2548 CG LYS A 677 -1.800 -0.215 -30.473 1.00 0.00
ATOM 2549 CD LYS A 677 -1.037 0.541 -31.565 1.00 0.00
ATOM 2550 CE LYS A 677 0.377 0.011 -31.813 1.00 0.00
ATOM 2551 NZ LYS A 677 0.959 0.660 -33.010 1.00 0.00
ATOM 2552 HN LYS A 677 -2.949 -1.328 -27.992 1.00 0.00
ATOM 2553 HA LYS A 677 -5.223 -0.419 -29.633 1.00 0.00
ATOM 2554 1HB LYS A 677 -3.327 1.153 -29.866 1.00 0.00
ATOM 2555 2HB LYS A 677 -3.659 0.316 -31.385 1.00 0.00
ATOM 2556 1HG LYS A 677 -1.743 -1.283 -30.680 1.00 0.00
ATOM 2557 2HG LYS A 677 -1.319 -0.026 -29.514 1.00 0.00
ATOM 2558 1HD LYS A 677 -0.970 1.590 -31.280 1.00 0.00
ATOM 2559 2HD LYS A 677 -1.601 0.474 -32.494 1.00 0.00
ATOM 2560 1HE LYS A 677 0.354 -1.065 -31.986 1.00 0.00
ATOM 2561 2HE LYS A 677 1.020 0.231 -30.961 1.00 0.00
ATOM 2562 1HZ LYS A 677 1.000 1.688 -32.862 1.00 0.00
ATOM 2563 2HZ LYS A 677 0.366 0.453 -33.839 1.00 0.00
ATOM 2564 3HZ LYS A 677 1.919 0.294 -33.171 1.00 0.00
ATOM 2565 N ASP A 678 -5.355 -2.780 -30.419 1.00 0.00
ATOM 2566 CA ASP A 678 -5.403 -3.975 -31.206 1.00 0.00
ATOM 2567 C ASP A 678 -5.302 -3.500 -32.613 1.00 0.00
ATOM 2568 O ASP A 678 -4.614 -4.095 -33.442 1.00 0.00
ATOM 2569 CB ASP A 678 -6.712 -4.768 -31.063 1.00 0.00
ATOM 2570 CG ASP A 678 -6.667 -5.508 -29.735 1.00 0.00
ATOM 2571 OD1 ASP A 678 -7.705 -6.119 -29.363 1.00 0.00
ATOM 2572 OD2 ASP A 678 -5.594 -5.476 -29.076 1.00 0.00
ATOM 2573 HN ASP A 678 -6.161 -2.459 -29.921 1.00 0.00
ATOM 2574 HA ASP A 678 -4.562 -4.588 -30.882 1.00 0.00
ATOM 2575 1HB ASP A 678 -6.815 -5.488 -31.875 1.00 0.00
ATOM 2576 2HB ASP A 678 -7.571 -4.096 -31.073 1.00 0.00
ATOM 2577 N GLY A 679 -5.989 -2.381 -32.908 1.00 0.00
ATOM 2578 CA GLY A 679 -5.943 -1.827 -34.223 1.00 0.00
ATOM 2579 C GLY A 679 -7.129 -0.938 -34.393 1.00 0.00
ATOM 2580 O GLY A 679 -7.322 0.016 -33.642 1.00 0.00
ATOM 2581 HN GLY A 679 -6.535 -1.934 -32.199 1.00 0.00
ATOM 2582 1HA GLY A 679 -5.978 -2.646 -34.940 1.00 0.00
ATOM 2583 2HA GLY A 679 -5.023 -1.253 -34.321 1.00 0.00
ATOM 2584 N LEU A 680 -7.974 -1.247 -35.390 1.00 0.00
ATOM 2585 CA LEU A 680 -9.110 -0.416 -35.644 1.00 0.00
ATOM 2586 C LEU A 680 -9.988 -0.447 -34.444 1.00 0.00
ATOM 2587 O LEU A 680 -10.549 0.573 -34.047 1.00 0.00
ATOM 2588 CB LEU A 680 -9.935 -0.874 -36.858 1.00 0.00
ATOM 2589 CG LEU A 680 -9.171 -0.731 -38.187 1.00 0.00
ATOM 2590 CD1 LEU A 680 -7.937 -1.648 -38.224 1.00 0.00
ATOM 2591 CD2 LEU A 680 -10.102 -0.926 -39.392 1.00 0.00
ATOM 2592 HN LEU A 680 -7.809 -2.056 -35.954 1.00 0.00
ATOM 2593 HA LEU A 680 -8.728 0.591 -35.810 1.00 0.00
ATOM 2594 1HB LEU A 680 -10.847 -0.280 -36.909 1.00 0.00
ATOM 2595 2HB LEU A 680 -10.214 -1.918 -36.722 1.00 0.00
ATOM 2596 HG LEU A 680 -8.853 0.304 -38.310 1.00 0.00

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ATOM  2597 1HD1 LEU A 680     -8.164  -2.616 -37.778  1.00  0.00
ATOM  2598 2HD1 LEU A 680     -7.118  -1.201 -37.661  1.00  0.00
ATOM  2599 3HD1 LEU A 680     -7.625  -1.816 -39.255  1.00  0.00
ATOM  2600 1HD2 LEU A 680    -10.902  -0.186 -39.385  1.00  0.00
ATOM  2601 2HD2 LEU A 680    -10.558  -1.916 -39.359  1.00  0.00
ATOM  2602 3HD2 LEU A 680     -9.544  -0.811 -40.321  1.00  0.00
ATOM  2603  N   LYS A 681    -10.116  -1.628 -33.820  1.00  0.00
ATOM  2604  CA  LYS A 681    -10.950  -1.737 -32.666  1.00  0.00
ATOM  2605  C   LYS A 681    -10.397  -0.839 -31.612  1.00  0.00
ATOM  2606  O   LYS A 681    -11.152  -0.186 -30.892  1.00  0.00
ATOM  2607  CB  LYS A 681    -10.994  -3.159 -32.086  1.00  0.00
ATOM  2608  CG  LYS A 681    -11.782  -4.143 -32.953  1.00  0.00
ATOM  2609  CD  LYS A 681    -13.264  -3.791 -33.083  1.00  0.00
ATOM  2610  CE  LYS A 681    -14.052  -4.774 -33.949  1.00  0.00
ATOM  2611  NZ  LYS A 681    -13.595  -4.689 -35.355  1.00  0.00
ATOM  2612  HN  LYS A 681     -9.628  -2.430 -34.164  1.00  0.00
ATOM  2613  HA  LYS A 681    -11.949  -1.428 -32.973  1.00  0.00
ATOM  2614 1HB  LYS A 681    -11.449  -3.121 -31.097  1.00  0.00
ATOM  2615 2HB  LYS A 681     -9.974  -3.526 -31.979  1.00  0.00
ATOM  2616 1HG  LYS A 681    -11.696  -5.138 -32.518  1.00  0.00
ATOM  2617 2HG  LYS A 681    -11.339  -4.164 -33.947  1.00  0.00
ATOM  2618 1HD  LYS A 681    -13.349  -2.796 -33.519  1.00  0.00
ATOM  2619 2HD  LYS A 681    -13.707  -3.768 -32.089  1.00  0.00
ATOM  2620 1HE  LYS A 681    -15.115  -4.536 -33.922  1.00  0.00
ATOM  2621 2HE  LYS A 681    -13.897  -5.795 -33.601  1.00  0.00
ATOM  2622 1HZ  LYS A 681    -12.583  -4.924 -35.405  1.00  0.00
ATOM  2623 2HZ  LYS A 681    -13.744  -3.724 -35.711  1.00  0.00
ATOM  2624 3HZ  LYS A 681    -14.135  -5.361 -35.937  1.00  0.00
ATOM  2625  N   SER A 682     -9.058  -0.771 -31.496  1.00  0.00
ATOM  2626  CA  SER A 682     -8.516   0.051 -30.459  1.00  0.00
ATOM  2627  C   SER A 682     -8.919   1.467 -30.694  1.00  0.00
ATOM  2628  O   SER A 682     -9.388   2.127 -29.772  1.00  0.00
ATOM  2629  CB  SER A 682     -6.978   0.012 -30.339  1.00  0.00
ATOM  2630  OG  SER A 682     -6.366   0.766 -31.373  1.00  0.00
ATOM  2631  HN  SER A 682     -8.462  -1.280 -32.115  1.00  0.00
ATOM  2632  HA  SER A 682     -8.965  -0.299 -29.529  1.00  0.00
ATOM  2633 1HB  SER A 682     -6.623  -1.016 -30.417  1.00  0.00
ATOM  2634 2HB  SER A 682     -6.667   0.434 -29.384  1.00  0.00
ATOM  2635  HG  SER A 682     -7.010   0.857 -32.062  1.00  0.00
ATOM  2636  N   GLN A 683     -8.804   1.975 -31.937  1.00  0.00
ATOM  2637  CA  GLN A 683     -9.159   3.355 -32.108  1.00  0.00
ATOM  2638  C   GLN A 683    -10.607   3.525 -31.795  1.00  0.00
ATOM  2639  O   GLN A 683    -11.012   4.550 -31.250  1.00  0.00
ATOM  2640  CB  GLN A 683     -8.907   3.961 -33.504  1.00  0.00
ATOM  2641  CG  GLN A 683     -9.702   3.344 -34.655  1.00  0.00
ATOM  2642  CD  GLN A 683     -8.737   2.506 -35.476  1.00  0.00
ATOM  2643  OE1 GLN A 683     -7.665   2.128 -35.005  1.00  0.00
ATOM  2644  NE2 GLN A 683     -9.115   2.226 -36.752  1.00  0.00
ATOM  2645  HN  GLN A 683     -8.486   1.417 -32.703  1.00  0.00
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ATOM 2646 HA GLN A 683 -8.576 3.903 -31.368 1.00 0.00
ATOM 2647 1HB GLN A 683 -7.848 3.855 -33.731 1.00 0.00
ATOM 2648 2HB GLN A 683 -9.146 5.022 -33.459 1.00 0.00
ATOM 2649 1HG GLN A 683 -10.134 4.122 -35.285 1.00 0.00
ATOM 2650 2HG GLN A 683 -10.502 2.709 -34.274 1.00 0.00
ATOM 2651 1HE2 GLN A 683 -8.460 1.811 -37.383 1.00 0.00
ATOM 2652 2HE2 GLN A 683 -10.039 2.429 -37.075 1.00 0.00
ATOM 2653 N GLU A 684 -11.433 2.521 -32.140 1.00 0.00
ATOM 2654 CA GLU A 684 -12.839 2.607 -31.877 1.00 0.00
ATOM 2655 C GLU A 684 -13.018 2.688 -30.394 1.00 0.00
ATOM 2656 O GLU A 684 -13.812 3.478 -29.888 1.00 0.00
ATOM 2657 CB GLU A 684 -13.597 1.362 -32.363 1.00 0.00
ATOM 2658 CG GLU A 684 -15.098 1.590 -32.521 1.00 0.00
ATOM 2659 CD GLU A 684 -15.285 2.313 -33.845 1.00 0.00
ATOM 2660 OE1 GLU A 684 -14.495 2.028 -34.784 1.00 0.00
ATOM 2661 OE2 GLU A 684 -16.211 3.162 -33.936 1.00 0.00
ATOM 2662 HN GLU A 684 -11.061 1.706 -32.584 1.00 0.00
ATOM 2663 HA GLU A 684 -13.203 3.496 -32.392 1.00 0.00
ATOM 2664 1HB GLU A 684 -13.438 0.554 -31.649 1.00 0.00
ATOM 2665 2HB GLU A 684 -13.186 1.055 -33.324 1.00 0.00
ATOM 2666 1HG GLU A 684 -15.486 2.204 -31.708 1.00 0.00
ATOM 2667 2HG GLU A 684 -15.636 0.642 -32.540 1.00 0.00
ATOM 2668 N LEU A 685 -12.256 1.860 -29.660 1.00 0.00
ATOM 2669 CA LEU A 685 -12.333 1.834 -28.230 1.00 0.00
ATOM 2670 C LEU A 685 -11.900 3.180 -27.745 1.00 0.00
ATOM 2671 O LEU A 685 -12.485 3.719 -26.809 1.00 0.00
ATOM 2672 CB LEU A 685 -11.418 0.741 -27.624 1.00 0.00
ATOM 2673 CG LEU A 685 -11.464 0.523 -26.089 1.00 0.00
ATOM 2674 CD1 LEU A 685 -10.495 -0.600 -25.688 1.00 0.00
ATOM 2675 CD2 LEU A 685 -11.179 1.793 -25.269 1.00 0.00
ATOM 2676 HN LEU A 685 -11.618 1.246 -30.124 1.00 0.00
ATOM 2677 HA LEU A 685 -13.374 1.643 -27.972 1.00 0.00
ATOM 2678 1HB LEU A 685 -10.393 0.988 -27.890 1.00 0.00
ATOM 2679 2HB LEU A 685 -11.679 -0.203 -28.097 1.00 0.00
ATOM 2680 HG LEU A 685 -12.477 0.258 -25.787 1.00 0.00
ATOM 2681 1HD1 LEU A 685 -9.565 -0.186 -25.300 1.00 0.00
ATOM 2682 2HD1 LEU A 685 -10.254 -1.217 -26.554 1.00 0.00
ATOM 2683 3HD1 LEU A 685 -10.939 -1.220 -24.909 1.00 0.00
ATOM 2684 1HD2 LEU A 685 -12.108 2.238 -24.912 1.00 0.00
ATOM 2685 2HD2 LEU A 685 -10.667 2.532 -25.886 1.00 0.00
ATOM 2686 3HD2 LEU A 685 -10.566 1.552 -24.401 1.00 0.00
ATOM 2687 N PHE A 686 -10.863 3.764 -28.371 1.00 0.00
ATOM 2688 CA PHE A 686 -10.358 5.027 -27.916 1.00 0.00
ATOM 2689 C PHE A 686 -11.389 6.090 -28.050 1.00 0.00
ATOM 2690 O PHE A 686 -11.546 6.926 -27.162 1.00 0.00
ATOM 2691 CB PHE A 686 -9.101 5.529 -28.657 1.00 0.00
ATOM 2692 CG PHE A 686 -7.902 4.803 -28.143 1.00 0.00
ATOM 2693 CD1 PHE A 686 -7.383 3.716 -28.806 1.00 0.00
ATOM 2694 CD2 PHE A 686 -7.315 5.198 -26.963 1.00 0.00

ATOM 2695 CE1 PHE A 686 -6.291 3.042 -28.311 1.00 0.00
ATOM 2696 CE2 PHE A 686 -6.225 4.527 -26.460 1.00 0.00
ATOM 2697 CZ PHE A 686 -5.709 3.448 -27.134 1.00 0.00
ATOM 2698 HN PHE A 686 -10.442 3.314 -29.159 1.00 0.00
ATOM 2699 HA PHE A 686 -10.131 4.898 -26.858 1.00 0.00
ATOM 2700 1HB PHE A 686 -8.971 6.599 -28.491 1.00 0.00
ATOM 2701 2HB PHE A 686 -9.199 5.348 -29.727 1.00 0.00
ATOM 2702 HD1 PHE A 686 -7.839 3.387 -29.728 1.00 0.00
ATOM 2703 HD2 PHE A 686 -7.715 6.044 -26.425 1.00 0.00
ATOM 2704 HE1 PHE A 686 -5.891 2.195 -28.848 1.00 0.00
ATOM 2705 HE2 PHE A 686 -5.773 4.850 -25.534 1.00 0.00
ATOM 2706 HZ PHE A 686 -4.852 2.920 -26.742 1.00 0.00
ATOM 2707 N ASP A 687 -12.135 6.092 -29.164 1.00 0.00
ATOM 2708 CA ASP A 687 -13.083 7.148 -29.329 1.00 0.00
ATOM 2709 C ASP A 687 -14.094 7.068 -28.235 1.00 0.00
ATOM 2710 O ASP A 687 -14.430 8.074 -27.612 1.00 0.00
ATOM 2711 CB ASP A 687 -13.841 7.083 -30.663 1.00 0.00
ATOM 2712 CG ASP A 687 -14.550 8.418 -30.818 1.00 0.00
ATOM 2713 OD1 ASP A 687 -14.445 9.244 -29.873 1.00 0.00
ATOM 2714 OD2 ASP A 687 -15.199 8.632 -31.876 1.00 0.00
ATOM 2715 HN ASP A 687 -12.030 5.378 -29.856 1.00 0.00
ATOM 2716 HA ASP A 687 -12.523 8.080 -29.263 1.00 0.00
ATOM 2717 1HB ASP A 687 -14.573 6.276 -30.656 1.00 0.00
ATOM 2718 2HB ASP A 687 -13.153 6.933 -31.495 1.00 0.00
ATOM 2719 N GLU A 688 -14.578 5.849 -27.942 1.00 0.00
ATOM 2720 CA GLU A 688 -15.609 5.742 -26.962 1.00 0.00
ATOM 2721 C GLU A 688 -15.131 6.282 -25.656 1.00 0.00
ATOM 2722 O GLU A 688 -15.805 7.105 -25.037 1.00 0.00
ATOM 2723 CB GLU A 688 -16.078 4.297 -26.724 1.00 0.00
ATOM 2724 CG GLU A 688 -17.293 4.220 -25.797 1.00 0.00
ATOM 2725 CD GLU A 688 -17.856 2.809 -25.859 1.00 0.00
ATOM 2726 OE1 GLU A 688 -17.087 1.874 -26.206 1.00 0.00
ATOM 2727 OE2 GLU A 688 -19.070 2.652 -25.564 1.00 0.00
ATOM 2728 HN GLU A 688 -14.223 5.035 -28.402 1.00 0.00
ATOM 2729 HA GLU A 688 -16.441 6.349 -27.319 1.00 0.00
ATOM 2730 1HB GLU A 688 -15.260 3.727 -26.283 1.00 0.00
ATOM 2731 2HB GLU A 688 -16.333 3.845 -27.681 1.00 0.00
ATOM 2732 1HG GLU A 688 -18.059 4.926 -26.116 1.00 0.00
ATOM 2733 2HG GLU A 688 -17.004 4.446 -24.771 1.00 0.00
ATOM 2734 N ILE A 689 -13.936 5.865 -25.202 1.00 0.00
ATOM 2735 CA ILE A 689 -13.526 6.370 -23.928 1.00 0.00
ATOM 2736 C ILE A 689 -13.262 7.842 -23.953 1.00 0.00
ATOM 2737 O ILE A 689 -13.552 8.537 -22.983 1.00 0.00
ATOM 2738 CB ILE A 689 -12.444 5.577 -23.235 1.00 0.00
ATOM 2739 CG1 ILE A 689 -11.151 5.446 -24.042 1.00 0.00
ATOM 2740 CG2 ILE A 689 -13.060 4.229 -22.839 1.00 0.00
ATOM 2741 CD1 ILE A 689 -10.067 4.699 -23.265 1.00 0.00
ATOM 2742 HN ILE A 689 -13.365 5.235 -25.728 1.00 0.00
ATOM 2743 HA ILE A 689 -14.422 6.382 -23.309 1.00 0.00

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ATOM  2744 HB  ILE A 689    -12.091   6.109 -22.350  1.00  0.00
ATOM  2745 1HG2 ILE A 689    -13.250   3.618 -23.722  1.00  0.00
ATOM  2746 2HG2 ILE A 689    -14.010   4.384 -22.327  1.00  0.00
ATOM  2747 3HG2 ILE A 689    -12.379   3.679 -22.189  1.00  0.00
ATOM  2748 1HG1 ILE A 689    -10.787   6.441 -24.298  1.00  0.00
ATOM  2749 2HG1 ILE A 689    -11.361   4.911 -24.968  1.00  0.00
ATOM  2750 1HD1 ILE A 689    -10.400   3.693 -23.010  1.00  0.00
ATOM  2751 2HD1 ILE A 689     -9.839   5.223 -22.337  1.00  0.00
ATOM  2752 3HD1 ILE A 689     -9.163   4.612 -23.868  1.00  0.00
ATOM  2753 N   ARG A 690    -12.745   8.378 -25.070  1.00  0.00
ATOM  2754 CA  ARG A 690    -12.504   9.793 -25.120  1.00  0.00
ATOM  2755 C   ARG A 690    -13.821  10.474 -24.910  1.00  0.00
ATOM  2756 O   ARG A 690    -13.918  11.457 -24.178  1.00  0.00
ATOM  2757 CB  ARG A 690    -11.949  10.243 -26.483  1.00  0.00
ATOM  2758 CG  ARG A 690    -10.620   9.572 -26.842  1.00  0.00
ATOM  2759 CD  ARG A 690    -10.025  10.023 -28.178  1.00  0.00
ATOM  2760 NE  ARG A 690     -9.259  11.276 -27.924  1.00  0.00
ATOM  2761 CZ  ARG A 690     -8.030  11.450 -28.490  1.00  0.00
ATOM  2762 NH1 ARG A 690     -7.500  10.477 -29.289  1.00  0.00
ATOM  2763 NH2 ARG A 690     -7.324  12.595 -28.252  1.00  0.00
ATOM  2764 HN  ARG A 690    -12.530   7.799 -25.857  1.00  0.00
ATOM  2765 HA  ARG A 690    -11.789  10.018 -24.328  1.00  0.00
ATOM  2766 1HB  ARG A 690    -11.804  11.323 -26.465  1.00  0.00
ATOM  2767 2HB  ARG A 690    -12.680  10.009 -27.256  1.00  0.00
ATOM  2768 1HG  ARG A 690    -10.776   8.495 -26.879  1.00  0.00
ATOM  2769 2HG  ARG A 690     -9.901   9.788 -26.053  1.00  0.00
ATOM  2770 1HD  ARG A 690    -10.805  10.246 -28.905  1.00  0.00
ATOM  2771 2HD  ARG A 690     -9.335   9.280 -28.576  1.00  0.00
ATOM  2772 HE  ARG A 690     -9.645  11.990 -27.339  1.00  0.00
ATOM  2773 1HH1 ARG A 690     -8.014   9.636 -29.460  1.00  0.00
ATOM  2774 2HH1 ARG A 690     -6.599  10.606 -29.703  1.00  0.00
ATOM  2775 1HH2 ARG A 690     -7.708  13.306 -27.663  1.00  0.00
ATOM  2776 2HH2 ARG A 690     -6.423  12.722 -28.667  1.00  0.00
ATOM  2777 N   MET A 691    -14.880   9.937 -25.544  1.00  0.00
ATOM  2778 CA  MET A 691    -16.196  10.500 -25.455  1.00  0.00
ATOM  2779 C   MET A 691    -16.711  10.474 -24.049  1.00  0.00
ATOM  2780 O   MET A 691    -17.297  11.450 -23.583  1.00  0.00
ATOM  2781 CB  MET A 691    -17.218   9.745 -26.318  1.00  0.00
ATOM  2782 CG  MET A 691    -18.627  10.331 -26.228  1.00  0.00
ATOM  2783 SD  MET A 691    -18.833  11.973 -26.976  1.00  0.00
ATOM  2784 CE  MET A 691    -20.569  12.136 -26.468  1.00  0.00
ATOM  2785 HN  MET A 691    -14.743   9.115 -26.097  1.00  0.00
ATOM  2786 HA  MET A 691    -16.117  11.536 -25.785  1.00  0.00
ATOM  2787 1HB  MET A 691    -17.248   8.705 -25.998  1.00  0.00
ATOM  2788 2HB  MET A 691    -16.891   9.774 -27.357  1.00  0.00
ATOM  2789 1HG  MET A 691    -18.904  10.410 -25.178  1.00  0.00
ATOM  2790 2HG  MET A 691    -19.318   9.652 -26.726  1.00  0.00
ATOM  2791 1HE  MET A 691    -20.636  12.085 -25.381  1.00  0.00
ATOM  2792 2HE  MET A 691    -21.157  11.321 -26.891  1.00  0.00
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ATOM 2793 3HE MET A 691 -20.963 13.097 -26.797 1.00 0.00
ATOM 2794 N THR A 692 -16.508 9.357 -23.329 1.00 0.00
ATOM 2795 CA THR A 692 -16.995 9.258 -21.982 1.00 0.00
ATOM 2796 C THR A 692 -16.283 10.306 -21.199 1.00 0.00
ATOM 2797 O THR A 692 -16.863 10.948 -20.323 1.00 0.00
ATOM 2798 CB THR A 692 -16.680 7.937 -21.344 1.00 0.00
ATOM 2799 OG1 THR A 692 -17.264 6.880 -22.089 1.00 0.00
ATOM 2800 CG2 THR A 692 -17.230 7.943 -19.907 1.00 0.00
ATOM 2801 HN THR A 692 -16.014 8.588 -23.736 1.00 0.00
ATOM 2802 HA THR A 692 -18.074 9.404 -22.029 1.00 0.00
ATOM 2803 HB THR A 692 -15.602 7.779 -21.316 1.00 0.00
ATOM 2804 HG1 THR A 692 -16.785 6.824 -22.905 1.00 0.00
ATOM 2805 1HG2 THR A 692 -18.113 8.578 -19.836 1.00 0.00
ATOM 2806 2HG2 THR A 692 -16.480 8.329 -19.218 1.00 0.00
ATOM 2807 3HG2 THR A 692 -17.516 6.934 -19.610 1.00 0.00
ATOM 2808 N TYR A 693 -14.990 10.511 -21.517 1.00 0.00
ATOM 2809 CA TYR A 693 -14.227 11.517 -20.844 1.00 0.00
ATOM 2810 C TYR A 693 -14.929 12.817 -20.883 1.00 0.00
ATOM 2811 O TYR A 693 -15.150 13.421 -19.838 1.00 0.00
ATOM 2812 CB TYR A 693 -12.888 11.823 -21.527 1.00 0.00
ATOM 2813 CG TYR A 693 -11.895 10.964 -20.883 1.00 0.00
ATOM 2814 CD1 TYR A 693 -11.864 9.613 -21.108 1.00 0.00
ATOM 2815 CD2 TYR A 693 -11.090 11.555 -19.944 1.00 0.00
ATOM 2816 CE1 TYR A 693 -11.078 8.830 -20.307 1.00 0.00
ATOM 2817 CE2 TYR A 693 -10.292 10.784 -19.157 1.00 0.00
ATOM 2818 CZ TYR A 693 -10.331 9.429 -19.322 1.00 0.00
ATOM 2819 OH TYR A 693 -9.721 8.651 -18.344 1.00 0.00
ATOM 2820 HN TYR A 693 -14.562 9.956 -22.230 1.00 0.00
ATOM 2821 HA TYR A 693 -14.054 11.149 -19.833 1.00 0.00
ATOM 2822 1HB TYR A 693 -12.616 12.871 -21.396 1.00 0.00
ATOM 2823 2HB TYR A 693 -12.937 11.603 -22.594 1.00 0.00
ATOM 2824 HD1 TYR A 693 -12.448 9.174 -21.902 1.00 0.00
ATOM 2825 HE1 TYR A 693 -11.046 7.760 -20.446 1.00 0.00
ATOM 2826 HD2 TYR A 693 -11.089 12.629 -19.830 1.00 0.00
ATOM 2827 HE2 TYR A 693 -9.643 11.233 -18.420 1.00 0.00
ATOM 2828 HH TYR A 693 -9.926 9.002 -17.487 1.00 0.00
ATOM 2829 N ILE A 694 -15.324 13.266 -22.084 1.00 0.00
ATOM 2830 CA ILE A 694 -15.905 14.570 -22.166 1.00 0.00
ATOM 2831 C ILE A 694 -17.151 14.605 -21.352 1.00 0.00
ATOM 2832 O ILE A 694 -17.425 15.590 -20.668 1.00 0.00
ATOM 2833 CB ILE A 694 -16.243 15.008 -23.564 1.00 0.00
ATOM 2834 CG1 ILE A 694 -16.539 16.517 -23.576 1.00 0.00
ATOM 2835 CG2 ILE A 694 -17.401 14.145 -24.087 1.00 0.00
ATOM 2836 CD1 ILE A 694 -16.577 17.126 -24.977 1.00 0.00
ATOM 2837 HN ILE A 694 -15.214 12.701 -22.902 1.00 0.00
ATOM 2838 HA ILE A 694 -15.179 15.256 -21.730 1.00 0.00
ATOM 2839 HB ILE A 694 -15.373 14.893 -24.210 1.00 0.00
ATOM 2840 1HG2 ILE A 694 -18.314 14.734 -24.170 1.00 0.00
ATOM 2841 2HG2 ILE A 694 -17.595 13.319 -23.402 1.00 0.00

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ATOM  2842 3HG2 ILE A 694   -17.162  13.753 -25.075  1.00  0.00
ATOM  2843 1HG1 ILE A 694   -15.771  17.028 -22.995  1.00  0.00
ATOM  2844 2HG1 ILE A 694   -17.502  16.688 -23.096  1.00  0.00
ATOM  2845 1HD1 ILE A 694   -17.351  16.652 -25.582  1.00  0.00
ATOM  2846 2HD1 ILE A 694   -15.621  16.978 -25.478  1.00  0.00
ATOM  2847 3HD1 ILE A 694   -16.801  18.191 -24.919  1.00  0.00
ATOM  2848  N   LYS A 695   -17.938  13.516 -21.384  1.00  0.00
ATOM  2849  CA  LYS A 695   -19.157  13.529 -20.639  1.00  0.00
ATOM  2850  C   LYS A 695   -18.843  13.722 -19.190  1.00  0.00
ATOM  2851  O   LYS A 695   -19.467  14.547 -18.523  1.00  0.00
ATOM  2852  CB  LYS A 695   -19.967  12.229 -20.781  1.00  0.00
ATOM  2853  CG  LYS A 695   -21.302  12.282 -20.036  1.00  0.00
ATOM  2854  CD  LYS A 695   -22.279  13.304 -20.617  1.00  0.00
ATOM  2855  CE  LYS A 695   -23.558  13.464 -19.793  1.00  0.00
ATOM  2856  NZ  LYS A 695   -23.266  14.222 -18.556  1.00  0.00
ATOM  2857  HN  LYS A 695   -17.674  12.713 -21.918  1.00  0.00
ATOM  2858  HA  LYS A 695   -19.739  14.373 -21.009  1.00  0.00
ATOM  2859 1HB  LYS A 695   -19.377  11.400 -20.390  1.00  0.00
ATOM  2860 2HB  LYS A 695   -20.158  12.045 -21.837  1.00  0.00
ATOM  2861 1HG  LYS A 695   -21.111  12.532 -18.993  1.00  0.00
ATOM  2862 2HG  LYS A 695   -21.763  11.296 -20.073  1.00  0.00
ATOM  2863 1HD  LYS A 695   -22.550  12.995 -21.626  1.00  0.00
ATOM  2864 2HD  LYS A 695   -21.780  14.270 -20.678  1.00  0.00
ATOM  2865 1HE  LYS A 695   -23.952  12.488 -19.510  1.00  0.00
ATOM  2866 2HE  LYS A 695   -24.310  14.013 -20.360  1.00  0.00
ATOM  2867 1HZ  LYS A 695   -22.898  15.162 -18.804  1.00  0.00
ATOM  2868 2HZ  LYS A 695   -22.557  13.709 -17.994  1.00  0.00
ATOM  2869 3HZ  LYS A 695   -24.139  14.328 -18.000  1.00  0.00
ATOM  2870  N   GLU A 696   -17.839  12.994 -18.659  1.00  0.00
ATOM  2871  CA  GLU A 696   -17.555  13.155 -17.265  1.00  0.00
ATOM  2872  C   GLU A 696   -17.124  14.559 -17.009  1.00  0.00
ATOM  2873  O   GLU A 696   -17.494  15.140 -15.989  1.00  0.00
ATOM  2874  CB  GLU A 696   -16.462  12.236 -16.677  1.00  0.00
ATOM  2875  CG  GLU A 696   -15.054  12.411 -17.246  1.00  0.00
ATOM  2876  CD  GLU A 696   -14.677  11.126 -17.965  1.00  0.00
ATOM  2877  OE1 GLU A 696   -15.592  10.298 -18.223  1.00  0.00
ATOM  2878  OE2 GLU A 696   -13.465  10.951 -18.262  1.00  0.00
ATOM  2879  HN  GLU A 696   -17.310  12.361 -19.224  1.00  0.00
ATOM  2880  HA  GLU A 696   -18.496  12.970 -16.749  1.00  0.00
ATOM  2881 1HB  GLU A 696   -16.766  11.204 -16.843  1.00  0.00
ATOM  2882 2HB  GLU A 696   -16.416  12.412 -15.604  1.00  0.00
ATOM  2883 1HG  GLU A 696   -14.338  12.600 -16.446  1.00  0.00
ATOM  2884 2HG  GLU A 696   -15.026  13.241 -17.952  1.00  0.00
ATOM  2885  N   LEU A 697   -16.332  15.163 -17.919  1.00  0.00
ATOM  2886  CA  LEU A 697   -15.923  16.501 -17.606  1.00  0.00
ATOM  2887  C   LEU A 697   -17.125  17.387 -17.521  1.00  0.00
ATOM  2888  O   LEU A 697   -17.223  18.217 -16.619  1.00  0.00
ATOM  2889  CB  LEU A 697   -14.934  17.177 -18.580  1.00  0.00
ATOM  2890  CG  LEU A 697   -13.522  16.555 -18.621  1.00  0.00
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ATOM 2891 CD1 LEU A 697 -13.050 16.137 -17.219 1.00 0.00
ATOM 2892 CD2 LEU A 697 -13.367 15.482 -19.702 1.00 0.00
ATOM 2893 HN LEU A 697 -16.049 14.705 -18.760 1.00 0.00
ATOM 2894 HA LEU A 697 -15.468 16.443 -16.618 1.00 0.00
ATOM 2895 1HB LEU A 697 -14.838 18.223 -18.297 1.00 0.00
ATOM 2896 2HB LEU A 697 -15.357 17.129 -19.582 1.00 0.00
ATOM 2897 HG LEU A 697 -12.821 17.280 -19.034 1.00 0.00
ATOM 2898 1HD1 LEU A 697 -13.342 15.109 -17.005 1.00 0.00
ATOM 2899 2HD1 LEU A 697 -13.501 16.780 -16.463 1.00 0.00
ATOM 2900 3HD1 LEU A 697 -11.964 16.199 -17.153 1.00 0.00
ATOM 2901 1HD2 LEU A 697 -12.720 15.834 -20.504 1.00 0.00
ATOM 2902 2HD2 LEU A 697 -14.338 15.241 -20.134 1.00 0.00
ATOM 2903 3HD2 LEU A 697 -12.921 14.583 -19.278 1.00 0.00
ATOM 2904 N GLY A 698 -18.088 17.215 -18.447 1.00 0.00
ATOM 2905 CA GLY A 698 -19.251 18.055 -18.451 1.00 0.00
ATOM 2906 C GLY A 698 -19.965 17.888 -17.151 1.00 0.00
ATOM 2907 O GLY A 698 -20.472 18.845 -16.571 1.00 0.00
ATOM 2908 HN GLY A 698 -17.990 16.497 -19.136 1.00 0.00
ATOM 2909 1HA GLY A 698 -19.891 17.744 -19.275 1.00 0.00
ATOM 2910 2HA GLY A 698 -18.923 19.087 -18.571 1.00 0.00
ATOM 2911 N LYS A 699 -20.020 16.646 -16.651 1.00 0.00
ATOM 2912 CA LYS A 699 -20.696 16.400 -15.419 1.00 0.00
ATOM 2913 C LYS A 699 -20.029 17.204 -14.345 1.00 0.00
ATOM 2914 O LYS A 699 -20.701 17.796 -13.502 1.00 0.00
ATOM 2915 CB LYS A 699 -20.667 14.897 -15.068 1.00 0.00
ATOM 2916 CG LYS A 699 -21.365 14.527 -13.762 1.00 0.00
ATOM 2917 CD LYS A 699 -20.564 14.961 -12.540 1.00 0.00
ATOM 2918 CE LYS A 699 -21.431 15.484 -11.408 1.00 0.00
ATOM 2919 NZ LYS A 699 -22.434 16.434 -11.943 1.00 0.00
ATOM 2920 HN LYS A 699 -19.587 15.891 -17.143 1.00 0.00
ATOM 2921 HA LYS A 699 -21.723 16.746 -15.540 1.00 0.00
ATOM 2922 1HB LYS A 699 -19.628 14.581 -15.002 1.00 0.00
ATOM 2923 2HB LYS A 699 -21.143 14.347 -15.879 1.00 0.00
ATOM 2924 1HG LYS A 699 -21.509 13.448 -13.729 1.00 0.00
ATOM 2925 2HG LYS A 699 -22.344 15.003 -13.734 1.00 0.00
ATOM 2926 1HD LYS A 699 -19.867 15.744 -12.838 1.00 0.00
ATOM 2927 2HD LYS A 699 -19.989 14.110 -12.178 1.00 0.00
ATOM 2928 1HE LYS A 699 -20.821 16.009 -10.673 1.00 0.00
ATOM 2929 2HE LYS A 699 -21.961 14.663 -10.925 1.00 0.00
ATOM 2930 1HZ LYS A 699 -23.137 15.914 -12.508 1.00 0.00
ATOM 2931 2HZ LYS A 699 -21.960 17.138 -12.543 1.00 0.00
ATOM 2932 3HZ LYS A 699 -22.911 16.915 -11.154 1.00 0.00
ATOM 2933 N ALA A 700 -18.684 17.255 -14.346 1.00 0.00
ATOM 2934 CA ALA A 700 -17.988 17.961 -13.307 1.00 0.00
ATOM 2935 C ALA A 700 -18.341 19.408 -13.349 1.00 0.00
ATOM 2936 O ALA A 700 -18.623 20.018 -12.318 1.00 0.00
ATOM 2937 CB ALA A 700 -16.460 17.857 -13.434 1.00 0.00
ATOM 2938 HN ALA A 700 -18.169 16.801 -15.072 1.00 0.00
ATOM 2939 HA ALA A 700 -18.316 17.528 -12.362 1.00 0.00

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ATOM  2940 1HB  ALA A 700    -16.123  18.273 -14.384  1.00  0.00
ATOM  2941 2HB  ALA A 700    -16.149  16.813 -13.394  1.00  0.00
ATOM  2942 3HB  ALA A 700    -15.976  18.415 -12.633  1.00  0.00
ATOM  2943  N   ILE A 701    -18.351  19.996 -14.557  1.00  0.00
ATOM  2944  CA  ILE A 701    -18.652  21.390 -14.648  1.00  0.00
ATOM  2945  C   ILE A 701    -20.060  21.594 -14.212  1.00  0.00
ATOM  2946  O   ILE A 701    -20.382  22.623 -13.631  1.00  0.00
ATOM  2947  CB  ILE A 701    -18.482  21.972 -16.021  1.00  0.00
ATOM  2948  CG1 ILE A 701    -19.449  21.343 -17.031  1.00  0.00
ATOM  2949  CG2 ILE A 701    -17.004  21.821 -16.406  1.00  0.00
ATOM  2950  CD1 ILE A 701    -19.478  22.085 -18.362  1.00  0.00
ATOM  2951  HN  ILE A 701    -18.151  19.465 -15.380  1.00  0.00
ATOM  2952  HA  ILE A 701    -17.982  21.892 -13.950  1.00  0.00
ATOM  2953  HB  ILE A 701    -18.767  23.024 -16.024  1.00  0.00
ATOM  2954 1HG2 ILE A 701    -16.712  20.771 -16.411  1.00  0.00
ATOM  2955 2HG2 ILE A 701    -16.372  22.343 -15.688  1.00  0.00
ATOM  2956 3HG2 ILE A 701    -16.832  22.222 -17.405  1.00  0.00
ATOM  2957 1HG1 ILE A 701    -20.452  21.342 -16.605  1.00  0.00
ATOM  2958 2HG1 ILE A 701    -19.152  20.310 -17.208  1.00  0.00
ATOM  2959 1HD1 ILE A 701    -18.490  22.088 -18.823  1.00  0.00
ATOM  2960 2HD1 ILE A 701    -19.781  23.121 -18.210  1.00  0.00
ATOM  2961 3HD1 ILE A 701    -20.170  21.598 -19.050  1.00  0.00
ATOM  2962  N   VAL A 702    -20.949  20.622 -14.475  1.00  0.00
ATOM  2963  CA  VAL A 702    -22.319  20.788 -14.085  1.00  0.00
ATOM  2964  C   VAL A 702    -22.425  20.931 -12.597  1.00  0.00
ATOM  2965  O   VAL A 702    -23.157  21.790 -12.105  1.00  0.00
ATOM  2966  CB  VAL A 702    -23.172  19.627 -14.482  1.00  0.00
ATOM  2967  CG1 VAL A 702    -24.594  19.863 -13.944  1.00  0.00
ATOM  2968  CG2 VAL A 702    -23.084  19.481 -16.010  1.00  0.00
ATOM  2969  HN  VAL A 702    -20.656  19.787 -14.941  1.00  0.00
ATOM  2970  HA  VAL A 702    -22.675  21.698 -14.568  1.00  0.00
ATOM  2971  HB  VAL A 702    -22.764  18.705 -14.067  1.00  0.00
ATOM  2972 1HG1 VAL A 702    -24.650  20.809 -13.406  1.00  0.00
ATOM  2973 2HG1 VAL A 702    -24.873  19.066 -13.255  1.00  0.00
ATOM  2974 3HG1 VAL A 702    -25.306  19.901 -14.769  1.00  0.00
ATOM  2975 1HG2 VAL A 702    -22.197  19.983 -16.395  1.00  0.00
ATOM  2976 2HG2 VAL A 702    -23.958  19.930 -16.482  1.00  0.00
ATOM  2977 3HG2 VAL A 702    -23.021  18.428 -16.285  1.00  0.00
ATOM  2978  N   LYS A 703    -21.685  20.107 -11.829  1.00  0.00
ATOM  2979  CA  LYS A 703    -21.780  20.209 -10.397  1.00  0.00
ATOM  2980  C   LYS A 703    -21.344  21.580 -10.022  1.00  0.00
ATOM  2981  O   LYS A 703    -21.933  22.232  -9.161  1.00  0.00
ATOM  2982  CB  LYS A 703    -20.815  19.297  -9.622  1.00  0.00
ATOM  2983  CG  LYS A 703    -21.180  17.821  -9.655  1.00  0.00
ATOM  2984  CD  LYS A 703    -20.112  16.900  -9.058  1.00  0.00
ATOM  2985  CE  LYS A 703    -18.706  17.078  -9.634  1.00  0.00
ATOM  2986  NZ  LYS A 703    -18.598  16.389 -10.938  1.00  0.00
ATOM  2987  HN  LYS A 703    -21.077  19.434 -12.250  1.00  0.00
ATOM  2988  HA  LYS A 703    -22.809  19.955 -10.143  1.00  0.00
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ATOM  2989 1HB  LYS A 703     -20.792  19.623  -8.583  1.00  0.00
ATOM  2990 2HB  LYS A 703     -19.817  19.415 -10.041  1.00  0.00
ATOM  2991 1HG  LYS A 703     -21.350  17.529 -10.691  1.00  0.00
ATOM  2992 2HG  LYS A 703     -22.108  17.681  -9.103  1.00  0.00
ATOM  2993 1HD  LYS A 703     -20.421  15.868  -9.220  1.00  0.00
ATOM  2994 2HD  LYS A 703     -20.067  17.080  -7.985  1.00  0.00
ATOM  2995 1HE  LYS A 703     -17.964  16.649  -8.961  1.00  0.00
ATOM  2996 2HE  LYS A 703     -18.492  18.135  -9.790  1.00  0.00
ATOM  2997 1HZ  LYS A 703     -19.292  16.791 -11.601  1.00  0.00
ATOM  2998 2HZ  LYS A 703     -18.788  15.375 -10.811  1.00  0.00
ATOM  2999 3HZ  LYS A 703     -17.639  16.517 -11.320  1.00  0.00
ATOM  3000 N    ARG A 704     -20.273  22.026 -10.690  1.00  0.00
ATOM  3001 CA   ARG A 704     -19.624  23.284 -10.496  1.00  0.00
ATOM  3002 C    ARG A 704     -20.553  24.375 -10.917  1.00  0.00
ATOM  3003 O    ARG A 704     -20.395  25.518 -10.507  1.00  0.00
ATOM  3004 CB   ARG A 704     -18.371  23.420 -11.373  1.00  0.00
ATOM  3005 CG   ARG A 704     -17.385  22.267 -11.197  1.00  0.00
ATOM  3006 CD   ARG A 704     -16.448  22.425 -10.001  1.00  0.00
ATOM  3007 NE   ARG A 704     -15.575  21.219  -9.975  1.00  0.00
ATOM  3008 CZ   ARG A 704     -14.439  21.179 -10.732  1.00  0.00
ATOM  3009 NH1  ARG A 704     -14.130  22.226 -11.549  1.00  0.00
ATOM  3010 NH2  ARG A 704     -13.615  20.093 -10.666  1.00  0.00
ATOM  3011 HN   ARG A 704     -19.893  21.422 -11.389  1.00  0.00
ATOM  3012 HA   ARG A 704     -19.357  23.344  -9.441  1.00  0.00
ATOM  3013 1HB  ARG A 704     -17.868  24.354 -11.123  1.00  0.00
ATOM  3014 2HB  ARG A 704     -18.677  23.465 -12.417  1.00  0.00
ATOM  3015 1HG  ARG A 704     -16.782  22.186 -12.100  1.00  0.00
ATOM  3016 2HG  ARG A 704     -17.949  21.344 -11.076  1.00  0.00
ATOM  3017 1HD  ARG A 704     -17.001  22.464  -9.064  1.00  0.00
ATOM  3018 2HD  ARG A 704     -15.813  23.303 -10.105  1.00  0.00
ATOM  3019 HE   ARG A 704     -15.820  20.437  -9.403  1.00  0.00
ATOM  3020 1HH1 ARG A 704     -14.735  23.021 -11.593  1.00  0.00
ATOM  3021 2HH1 ARG A 704     -13.299  22.198 -12.103  1.00  0.00
ATOM  3022 1HH2 ARG A 704     -12.867  19.992 -11.323  1.00  0.00
ATOM  3023 2HH2 ARG A 704     -13.759  19.398  -9.962  1.00  0.00
ATOM  3024 N    GLU A 705     -21.526  24.047 -11.784  1.00  0.00
ATOM  3025 CA   GLU A 705     -22.452  24.985 -12.346  1.00  0.00
ATOM  3026 C    GLU A 705     -23.197  25.603 -11.225  1.00  0.00
ATOM  3027 O    GLU A 705     -23.701  26.719 -11.350  1.00  0.00
ATOM  3028 CB   GLU A 705     -23.467  24.326 -13.296  1.00  0.00
ATOM  3029 CG   GLU A 705     -24.376  25.332 -14.004  1.00  0.00
ATOM  3030 CD   GLU A 705     -23.519  26.124 -14.981  1.00  0.00
ATOM  3031 OE1  GLU A 705     -23.147  27.278 -14.637  1.00  0.00
ATOM  3032 OE2  GLU A 705     -23.216  25.584 -16.078  1.00  0.00
ATOM  3033 HN   GLU A 705     -21.610  23.087 -12.052  1.00  0.00
ATOM  3034 HA   GLU A 705     -21.859  25.724 -12.885  1.00  0.00
ATOM  3035 1HB  GLU A 705     -24.086  23.637 -12.723  1.00  0.00
ATOM  3036 2HB  GLU A 705     -22.924  23.755 -14.047  1.00  0.00
ATOM  3037 1HG  GLU A 705     -24.829  26.014 -13.285  1.00  0.00
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ATOM 3038 2HG GLU A 705 -25.166 24.816 -14.552 1.00 0.00
ATOM 3039 N GLY A 706 -23.302 24.865 -10.105 1.00 0.00
ATOM 3040 CA GLY A 706 -23.959 25.401 -8.954 1.00 0.00
ATOM 3041 C GLY A 706 -23.259 26.696 -8.655 1.00 0.00
ATOM 3042 O GLY A 706 -23.896 27.696 -8.328 1.00 0.00
ATOM 3043 HN GLY A 706 -22.920 23.941 -10.078 1.00 0.00
ATOM 3044 1HA GLY A 706 -23.850 24.701 -8.127 1.00 0.00
ATOM 3045 2HA GLY A 706 -25.007 25.573 -9.194 1.00 0.00
ATOM 3046 N ASN A 707 -21.914 26.694 -8.773 1.00 0.00
ATOM 3047 CA ASN A 707 -21.090 27.862 -8.605 1.00 0.00
ATOM 3048 C ASN A 707 -20.904 28.564 -9.933 1.00 0.00
ATOM 3049 O ASN A 707 -21.800 28.531 -10.775 1.00 0.00
ATOM 3050 CB ASN A 707 -19.699 27.572 -8.022 1.00 0.00
ATOM 3051 CG ASN A 707 -19.889 27.364 -6.528 1.00 0.00
ATOM 3052 OD1 ASN A 707 -20.915 27.749 -5.970 1.00 0.00
ATOM 3053 ND2 ASN A 707 -18.874 26.755 -5.859 1.00 0.00
ATOM 3054 HN ASN A 707 -21.465 25.829 -8.991 1.00 0.00
ATOM 3055 HA ASN A 707 -21.637 28.529 -7.940 1.00 0.00
ATOM 3056 1HB ASN A 707 -19.024 28.411 -8.192 1.00 0.00
ATOM 3057 2HB ASN A 707 -19.270 26.674 -8.466 1.00 0.00
ATOM 3058 1HD2 ASN A 707 -18.885 26.730 -4.860 1.00 0.00
ATOM 3059 2HD2 ASN A 707 -18.114 26.329 -6.349 1.00 0.00
ATOM 3060 N SER A 708 -19.744 29.240 -10.159 1.00 0.00
ATOM 3061 CA SER A 708 -19.586 29.964 -11.400 1.00 0.00
ATOM 3062 C SER A 708 -18.214 29.833 -12.019 1.00 0.00
ATOM 3063 O SER A 708 -17.723 28.727 -12.234 1.00 0.00
ATOM 3064 CB SER A 708 -19.894 31.469 -11.261 1.00 0.00
ATOM 3065 OG SER A 708 -19.957 32.087 -12.539 1.00 0.00
ATOM 3066 HN SER A 708 -19.014 29.235 -9.477 1.00 0.00
ATOM 3067 HA SER A 708 -20.268 29.507 -12.117 1.00 0.00
ATOM 3068 1HB SER A 708 -19.110 31.962 -10.685 1.00 0.00
ATOM 3069 2HB SER A 708 -20.854 31.613 -10.767 1.00 0.00
ATOM 3070 HG SER A 708 -20.537 31.556 -13.070 1.00 0.00
ATOM 3071 N SER A 709 -17.553 30.988 -12.286 1.00 0.00
ATOM 3072 CA SER A 709 -16.308 31.118 -13.009 1.00 0.00
ATOM 3073 C SER A 709 -15.219 30.341 -12.359 1.00 0.00
ATOM 3074 O SER A 709 -14.309 29.834 -13.014 1.00 0.00
ATOM 3075 CB SER A 709 -15.830 32.578 -13.122 1.00 0.00
ATOM 3076 OG SER A 709 -14.609 32.634 -13.845 1.00 0.00
ATOM 3077 HN SER A 709 -17.968 31.831 -11.950 1.00 0.00
ATOM 3078 HA SER A 709 -16.478 30.703 -14.002 1.00 0.00
ATOM 3079 1HB SER A 709 -15.661 32.998 -12.130 1.00 0.00
ATOM 3080 2HB SER A 709 -16.570 33.178 -13.651 1.00 0.00
ATOM 3081 HG SER A 709 -14.089 31.895 -13.560 1.00 0.00
ATOM 3082 N GLN A 710 -15.304 30.190 -11.034 1.00 0.00
ATOM 3083 CA GLN A 710 -14.320 29.451 -10.309 1.00 0.00
ATOM 3084 C GLN A 710 -14.284 28.076 -10.903 1.00 0.00
ATOM 3085 O GLN A 710 -13.284 27.368 -10.796 1.00 0.00
ATOM 3086 CB GLN A 710 -14.666 29.304 -8.816 1.00 0.00

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ATOM  3087 CG  GLN A 710   -14.694  30.629  -8.052  1.00  0.00
ATOM  3088 CD  GLN A 710   -15.988  31.361  -8.386  1.00  0.00
ATOM  3089 OE1 GLN A 710   -16.882  30.818  -9.034  1.00  0.00
ATOM  3090 NE2 GLN A 710   -16.096  32.635  -7.923  1.00  0.00
ATOM  3091 HN  GLN A 710   -16.071  30.602 -10.541  1.00  0.00
ATOM  3092 HA  GLN A 710   -13.378  29.988 -10.425  1.00  0.00
ATOM  3093 1HB GLN A 710   -13.930  28.649  -8.352  1.00  0.00
ATOM  3094 2HB GLN A 710   -15.645  28.833  -8.732  1.00  0.00
ATOM  3095 1HG GLN A 710   -13.847  31.251  -8.341  1.00  0.00
ATOM  3096 2HG GLN A 710   -14.653  30.448  -6.978  1.00  0.00
ATOM  3097 1HE2 GLN A 710  -15.346  33.036  -7.396  1.00  0.00
ATOM  3098 2HE2 GLN A 710  -16.913  33.183  -8.100  1.00  0.00
ATOM  3099 N   ASN A 711   -15.380  27.657 -11.559  1.00  0.00
ATOM  3100 CA  ASN A 711   -15.461  26.323 -12.067  1.00  0.00
ATOM  3101 C   ASN A 711   -14.298  25.993 -12.953  1.00  0.00
ATOM  3102 O   ASN A 711   -13.698  24.930 -12.804  1.00  0.00
ATOM  3103 CB  ASN A 711   -16.751  26.026 -12.870  1.00  0.00
ATOM  3104 CG  ASN A 711   -16.691  26.627 -14.274  1.00  0.00
ATOM  3105 OD1 ASN A 711   -16.897  25.908 -15.250  1.00  0.00
ATOM  3106 ND2 ASN A 711   -16.393  27.948 -14.394  1.00  0.00
ATOM  3107 HN  ASN A 711   -16.147  28.285 -11.693  1.00  0.00
ATOM  3108 HA  ASN A 711   -15.404  25.663 -11.202  1.00  0.00
ATOM  3109 1HB ASN A 711   -17.611  26.448 -12.352  1.00  0.00
ATOM  3110 2HB ASN A 711   -16.885  24.948 -12.964  1.00  0.00
ATOM  3111 1HD2 ASN A 711  -16.200  28.333 -15.296  1.00  0.00
ATOM  3112 2HD2 ASN A 711  -16.363  28.547 -13.594  1.00  0.00
ATOM  3113 N   TRP A 712   -13.916  26.884 -13.887  1.00  0.00
ATOM  3114 CA  TRP A 712   -12.853  26.497 -14.765  1.00  0.00
ATOM  3115 C   TRP A 712   -11.591  26.323 -13.993  1.00  0.00
ATOM  3116 O   TRP A 712   -10.832  25.390 -14.243  1.00  0.00
ATOM  3117 CB  TRP A 712   -12.619  27.465 -15.943  1.00  0.00
ATOM  3118 CG  TRP A 712   -12.309  28.896 -15.583  1.00  0.00
ATOM  3119 CD1 TRP A 712   -13.148  29.967 -15.494  1.00  0.00
ATOM  3120 CD2 TRP A 712   -10.988  29.388 -15.317  1.00  0.00
ATOM  3121 NE1 TRP A 712   -12.434  31.097 -15.174  1.00  0.00
ATOM  3122 CE2 TRP A 712   -11.101  30.754 -15.067  1.00  0.00
ATOM  3123 CE3 TRP A 712    -9.779  28.754 -15.292  1.00  0.00
ATOM  3124 CZ2 TRP A 712   -10.001  31.512 -14.785  1.00  0.00
ATOM  3125 CZ3 TRP A 712    -8.671  29.521 -15.011  1.00  0.00
ATOM  3126 CH2 TRP A 712    -8.781  30.873 -14.762  1.00  0.00
ATOM  3127 HN  TRP A 712   -14.356  27.778 -13.963  1.00  0.00
ATOM  3128 HA  TRP A 712   -13.116  25.510 -15.145  1.00  0.00
ATOM  3129 1HB TRP A 712   -13.514  27.473 -16.563  1.00  0.00
ATOM  3130 2HB TRP A 712   -11.783  27.091 -16.532  1.00  0.00
ATOM  3131 HE3 TRP A 712    -9.696  27.695 -15.485  1.00  0.00
ATOM  3132 HD1 TRP A 712   -14.216  29.933 -15.652  1.00  0.00
ATOM  3133 HE1 TRP A 712   -12.807  31.993 -15.043  1.00  0.00
ATOM  3134 HZ2 TRP A 712   -10.084  32.570 -14.587  1.00  0.00
ATOM  3135 HZ3 TRP A 712    -7.697  29.055 -14.985  1.00  0.00
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ATOM  3136 HH2 TRP A 712    -7.891  31.444 -14.544  1.00  0.00
ATOM  3137  N  GLN A 713   -11.330  27.211 -13.017  1.00  0.00
ATOM  3138  CA GLN A 713   -10.107  27.075 -12.282  1.00  0.00
ATOM  3139  C  GLN A 713   -10.089  25.802 -11.491  1.00  0.00
ATOM  3140  O  GLN A 713    -9.093  25.080 -11.508  1.00  0.00
ATOM  3141  CB GLN A 713    -9.821  28.261 -11.342  1.00  0.00
ATOM  3142  CG GLN A 713   -10.838  28.460 -10.220  1.00  0.00
ATOM  3143  CD GLN A 713   -10.394  29.664  -9.403  1.00  0.00
ATOM  3144  OE1 GLN A 713    -9.241  29.755  -8.985  1.00  0.00
ATOM  3145  NE2 GLN A 713   -11.331  30.626  -9.180  1.00  0.00
ATOM  3146  HN  GLN A 713   -11.973  27.947 -12.809  1.00  0.00
ATOM  3147  HA  GLN A 713    -9.311  26.985 -13.021  1.00  0.00
ATOM  3148 1HB  GLN A 713    -9.789  29.171 -11.939  1.00  0.00
ATOM  3149 2HB  GLN A 713    -8.840  28.112 -10.892  1.00  0.00
ATOM  3150 1HG  GLN A 713   -10.877  27.581  -9.577  1.00  0.00
ATOM  3151 2HG  GLN A 713   -11.830  28.646 -10.630  1.00  0.00
ATOM  3152 1HE2 GLN A 713   -12.287  30.451  -9.415  1.00  0.00
ATOM  3153 2HE2 GLN A 713   -11.082  31.509  -8.783  1.00  0.00
ATOM  3154  N  ARG A 714   -11.197  25.461 -10.801  1.00  0.00
ATOM  3155  CA ARG A 714   -11.173  24.266 -10.001  1.00  0.00
ATOM  3156  C  ARG A 714   -10.968  23.072 -10.861  1.00  0.00
ATOM  3157  O  ARG A 714   -10.272  22.135 -10.473  1.00  0.00
ATOM  3158  CB ARG A 714   -12.450  23.958  -9.200  1.00  0.00
ATOM  3159  CG ARG A 714   -12.332  22.584  -8.521  1.00  0.00
ATOM  3160  CD ARG A 714   -13.646  21.995  -8.004  1.00  0.00
ATOM  3161  NE ARG A 714   -13.923  22.565  -6.658  1.00  0.00
ATOM  3162  CZ ARG A 714   -13.668  21.828  -5.538  1.00  0.00
ATOM  3163 NH1 ARG A 714   -13.907  22.359  -4.303  1.00  0.00
ATOM  3164 NH2 ARG A 714   -13.186  20.556  -5.651  1.00  0.00
ATOM  3165  HN  ARG A 714   -12.019  26.028 -10.846  1.00  0.00
ATOM  3166  HA  ARG A 714   -10.337  24.388  -9.313  1.00  0.00
ATOM  3167 1HB  ARG A 714   -13.310  23.963  -9.869  1.00  0.00
ATOM  3168 2HB  ARG A 714   -12.601  24.728  -8.443  1.00  0.00
ATOM  3169 1HG  ARG A 714   -11.647  22.677  -7.680  1.00  0.00
ATOM  3170 2HG  ARG A 714   -11.905  21.885  -9.238  1.00  0.00
ATOM  3171 1HD  ARG A 714   -13.576  20.913  -7.899  1.00  0.00
ATOM  3172 2HD  ARG A 714   -14.478  22.260  -8.656  1.00  0.00
ATOM  3173  HE  ARG A 714   -14.297  23.489  -6.573  1.00  0.00
ATOM  3174 1HH1 ARG A 714   -14.268  23.288  -4.219  1.00  0.00
ATOM  3175 2HH1 ARG A 714   -13.720  21.819  -3.482  1.00  0.00
ATOM  3176 1HH2 ARG A 714   -12.724  20.126  -4.876  1.00  0.00
ATOM  3177 2HH2 ARG A 714   -13.296  20.054  -6.509  1.00  0.00
ATOM  3178  N  PHE A 715   -11.573  23.082 -12.059  1.00  0.00
ATOM  3179  CA PHE A 715   -11.501  21.952 -12.932  1.00  0.00
ATOM  3180  C  PHE A 715   -10.049  21.682 -13.163  1.00  0.00
ATOM  3181  O  PHE A 715    -9.574  20.558 -12.995  1.00  0.00
ATOM  3182  CB PHE A 715   -12.180  22.267 -14.278  1.00  0.00
ATOM  3183  CG PHE A 715   -12.190  21.056 -15.138  1.00  0.00
ATOM  3184  CD1 PHE A 715   -11.089  20.730 -15.896  1.00  0.00
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ATOM 3185 CD2 PHE A 715 -13.348 20.329 -15.286 1.00 0.00
ATOM 3186 CE1 PHE A 715 -11.142 19.685 -16.784 1.00 0.00
ATOM 3187 CE2 PHE A 715 -13.406 19.282 -16.173 1.00 0.00
ATOM 3188 CZ PHE A 715 -12.305 18.969 -16.931 1.00 0.00
ATOM 3189 HN PHE A 715 -12.083 23.893 -12.345 1.00 0.00
ATOM 3190 HA PHE A 715 -12.003 21.124 -12.432 1.00 0.00
ATOM 3191 1HB PHE A 715 -11.639 23.063 -14.790 1.00 0.00
ATOM 3192 2HB PHE A 715 -13.207 22.591 -14.109 1.00 0.00
ATOM 3193 HD1 PHE A 715 -10.178 21.300 -15.792 1.00 0.00
ATOM 3194 HD2 PHE A 715 -14.219 20.583 -14.700 1.00 0.00
ATOM 3195 HE1 PHE A 715 -10.271 19.426 -17.367 1.00 0.00
ATOM 3196 HE2 PHE A 715 -14.315 18.707 -16.273 1.00 0.00
ATOM 3197 HZ PHE A 715 -12.353 18.159 -17.643 1.00 0.00
ATOM 3198 N TYR A 716 -9.289 22.737 -13.493 1.00 0.00
ATOM 3199 CA TYR A 716 -7.900 22.550 -13.770 1.00 0.00
ATOM 3200 C TYR A 716 -7.194 22.064 -12.541 1.00 0.00
ATOM 3201 O TYR A 716 -6.394 21.132 -12.613 1.00 0.00
ATOM 3202 CB TYR A 716 -7.222 23.842 -14.256 1.00 0.00
ATOM 3203 CG TYR A 716 -5.825 23.506 -14.644 1.00 0.00
ATOM 3204 CD1 TYR A 716 -5.581 22.804 -15.802 1.00 0.00
ATOM 3205 CD2 TYR A 716 -4.758 23.997 -13.927 1.00 0.00
ATOM 3206 CE1 TYR A 716 -4.294 22.552 -16.214 1.00 0.00
ATOM 3207 CE2 TYR A 716 -3.468 23.756 -14.339 1.00 0.00
ATOM 3208 CZ TYR A 716 -3.235 23.028 -15.481 1.00 0.00
ATOM 3209 OH TYR A 716 -1.912 22.781 -15.905 1.00 0.00
ATOM 3210 HN TYR A 716 -9.693 23.650 -13.544 1.00 0.00
ATOM 3211 HA TYR A 716 -7.833 21.779 -14.537 1.00 0.00
ATOM 3212 1HB TYR A 716 -7.211 24.589 -13.462 1.00 0.00
ATOM 3213 2HB TYR A 716 -7.751 24.251 -15.116 1.00 0.00
ATOM 3214 HD1 TYR A 716 -6.411 22.446 -16.394 1.00 0.00
ATOM 3215 HE1 TYR A 716 -4.116 21.980 -17.113 1.00 0.00
ATOM 3216 HD2 TYR A 716 -4.936 24.578 -13.034 1.00 0.00
ATOM 3217 HE2 TYR A 716 -2.638 24.140 -13.764 1.00 0.00
ATOM 3218 HH TYR A 716 -1.407 22.435 -15.181 1.00 0.00
ATOM 3219 N GLN A 717 -7.480 22.658 -11.365 1.00 0.00
ATOM 3220 CA GLN A 717 -6.767 22.208 -10.203 1.00 0.00
ATOM 3221 C GLN A 717 -7.093 20.799 -9.825 1.00 0.00
ATOM 3222 O GLN A 717 -6.242 20.068 -9.319 1.00 0.00
ATOM 3223 CB GLN A 717 -6.848 23.111 -8.952 1.00 0.00
ATOM 3224 CG GLN A 717 -8.239 23.434 -8.409 1.00 0.00
ATOM 3225 CD GLN A 717 -8.473 24.912 -8.692 1.00 0.00
ATOM 3226 OE1 GLN A 717 -9.459 25.503 -8.254 1.00 0.00
ATOM 3227 NE2 GLN A 717 -7.511 25.541 -9.419 1.00 0.00
ATOM 3228 HN GLN A 717 -8.165 23.384 -11.305 1.00 0.00
ATOM 3229 HA GLN A 717 -5.726 22.118 -10.514 1.00 0.00
ATOM 3230 1HB GLN A 717 -6.359 24.053 -9.192 1.00 0.00
ATOM 3231 2HB GLN A 717 -6.287 22.625 -8.156 1.00 0.00
ATOM 3232 1HG GLN A 717 -8.292 23.251 -7.336 1.00 0.00
ATOM 3233 2HG GLN A 717 -9.002 22.838 -8.910 1.00 0.00

ATOM 3234 1HE2 GLN A 717 -7.086 25.069 -10.191 1.00 0.00
ATOM 3235 2HE2 GLN A 717 -7.218 26.470 -9.196 1.00 0.00
ATOM 3236 N LEU A 718 -8.345 20.378 -10.043 1.00 0.00
ATOM 3237 CA LEU A 718 -8.759 19.061 -9.662 1.00 0.00
ATOM 3238 C LEU A 718 -7.997 18.065 -10.503 1.00 0.00
ATOM 3239 O LEU A 718 -7.428 17.099 -9.995 1.00 0.00
ATOM 3240 CB LEU A 718 -10.288 18.979 -9.871 1.00 0.00
ATOM 3241 CG LEU A 718 -11.062 17.937 -9.047 1.00 0.00
ATOM 3242 CD1 LEU A 718 -10.887 16.514 -9.571 1.00 0.00
ATOM 3243 CD2 LEU A 718 -10.734 18.069 -7.552 1.00 0.00
ATOM 3244 HN LEU A 718 -9.000 20.994 -10.479 1.00 0.00
ATOM 3245 HA LEU A 718 -8.493 18.913 -8.616 1.00 0.00
ATOM 3246 1HB LEU A 718 -10.466 18.767 -10.923 1.00 0.00
ATOM 3247 2HB LEU A 718 -10.705 19.958 -9.640 1.00 0.00
ATOM 3248 HG LEU A 718 -12.122 18.190 -9.065 1.00 0.00
ATOM 3249 1HD1 LEU A 718 -9.911 16.395 -10.041 1.00 0.00
ATOM 3250 2HD1 LEU A 718 -11.650 16.290 -10.315 1.00 0.00
ATOM 3251 3HD1 LEU A 718 -10.955 15.800 -8.750 1.00 0.00
ATOM 3252 1HD2 LEU A 718 -10.835 19.104 -7.226 1.00 0.00
ATOM 3253 2HD2 LEU A 718 -9.708 17.754 -7.363 1.00 0.00
ATOM 3254 3HD2 LEU A 718 -11.419 17.461 -6.962 1.00 0.00
ATOM 3255 N THR A 719 -7.913 18.326 -11.823 1.00 0.00
ATOM 3256 CA THR A 719 -7.266 17.449 -12.761 1.00 0.00
ATOM 3257 C THR A 719 -5.793 17.323 -12.512 1.00 0.00
ATOM 3258 O THR A 719 -5.244 16.230 -12.641 1.00 0.00
ATOM 3259 CB THR A 719 -7.433 17.911 -14.178 1.00 0.00
ATOM 3260 OG1 THR A 719 -6.820 19.179 -14.356 1.00 0.00
ATOM 3261 CG2 THR A 719 -8.936 18.002 -14.489 1.00 0.00
ATOM 3262 HN THR A 719 -8.322 19.171 -12.167 1.00 0.00
ATOM 3263 HA THR A 719 -7.712 16.463 -12.630 1.00 0.00
ATOM 3264 HB THR A 719 -6.963 17.206 -14.864 1.00 0.00
ATOM 3265 HG1 THR A 719 -5.901 19.069 -14.148 1.00 0.00
ATOM 3266 1HG2 THR A 719 -9.482 18.409 -13.638 1.00 0.00
ATOM 3267 2HG2 THR A 719 -9.337 17.011 -14.704 1.00 0.00
ATOM 3268 3HG2 THR A 719 -9.105 18.658 -15.343 1.00 0.00
ATOM 3269 N LYS A 720 -5.093 18.417 -12.150 1.00 0.00
ATOM 3270 CA LYS A 720 -3.672 18.243 -12.010 1.00 0.00
ATOM 3271 C LYS A 720 -3.334 17.332 -10.872 1.00 0.00
ATOM 3272 O LYS A 720 -2.267 16.722 -10.867 1.00 0.00
ATOM 3273 CB LYS A 720 -2.780 19.505 -11.921 1.00 0.00
ATOM 3274 CG LYS A 720 -2.797 20.308 -10.622 1.00 0.00
ATOM 3275 CD LYS A 720 -4.022 21.194 -10.462 1.00 0.00
ATOM 3276 CE LYS A 720 -4.127 22.275 -11.542 1.00 0.00
ATOM 3277 NZ LYS A 720 -2.912 23.122 -11.534 1.00 0.00
ATOM 3278 HN LYS A 720 -5.536 19.298 -11.988 1.00 0.00
ATOM 3279 HA LYS A 720 -3.369 17.661 -12.880 1.00 0.00
ATOM 3280 1HB LYS A 720 -3.081 20.175 -12.723 1.00 0.00
ATOM 3281 2HB LYS A 720 -1.753 19.192 -12.098 1.00 0.00
ATOM 3282 1HG LYS A 720 -1.907 20.935 -10.590 1.00 0.00

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ATOM  3283 2HG LYS A 720    -2.757  19.614  -9.784  1.00  0.00
ATOM  3284 1HD LYS A 720    -3.982  21.675  -9.485  1.00  0.00
ATOM  3285 2HD LYS A 720    -4.914  20.570 -10.501  1.00  0.00
ATOM  3286 1HE LYS A 720    -4.989  22.916 -11.355  1.00  0.00
ATOM  3287 2HE LYS A 720    -4.216  21.819 -12.528  1.00  0.00
ATOM  3288 1HZ LYS A 720    -2.077  22.532 -11.722  1.00  0.00
ATOM  3289 2HZ LYS A 720    -2.813  23.577 -10.604  1.00  0.00
ATOM  3290 3HZ LYS A 720    -2.993  23.852 -12.270  1.00  0.00
ATOM  3291  N  LEU A 721    -4.227  17.216  -9.873  1.00  0.00
ATOM  3292  CA LEU A 721    -3.978  16.374  -8.733  1.00  0.00
ATOM  3293  C  LEU A 721    -3.756  14.989  -9.260  1.00  0.00
ATOM  3294  O  LEU A 721    -2.949  14.229  -8.726  1.00  0.00
ATOM  3295  CB LEU A 721    -5.180  16.384  -7.757  1.00  0.00
ATOM  3296  CG LEU A 721    -5.050  15.608  -6.423  1.00  0.00
ATOM  3297  CD1 LEU A 721    -6.341  15.751  -5.601  1.00  0.00
ATOM  3298  CD2 LEU A 721    -4.679  14.127  -6.606  1.00  0.00
ATOM  3299  HN LEU A 721    -5.085  17.728  -9.924  1.00  0.00
ATOM  3300  HA LEU A 721    -3.084  16.757  -8.241  1.00  0.00
ATOM  3301 1HB LEU A 721    -6.036  15.975  -8.290  1.00  0.00
ATOM  3302 2HB LEU A 721    -5.391  17.423  -7.510  1.00  0.00
ATOM  3303  HG LEU A 721    -4.208  15.999  -5.853  1.00  0.00
ATOM  3304 1HD1 LEU A 721   -7.158  15.200  -6.068  1.00  0.00
ATOM  3305 2HD1 LEU A 721   -6.634  16.799  -5.538  1.00  0.00
ATOM  3306 3HD1 LEU A 721   -6.195  15.350  -4.598  1.00  0.00
ATOM  3307 1HD2 LEU A 721   -3.597  13.999  -6.607  1.00  0.00
ATOM  3308 2HD2 LEU A 721   -5.064  13.757  -7.556  1.00  0.00
ATOM  3309 3HD2 LEU A 721   -5.088  13.534  -5.788  1.00  0.00
ATOM  3310  N  LEU A 722    -4.443  14.633 -10.356  1.00  0.00
ATOM  3311  CA LEU A 722    -4.320  13.307 -10.888  1.00  0.00
ATOM  3312  C  LEU A 722    -2.887  13.009 -11.191  1.00  0.00
ATOM  3313  O  LEU A 722    -2.442  11.872 -11.040  1.00  0.00
ATOM  3314  CB LEU A 722    -5.125  13.093 -12.177  1.00  0.00
ATOM  3315  CG LEU A 722    -6.645  13.143 -11.952  1.00  0.00
ATOM  3316  CD1 LEU A 722    -7.109  14.534 -11.493  1.00  0.00
ATOM  3317  CD2 LEU A 722    -7.396  12.646 -13.191  1.00  0.00
ATOM  3318  HN LEU A 722    -5.044  15.296 -10.804  1.00  0.00
ATOM  3319  HA LEU A 722    -4.672  12.628 -10.111  1.00  0.00
ATOM  3320 1HB LEU A 722    -4.863  12.123 -12.598  1.00  0.00
ATOM  3321 2HB LEU A 722    -4.850  13.864 -12.895  1.00  0.00
ATOM  3322  HG LEU A 722    -6.920  12.407 -11.197  1.00  0.00
ATOM  3323 1HD1 LEU A 722   -6.709  15.309 -12.147  1.00  0.00
ATOM  3324 2HD1 LEU A 722   -6.756  14.733 -10.481  1.00  0.00
ATOM  3325 3HD1 LEU A 722   -8.196  14.597 -11.521  1.00  0.00
ATOM  3326 1HD2 LEU A 722   -6.803  11.906 -13.729  1.00  0.00
ATOM  3327 2HD2 LEU A 722   -7.595  13.476 -13.869  1.00  0.00
ATOM  3328 3HD2 LEU A 722   -8.336  12.178 -12.899  1.00  0.00
ATOM  3329  N  ASP A 723    -2.119  14.019 -11.633  1.00  0.00
ATOM  3330  CA ASP A 723    -0.741  13.792 -11.962  1.00  0.00
ATOM  3331  C  ASP A 723    -0.010  13.274 -10.759  1.00  0.00
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ATOM  3332  O   ASP A 723      0.743  12.305 -10.854  1.00  0.00
ATOM  3333  CB  ASP A 723     -0.030  15.083 -12.405  1.00  0.00
ATOM  3334  CG  ASP A 723      1.370  14.732 -12.890  1.00  0.00
ATOM  3335  OD1 ASP A 723      2.107  15.674 -13.288  1.00  0.00
ATOM  3336  OD2 ASP A 723      1.720  13.522 -12.876  1.00  0.00
ATOM  3337  HN  ASP A 723     -2.510  14.934 -11.733  1.00  0.00
ATOM  3338  HA  ASP A 723     -0.725  13.057 -12.767  1.00  0.00
ATOM  3339 1HB  ASP A 723      0.047  15.779 -11.569  1.00  0.00
ATOM  3340 2HB  ASP A 723     -0.580  15.560 -13.216  1.00  0.00
ATOM  3341  N   SER A 724     -0.232  13.895  -9.585  1.00  0.00
ATOM  3342  CA  SER A 724      0.455  13.494  -8.388  1.00  0.00
ATOM  3343  C   SER A 724      0.075  12.088  -8.070  1.00  0.00
ATOM  3344  O   SER A 724      0.909  11.279  -7.664  1.00  0.00
ATOM  3345  CB  SER A 724      0.076  14.348  -7.166  1.00  0.00
ATOM  3346  OG  SER A 724      0.481  15.694  -7.363  1.00  0.00
ATOM  3347  HN  SER A 724     -0.888  14.649  -9.546  1.00  0.00
ATOM  3348  HA  SER A 724      1.521  13.587  -8.595  1.00  0.00
ATOM  3349 1HB  SER A 724      0.573  13.970  -6.273  1.00  0.00
ATOM  3350 2HB  SER A 724     -1.003  14.336  -7.016  1.00  0.00
ATOM  3351  HG  SER A 724      1.389  15.668  -7.634  1.00  0.00
ATOM  3352  N   MET A 725     -1.212  11.757  -8.261  1.00  0.00
ATOM  3353  CA  MET A 725     -1.668  10.440  -7.944  1.00  0.00
ATOM  3354  C   MET A 725     -0.915   9.461  -8.785  1.00  0.00
ATOM  3355  O   MET A 725     -0.510   8.408  -8.298  1.00  0.00
ATOM  3356  CB  MET A 725     -3.164  10.256  -8.196  1.00  0.00
ATOM  3357  CG  MET A 725     -4.058  11.063  -7.257  1.00  0.00
ATOM  3358  SD  MET A 725     -5.826  10.823  -7.583  1.00  0.00
ATOM  3359  CE  MET A 725     -5.715   9.033  -7.303  1.00  0.00
ATOM  3360  HN  MET A 725     -1.852  12.434  -8.625  1.00  0.00
ATOM  3361  HA  MET A 725     -1.441  10.276  -6.890  1.00  0.00
ATOM  3362 1HB  MET A 725     -3.408   9.200  -8.083  1.00  0.00
ATOM  3363 2HB  MET A 725     -3.382  10.551  -9.221  1.00  0.00
ATOM  3364 1HG  MET A 725     -3.832  12.123  -7.370  1.00  0.00
ATOM  3365 2HG  MET A 725     -3.858  10.767  -6.228  1.00  0.00
ATOM  3366 1HE  MET A 725     -5.897   8.818  -6.250  1.00  0.00
ATOM  3367 2HE  MET A 725     -4.719   8.677  -7.564  1.00  0.00
ATOM  3368 3HE  MET A 725     -6.469   8.517  -7.898  1.00  0.00
ATOM  3369  N   HIS A 726     -0.694   9.788 -10.072  1.00  0.00
ATOM  3370  CA  HIS A 726      0.036   8.910 -10.943  1.00  0.00
ATOM  3371  C   HIS A 726      1.424   8.772 -10.390  1.00  0.00
ATOM  3372  O   HIS A 726      2.024   7.699 -10.419  1.00  0.00
ATOM  3373  CB  HIS A 726      0.161   9.465 -12.373  1.00  0.00
ATOM  3374  CG  HIS A 726      0.837   8.528 -13.331  1.00  0.00
ATOM  3375  ND1 HIS A 726      0.193   7.499 -13.981  1.00  0.00
ATOM  3376  CD2 HIS A 726      2.124   8.498 -13.772  1.00  0.00
ATOM  3377  CE1 HIS A 726      1.115   6.900 -14.777  1.00  0.00
ATOM  3378  NE2 HIS A 726      2.302   7.471 -14.685  1.00  0.00
ATOM  3379  HN  HIS A 726     -1.044  10.655 -10.426  1.00  0.00
ATOM  3380  HA  HIS A 726     -0.500   7.962 -10.953  1.00  0.00
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ATOM  3381 1HB  HIS A 726     0.734  10.391 -12.345  1.00  0.00
ATOM  3382 2HB  HIS A 726    -0.836   9.679 -12.758  1.00  0.00
ATOM  3383  HD2 HIS A 726     2.899   9.179 -13.455  1.00  0.00
ATOM  3384  HD1 HIS A 726    -0.750   7.247 -13.886  1.00  0.00
ATOM  3385  HE1 HIS A 726     0.903   6.054 -15.412  1.00  0.00
ATOM  3386  N   GLU A 727     1.986   9.871  -9.863  1.00  0.00
ATOM  3387  CA  GLU A 727     3.321   9.790  -9.352  1.00  0.00
ATOM  3388  C   GLU A 727     3.378   8.829  -8.205  1.00  0.00
ATOM  3389  O   GLU A 727     4.243   7.955  -8.158  1.00  0.00
ATOM  3390  CB  GLU A 727     3.841  11.150  -8.853  1.00  0.00
ATOM  3391  CG  GLU A 727     5.295  11.127  -8.376  1.00  0.00
ATOM  3392  CD  GLU A 727     5.332  10.686  -6.918  1.00  0.00
ATOM  3393  OE1 GLU A 727     6.457  10.435  -6.410  1.00  0.00
ATOM  3394  OE2 GLU A 727     4.242  10.600  -6.293  1.00  0.00
ATOM  3395  HN  GLU A 727     1.479  10.733  -9.827  1.00  0.00
ATOM  3396  HA  GLU A 727     3.947   9.424 -10.166  1.00  0.00
ATOM  3397 1HB  GLU A 727     3.211  11.481  -8.028  1.00  0.00
ATOM  3398 2HB  GLU A 727     3.754  11.873  -9.663  1.00  0.00
ATOM  3399 1HG  GLU A 727     5.736  12.121  -8.458  1.00  0.00
ATOM  3400 2HG  GLU A 727     5.879  10.428  -8.974  1.00  0.00
ATOM  3401  N   VAL A 728     2.426   8.949  -7.260  1.00  0.00
ATOM  3402  CA  VAL A 728     2.421   8.126  -6.084  1.00  0.00
ATOM  3403  C   VAL A 728     2.245   6.693  -6.460  1.00  0.00
ATOM  3404  O   VAL A 728     2.901   5.819  -5.893  1.00  0.00
ATOM  3405  CB  VAL A 728     1.307   8.467  -5.137  1.00  0.00
ATOM  3406  CG1 VAL A 728     1.343   7.471  -3.965  1.00  0.00
ATOM  3407  CG2 VAL A 728     1.458   9.936  -4.705  1.00  0.00
ATOM  3408  HN  VAL A 728     1.704   9.629  -7.382  1.00  0.00
ATOM  3409  HA  VAL A 728     3.385   8.272  -5.597  1.00  0.00
ATOM  3410  HB  VAL A 728     0.348   8.405  -5.650  1.00  0.00
ATOM  3411 1HG1 VAL A 728     2.370   7.266  -3.664  1.00  0.00
ATOM  3412 2HG1 VAL A 728     0.883   6.527  -4.259  1.00  0.00
ATOM  3413 3HG1 VAL A 728     0.816   7.883  -3.104  1.00  0.00
ATOM  3414 1HG2 VAL A 728     1.409  10.598  -5.570  1.00  0.00
ATOM  3415 2HG2 VAL A 728     2.420  10.088  -4.217  1.00  0.00
ATOM  3416 3HG2 VAL A 728     0.653  10.212  -4.023  1.00  0.00
ATOM  3417  N   VAL A 729     1.351   6.419  -7.432  1.00  0.00
ATOM  3418  CA  VAL A 729     1.114   5:066  -7.846  1.00  0.00
ATOM  3419  C   VAL A 729     2.347   4.436  -8.386  1.00  0.00
ATOM  3420  O   VAL A 729     2.634   3.280  -8.079  1.00  0.00
ATOM  3421  CB  VAL A 729     0.025   4.898  -8.881  1.00  0.00
ATOM  3422  CG1 VAL A 729    -0.103   6.135  -9.771  1.00  0.00
ATOM  3423  CG2 VAL A 729     0.399   3.659  -9.717  1.00  0.00
ATOM  3424  HN  VAL A 729     0.849   7.166  -7.868  1.00  0.00
ATOM  3425  HA  VAL A 729     0.849   4.516  -6.943  1.00  0.00
ATOM  3426  HB  VAL A 729    -0.924   4.719  -8.377  1.00  0.00
ATOM  3427 1HG1 VAL A 729     0.243   5.920 -10.781  1.00  0.00
ATOM  3428 2HG1 VAL A 729     0.502   6.949  -9.373  1.00  0.00
ATOM  3429 3HG1 VAL A 729    -1.145   6.449  -9.831  1.00  0.00
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ATOM 3430 1HG2 VAL A 729 0.802 2.871 -9.080 1.00 0.00
ATOM 3431 2HG2 VAL A 729 1.160 3.918 -10.454 1.00 0.00
ATOM 3432 3HG2 VAL A 729 -0.482 3.266 -10.223 1.00 0.00
ATOM 3433 N GLU A 730 3.121 5.177 -9.194 1.00 0.00
ATOM 3434 CA GLU A 730 4.298 4.583 -9.753 1.00 0.00
ATOM 3435 C GLU A 730 5.209 4.190 -8.637 1.00 0.00
ATOM 3436 O GLU A 730 5.754 3.088 -8.626 1.00 0.00
ATOM 3437 CB GLU A 730 5.081 5.542 -10.669 1.00 0.00
ATOM 3438 CG GLU A 730 4.352 5.894 -11.968 1.00 0.00
ATOM 3439 CD GLU A 730 5.250 6.829 -12.770 1.00 0.00
ATOM 3440 OE1 GLU A 730 4.873 7.167 -13.923 1.00 0.00
ATOM 3441 OE2 GLU A 730 6.327 7.211 -12.241 1.00 0.00
ATOM 3442 HN GLU A 730 2.880 6.125 -9.400 1.00 0.00
ATOM 3443 HA GLU A 730 3.967 3.712 -10.319 1.00 0.00
ATOM 3444 1HB GLU A 730 6.035 5.080 -10.920 1.00 0.00
ATOM 3445 2HB GLU A 730 5.278 6.462 -10.121 1.00 0.00
ATOM 3446 1HG GLU A 730 3.408 6.395 -11.755 1.00 0.00
ATOM 3447 2HG GLU A 730 4.154 4.995 -12.552 1.00 0.00
ATOM 3448 N ASN A 731 5.383 5.085 -7.649 1.00 0.00
ATOM 3449 CA ASN A 731 6.262 4.803 -6.553 1.00 0.00
ATOM 3450 C ASN A 731 5.724 3.642 -5.785 1.00 0.00
ATOM 3451 O ASN A 731 6.482 2.778 -5.346 1.00 0.00
ATOM 3452 CB ASN A 731 6.391 5.978 -5.566 1.00 0.00
ATOM 3453 CG ASN A 731 7.092 7.133 -6.272 1.00 0.00
ATOM 3454 OD1 ASN A 731 6.004 6.959 -5.719 1.00 0.00
ATOM 3455 ND2 ASN A 731 8.213 6.414 -6.535 1.00 0.00
ATOM 3456 HN ASN A 731 4.894 5.957 -7.679 1.00 0.00
ATOM 3457 HA ASN A 731 7.235 4.570 -6.986 1.00 0.00
ATOM 3458 1HB ASN A 731 6.978 5.682 -4.697 1.00 0.00
ATOM 3459 2HB ASN A 731 5.406 6.307 -5.236 1.00 0.00
ATOM 3460 1HD2 ASN A 731 8.909 6.788 -7.148 1.00 0.00
ATOM 3461 2HD2 ASN A 731 8.358 5.513 -6.126 1.00 0.00
ATOM 3462 N LEU A 732 4.389 3.608 -5.654 1.00 0.00
ATOM 3463 CA LEU A 732 3.673 2.603 -4.884 1.00 0.00
ATOM 3464 C LEU A 732 3.997 1.198 -5.395 1.00 0.00
ATOM 3465 O LEU A 732 4.352 0.318 -4.621 1.00 0.00
ATOM 3466 CB LEU A 732 2.167 2.913 -4.937 1.00 0.00
ATOM 3467 CG LEU A 732 1.276 2.084 -4.002 1.00 0.00
ATOM 3468 CD1 LEU A 732 -0.051 2.820 -3.762 1.00 0.00
ATOM 3469 CD2 LEU A 732 1.004 0.675 -4.542 1.00 0.00
ATOM 3470 HN LEU A 732 3.877 4.336 -6.105 1.00 0.00
ATOM 3471 HA LEU A 732 4.037 2.690 -3.860 1.00 0.00
ATOM 3472 1HB LEU A 732 1.790 2.817 -5.951 1.00 0.00
ATOM 3473 2HB LEU A 732 2.044 3.962 -4.666 1.00 0.00
ATOM 3474 HG LEU A 732 1.791 1.986 -3.050 1.00 0.00
ATOM 3475 1HD1 LEU A 732 -0.731 2.224 -3.158 1.00 0.00
ATOM 3476 2HD1 LEU A 732 -0.557 3.042 -4.701 1.00 0.00
ATOM 3477 3HD1 LEU A 732 0.112 3.764 -3.240 1.00 0.00
ATOM 3478 1HD2 LEU A 732 0.728 0.714 -5.592 1.00 0.00

ATOM 3479 2HD2 LEU A 732 0.188 0.202 -3.998 1.00 0.00
ATOM 3480 3HD2 LEU A 732 1.865 0.018 -4.444 1.00 0.00
ATOM 3481 N LEU A 733 3.882 1.025 -6.730 1.00 0.00
ATOM 3482 CA LEU A 733 4.123 -0.307 -7.268 1.00 0.00
ATOM 3483 C LEU A 733 5.569 -0.716 -7.057 1.00 0.00
ATOM 3484 O LEU A 733 5.843 -1.876 -6.783 1.00 0.00
ATOM 3485 CB LEU A 733 3.761 -0.454 -8.753 1.00 0.00
ATOM 3486 CG LEU A 733 2.286 -0.825 -8.982 1.00 0.00
ATOM 3487 CD1 LEU A 733 1.429 0.428 -9.126 1.00 0.00
ATOM 3488 CD2 LEU A 733 2.141 -1.718 -10.214 1.00 0.00
ATOM 3489 HN LEU A 733 3.603 1.798 -7.310 1.00 0.00
ATOM 3490 HA LEU A 733 3.518 -0.998 -6.677 1.00 0.00
ATOM 3491 1HB LEU A 733 4.363 -1.258 -9.182 1.00 0.00
ATOM 3492 2HB LEU A 733 4.043 0.440 -9.313 1.00 0.00
ATOM 3493 HG LEU A 733 1.916 -1.402 -8.133 1.00 0.00
ATOM 3494 1HD1 LEU A 733 1.798 1.058 -9.937 1.00 0.00
ATOM 3495 2HD1 LEU A 733 1.450 1.008 -8.204 1.00 0.00
ATOM 3496 3HD1 LEU A 733 0.392 0.179 -9.350 1.00 0.00
ATOM 3497 1HD2 LEU A 733 2.708 -2.644 -10.104 1.00 0.00
ATOM 3498 2HD2 LEU A 733 2.518 -1.194 -11.090 1.00 0.00
ATOM 3499 3HD2 LEU A 733 1.101 -1.995 -10.389 1.00 0.00
ATOM 3500 N ASN A 734 6.483 0.268 -7.192 1.00 0.00
ATOM 3501 CA ASN A 734 7.872 -0.044 -7.046 1.00 0.00
ATOM 3502 C ASN A 734 8.076 -0.607 -5.680 1.00 0.00
ATOM 3503 O ASN A 734 8.776 -1.603 -5.507 1.00 0.00
ATOM 3504 CB ASN A 734 8.785 1.188 -7.172 1.00 0.00
ATOM 3505 CG ASN A 734 8.736 1.676 -8.611 1.00 0.00
ATOM 3506 OD1 ASN A 734 8.794 0.888 -9.554 1.00 0.00
ATOM 3507 ND2 ASN A 734 8.622 3.020 -8.790 1.00 0.00
ATOM 3508 HN ASN A 734 6.201 1.201 -7.415 1.00 0.00
ATOM 3509 HA ASN A 734 8.111 -0.767 -7.826 1.00 0.00
ATOM 3510 1HB ASN A 734 9.812 0.928 -6.916 1.00 0.00
ATOM 3511 2HB ASN A 734 8.444 1.984 -6.511 1.00 0.00
ATOM 3512 1HD2 ASN A 734 8.576 3.623 -7.994 1.00 0.00
ATOM 3513 2HD2 ASN A 734 8.584 3.419 -9.706 1.00 0.00
ATOM 3514 N TYR A 735 7.472 0.061 -4.663 1.00 0.00
ATOM 3515 CA TYR A 735 7.712 -0.419 -3.297 1.00 0.00
ATOM 3516 C TYR A 735 6.993 -1.750 -3.052 1.00 0.00
ATOM 3517 O TYR A 735 7.519 -2.627 -2.381 1.00 0.00
ATOM 3518 CB TYR A 735 7.350 0.616 -2.209 1.00 0.00
ATOM 3519 CG TYR A 735 7.674 0.144 -0.800 1.00 0.00
ATOM 3520 CD1 TYR A 735 8.850 -0.555 -0.517 1.00 0.00
ATOM 3521 CD2 TYR A 735 6.788 0.380 0.250 1.00 0.00
ATOM 3522 CE1 TYR A 735 9.119 -1.018 0.764 1.00 0.00
ATOM 3523 CE2 TYR A 735 7.061 -0.082 1.536 1.00 0.00
ATOM 3524 CZ TYR A 735 8.232 -0.775 1.800 1.00 0.00
ATOM 3525 OH TYR A 735 8.521 -1.222 3.077 1.00 0.00
ATOM 3526 HN TYR A 735 6.917 0.875 -4.864 1.00 0.00
ATOM 3527 HA TYR A 735 8.784 -0.616 -3.250 1.00 0.00

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ATOM  3528 1HB  TYR A 735     6.287  0.852 -2.275 1.00 0.00
ATOM  3529 2HB  TYR A 735     7.886  1.547 -2.393 1.00 0.00
ATOM  3530  HD1 TYR A 735     9.577 -0.763 -1.285 1.00 0.00
ATOM  3531  HE1 TYR A 735    10.023 -1.577  0.952 1.00 0.00
ATOM  3532  HD2 TYR A 735     5.867  0.913  0.069 1.00 0.00
ATOM  3533  HE2 TYR A 735     6.349  0.077  2.330 1.00 0.00
ATOM  3534  HH  TYR A 735     9.007 -0.572  3.589 1.00 0.00
ATOM  3535  N   CYS A 736     5.797 -1.868 -3.656 1.00 0.00
ATOM  3536  CA  CYS A 736     5.021 -3.096 -3.545 1.00 0.00
ATOM  3537  C   CYS A 736     5.847 -4.286 -4.026 1.00 0.00
ATOM  3538  O   CYS A 736     5.925 -5.320 -3.369 1.00 0.00
ATOM  3539  CB  CYS A 736     3.696 -2.947 -4.303 1.00 0.00
ATOM  3540  SG  CYS A 736     2.461 -4.186 -3.834 1.00 0.00
ATOM  3541  HN  CYS A 736     5.452 -1.090 -4.182 1.00 0.00
ATOM  3542  HA  CYS A 736     4.829 -3.258 -2.490 1.00 0.00
ATOM  3543 1HB  CYS A 736     3.856 -2.988 -5.382 1.00 0.00
ATOM  3544 2HB  CYS A 736     3.270 -1.966 -4.093 1.00 0.00
ATOM  3545  HG  CYS A 736     1.304 -3.914 -4.440 1.00 0.00
ATOM  3546  N   PHE A 737     6.506 -4.064 -5.183 1.00 0.00
ATOM  3547  CA  PHE A 737     7.249 -5.179 -5.733 1.00 0.00
ATOM  3548  C   PHE A 737     8.514 -5.457 -4.926 1.00 0.00
ATOM  3549  O   PHE A 737     8.950 -6.593 -4.862 1.00 0.00
ATOM  3550  CB  PHE A 737     7.421 -5.145 -7.268 1.00 0.00
ATOM  3551  CG  PHE A 737     8.665 -4.481 -7.801 1.00 0.00
ATOM  3552  CD1 PHE A 737     8.577 -3.263 -8.460 1.00 0.00
ATOM  3553  CD2 PHE A 737     9.914 -5.087 -7.676 1.00 0.00
ATOM  3554  CE1 PHE A 737     9.711 -2.651 -8.980 1.00 0.00
ATOM  3555  CE2 PHE A 737    11.052 -4.479 -8.191 1.00 0.00
ATOM  3556  CZ  PHE A 737    10.951 -3.258 -8.843 1.00 0.00
ATOM  3557  HN  PHE A 737     6.446 -3.190 -5.666 1.00 0.00
ATOM  3558  HA  PHE A 737     6.610 -6.051 -5.573 1.00 0.00
ATOM  3559 1HB  PHE A 737     6.537 -4.699 -7.727 1.00 0.00
ATOM  3560 2HB  PHE A 737     7.444 -6.174 -7.632 1.00 0.00
ATOM  3561  HD1 PHE A 737     7.613 -2.789 -8.574 1.00 0.00
ATOM  3562  HD2 PHE A 737    10.007 -6.045 -7.184 1.00 0.00
ATOM  3563  HE1 PHE A 737     9.625 -1.701 -9.490 1.00 0.00
ATOM  3564  HE2 PHE A 737    12.014 -4.959 -8.085 1.00 0.00
ATOM  3565  HZ  PHE A 737    11.833 -2.781 -9.246 1.00 0.00
ATOM  3566  N   GLN A 738     9.120 -4.415 -4.322 1.00 0.00
ATOM  3567  CA  GLN A 738    10.282 -4.659 -3.514 1.00 0.00
ATOM  3568  C   GLN A 738     9.894 -5.407 -2.272 1.00 0.00
ATOM  3569  O   GLN A 738    10.561 -6.363 -1.882 1.00 0.00
ATOM  3570  CB  GLN A 738    11.000 -3.359 -3.105 1.00 0.00
ATOM  3571  CG  GLN A 738    12.352 -3.577 -2.418 1.00 0.00
ATOM  3572  CD  GLN A 738    12.102 -3.957 -0.966 1.00 0.00
ATOM  3573  OE1 GLN A 738    11.251 -3.369 -0.301 1.00 0.00
ATOM  3574  NE2 GLN A 738    12.856 -4.970 -0.462 1.00 0.00
ATOM  3575  HN  GLN A 738     8.801 -3.479 -4.470 1.00 0.00
ATOM  3576  HA  GLN A 738    10.949 -5.287 -4.104 1.00 0.00
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ATOM 3577 1HB GLN A 738 10.353 -2.805 -2.427 1.00 0.00
ATOM 3578 2HB GLN A 738 11.159 -2.756 -3.998 1.00 0.00
ATOM 3579 1HG GLN A 738 12.948 -2.665 -2.452 1.00 0.00
ATOM 3580 2HG GLN A 738 12.903 -4.381 -2.908 1.00 0.00
ATOM 3581 1HE2 GLN A 738 13.630 -5.321 -0.989 1.00 0.00
ATOM 3582 2HE2 GLN A 738 12.652 -5.374 0.429 1.00 0.00
ATOM 3583 N THR A 739 8.777 -4.983 -1.675 1.00 0.00
ATOM 3584 CA THR A 739 8.229 -5.599 -0.472 1.00 0.00
ATOM 3585 C THR A 739 7.769 -7.048 -0.725 1.00 0.00
ATOM 3586 O THR A 739 7.590 -7.863 0.163 1.00 0.00
ATOM 3587 CB THR A 739 7.024 -4.732 -0.074 1.00 0.00
ATOM 3588 OG1 THR A 739 7.468 -3.420 0.223 1.00 0.00
ATOM 3589 CG2 THR A 739 6.312 -5.263 1.159 1.00 0.00
ATOM 3590 HN THR A 739 8.305 -4.212 -2.093 1.00 0.00
ATOM 3591 HA THR A 739 9.007 -5.592 0.292 1.00 0.00
ATOM 3592 HB THR A 739 6.279 -4.716 -0.884 1.00 0.00
ATOM 3593 HG1 THR A 739 7.587 -2.915 -0.587 1.00 0.00
ATOM 3594 1HG2 THR A 739 6.996 -5.820 1.792 1.00 0.00
ATOM 3595 2HG2 THR A 739 5.517 -5.941 0.871 1.00 0.00
ATOM 3596 3HG2 THR A 739 5.874 -4.459 1.746 1.00 0.00
ATOM 3597 N PHE A 740 7.539 -7.292 -2.006 1.00 0.00
ATOM 3598 CA PHE A 740 7.217 -8.590 -2.519 1.00 0.00
ATOM 3599 C PHE A 740 8.461 -9.389 -2.770 1.00 0.00
ATOM 3600 O PHE A 740 8.539 -10.564 -2.415 1.00 0.00
ATOM 3601 CB PHE A 740 6.466 -8.465 -3.856 1.00 0.00
ATOM 3602 CG PHE A 740 6.007 -9.806 -4.302 1.00 0.00
ATOM 3603 CD1 PHE A 740 6.865 -10.669 -4.944 1.00 0.00
ATOM 3604 CD2 PHE A 740 4.676 -10.138 -4.199 1.00 0.00
ATOM 3605 CE1 PHE A 740 6.402 -11.859 -5.454 1.00 0.00
ATOM 3606 CE2 PHE A 740 4.207 -11.323 -4.709 1.00 0.00
ATOM 3607 CZ PHE A 740 5.072 -12.183 -5.342 1.00 0.00
ATOM 3608 HN PHE A 740 7.342 -6.493 -2.574 1.00 0.00
ATOM 3609 HA PHE A 740 6.596 -9.089 -1.774 1.00 0.00
ATOM 3610 1HB PHE A 740 7.124 -8.042 -4.615 1.00 0.00
ATOM 3611 2HB PHE A 740 5.601 -7.813 -3.738 1.00 0.00
ATOM 3612 HD1 PHE A 740 7.908 -10.410 -5.047 1.00 0.00
ATOM 3613 HD2 PHE A 740 3.992 -9.458 -3.712 1.00 0.00
ATOM 3614 HE1 PHE A 740 7.085 -12.539 -5.941 1.00 0.00
ATOM 3615 HE2 PHE A 740 3.163 -11.580 -4.612 1.00 0.00
ATOM 3616 HZ PHE A 740 4.706 -13.112 -5.753 1.00 0.00
ATOM 3617 N LEU A 741 9.481 -8.749 -3.373 1.00 0.00
ATOM 3618 CA LEU A 741 10.675 -9.435 -3.772 1.00 0.00
ATOM 3619 C LEU A 741 11.407 -10.008 -2.617 1.00 0.00
ATOM 3620 O LEU A 741 11.870 -11.146 -2.694 1.00 0.00
ATOM 3621 CB LEU A 741 11.668 -8.553 -4.549 1.00 0.00
ATOM 3622 CG LEU A 741 12.941 -9.319 -4.958 1.00 0.00
ATOM 3623 CD1 LEU A 741 12.608 -10.522 -5.851 1.00 0.00
ATOM 3624 CD2 LEU A 741 13.977 -8.382 -5.600 1.00 0.00
ATOM 3625 HN LEU A 741 9.403 -7.768 -3.547 1.00 0.00

ATOM 3626 HA LEU A 741 10.356 -10.270 -4.395 1.00 0.00
ATOM 3627 1HB LEU A 741 11.950 -7.704 -3.927 1.00 0.00
ATOM 3628 2HB LEU A 741 11.179 -8.174 -5.445 1.00 0.00
ATOM 3629 HG LEU A 741 13.455 -9.667 -4.062 1.00 0.00
ATOM 3630 1HD1 LEU A 741 11.955 -10.224 -6.671 1.00 0.00
ATOM 3631 2HD1 LEU A 741 12.094 -11.290 -5.273 1.00 0.00
ATOM 3632 3HD1 LEU A 741 13.521 -10.937 -6.280 1.00 0.00
ATOM 3633 1HD2 LEU A 741 14.269 -7.596 -4.904 1.00 0.00
ATOM 3634 2HD2 LEU A 741 13.557 -7.908 -6.487 1.00 0.00
ATOM 3635 3HD2 LEU A 741 14.872 -8.941 -5.873 1.00 0.00
ATOM 3636 N ASP A 742 11.534 -9.248 -1.511 1.00 0.00
ATOM 3637 CA ASP A 742 12.265 -9.803 -0.414 1.00 0.00
ATOM 3638 C ASP A 742 11.571 -11.053 0.018 1.00 0.00
ATOM 3639 O ASP A 742 10.347 -11.162 -0.050 1.00 0.00
ATOM 3640 CB ASP A 742 12.541 -8.820 0.746 1.00 0.00
ATOM 3641 CG ASP A 742 11.249 -8.276 1.322 1.00 0.00
ATOM 3642 OD1 ASP A 742 10.245 -9.033 1.325 1.00 0.00
ATOM 3643 OD2 ASP A 742 11.246 -7.093 1.757 1.00 0.00
ATOM 3644 HN ASP A 742 11.134 -8.333 -1.460 1.00 0.00
ATOM 3645 HA ASP A 742 13.209 -10.156 -0.828 1.00 0.00
ATOM 3646 1HB ASP A 742 13.139 -7.982 0.386 1.00 0.00
ATOM 3647 2HB ASP A 742 13.086 -9.330 1.540 1.00 0.00
ATOM 3648 N LYS A 743 12.368 -12.049 0.448 1.00 0.00
ATOM 3649 CA LYS A 743 11.832 -13.346 0.724 1.00 0.00
ATOM 3650 C LYS A 743 10.692 -13.275 1.663 1.00 0.00
ATOM 3651 O LYS A 743 9.628 -13.837 1.400 1.00 0.00
ATOM 3652 CB LYS A 743 12.806 -14.309 1.412 1.00 0.00
ATOM 3653 CG LYS A 743 12.044 -15.542 1.902 1.00 0.00
ATOM 3654 CD LYS A 743 12.883 -16.607 2.605 1.00 0.00
ATOM 3655 CE LYS A 743 12.022 -17.662 3.304 1.00 0.00
ATOM 3656 NZ LYS A 743 11.056 -16.998 4.210 1.00 0.00
ATOM 3657 HN LYS A 743 13.345 -11.880 0.575 1.00 0.00
ATOM 3658 HA LYS A 743 11.525 -13.758 -0.236 1.00 0.00
ATOM 3659 1HB LYS A 743 13.284 -13.811 2.255 1.00 0.00
ATOM 3660 2HB LYS A 743 13.583 -14.611 0.709 1.00 0.00
ATOM 3661 1HG LYS A 743 11.560 -16.005 1.044 1.00 0.00
ATOM 3662 2HG LYS A 743 11.272 -15.210 2.594 1.00 0.00
ATOM 3663 1HD LYS A 743 13.523 -16.124 3.344 1.00 0.00
ATOM 3664 2HD LYS A 743 13.520 -17.098 1.870 1.00 0.00
ATOM 3665 1HE LYS A 743 12.645 -18.329 3.899 1.00 0.00
ATOM 3666 2HE LYS A 743 11.460 -18.241 2.571 1.00 0.00
ATOM 3667 1HZ LYS A 743 10.178 -16.794 3.691 1.00 0.00
ATOM 3668 2HZ LYS A 743 11.465 -16.109 4.561 1.00 0.00
ATOM 3669 3HZ LYS A 743 10.847 -17.625 5.013 1.00 0.00
ATOM 3670 N THR A 744 10.866 -12.578 2.792 1.00 0.00
ATOM 3671 CA THR A 744 9.773 -12.650 3.697 1.00 0.00
ATOM 3672 C THR A 744 9.253 -11.262 3.862 1.00 0.00
ATOM 3673 O THR A 744 9.960 -10.390 4.369 1.00 0.00
ATOM 3674 CB THR A 744 10.206 -13.141 5.048 1.00 0.00

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ATOM  3675  OG1 THR A 744      11.103 -14.232   4.899  1.00  0.00
ATOM  3676  CG2 THR A 744       8.960 -13.680   5.773  1.00  0.00
ATOM  3677  HN  THR A 744      11.693 -12.052   2.981  1.00  0.00
ATOM  3678  HA  THR A 744       9.043 -13.332   3.261  1.00  0.00
ATOM  3679  HB  THR A 744      10.718 -12.349   5.594  1.00  0.00
ATOM  3680  HG1 THR A 744      11.846 -13.909   4.407  1.00  0.00
ATOM  3681 1HG2 THR A 744       8.820 -14.740   5.563  1.00  0.00
ATOM  3682 2HG2 THR A 744       8.069 -13.150   5.436  1.00  0.00
ATOM  3683 3HG2 THR A 744       9.071 -13.562   6.851  1.00  0.00
ATOM  3684  N   MET A 745       8.018 -10.964   3.408  1.00  0.00
ATOM  3685  CA  MET A 745       7.428  -9.642   3.726  1.00  0.00
ATOM  3686  C   MET A 745       5.989  -9.601   3.232  1.00  0.00
ATOM  3687  O   MET A 745       5.055  -9.884   3.973  1.00  0.00
ATOM  3688  CB  MET A 745       8.233  -8.382   3.310  1.00  0.00
ATOM  3689  CG  MET A 745       7.813  -7.093   4.023  1.00  0.00
ATOM  3690  SD  MET A 745       9.021  -5.787   3.661  1.00  0.00
ATOM  3691  CE  MET A 745       7.992  -4.302   3.617  1.00  0.00
ATOM  3692  HN  MET A 745       7.516 -11.616   2.840  1.00  0.00
ATOM  3693  HA  MET A 745       7.362  -9.591   4.801  1.00  0.00
ATOM  3694 1HB  MET A 745       8.199  -8.227   2.245  1.00  0.00
ATOM  3695 2HB  MET A 745       9.288  -8.489   3.533  1.00  0.00
ATOM  3696 1HG  MET A 745       7.795  -7.286   5.094  1.00  0.00
ATOM  3697 2HG  MET A 745       6.810  -6.798   3.719  1.00  0.00
ATOM  3698 1HE  MET A 745       8.417  -3.530   4.257  1.00  0.00
ATOM  3699 2HE  MET A 745       6.972  -4.501   3.945  1.00  0.00
ATOM  3700 3HE  MET A 745       7.986  -3.875   2.615  1.00  0.00
ATOM  3701  N   SER A 746       5.851  -9.230   1.946  1.00  0.00
ATOM  3702  CA  SER A 746       4.516  -9.190   1.377  1.00  0.00
ATOM  3703  C   SER A 746       4.071 -10.623   1.276  1.00  0.00
ATOM  3704  O   SER A 746       4.874 -11.495   0.961  1.00  0.00
ATOM  3705  CB  SER A 746       4.501  -8.593  -0.037  1.00  0.00
ATOM  3706  OG  SER A 746       3.188  -8.162  -0.377  1.00  0.00
ATOM  3707  HN  SER A 746       6.665  -9.030   1.391  1.00  0.00
ATOM  3708  HA  SER A 746       3.877  -8.626   2.057  1.00  0.00
ATOM  3709 1HB  SER A 746       4.846  -9.345  -0.755  1.00  0.00
ATOM  3710 2HB  SER A 746       5.187  -7.749  -0.090  1.00  0.00
ATOM  3711  HG  SER A 746       3.159  -7.827  -1.275  1.00  0.00
ATOM  3712  N   ILE A 747       2.778 -10.859   1.568  1.00  0.00
ATOM  3713  CA  ILE A 747       2.333 -12.194   1.377  1.00  0.00
ATOM  3714  C   ILE A 747       2.368 -12.310  -0.104  1.00  0.00
ATOM  3715  O   ILE A 747       1.618 -11.654  -0.825  1.00  0.00
ATOM  3716  CB  ILE A 747       0.939 -12.479   1.863  1.00  0.00
ATOM  3717  CG1 ILE A 747       0.778 -12.082   3.341  1.00  0.00
ATOM  3718  CG2 ILE A 747       0.700 -13.986   1.658  1.00  0.00
ATOM  3719  CD1 ILE A 747       0.813 -10.575   3.581  1.00  0.00
ATOM  3720  HN  ILE A 747       2.179 -10.147   1.933  1.00  0.00
ATOM  3721  HA  ILE A 747       3.042 -12.826   1.911  1.00  0.00
ATOM  3722  HB  ILE A 747       0.211 -11.897   1.297  1.00  0.00
ATOM  3723 1HG2 ILE A 747       1.303 -14.570   2.353  1.00  0.00
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ATOM 3724 2HG2 ILE A 747 0.978 -14.277 0.645 1.00 0.00
ATOM 3725 3HG2 ILE A 747 -0.348 -14.228 1.835 1.00 0.00
ATOM 3726 1HG1 ILE A 747 1.579 -12.545 3.916 1.00 0.00
ATOM 3727 2HG1 ILE A 747 -0.173 -12.471 3.704 1.00 0.00
ATOM 3728 1HD1 ILE A 747 0.129 -10.061 2.906 1.00 0.00
ATOM 3729 2HD1 ILE A 747 1.816 -10.189 3.403 1.00 0.00
ATOM 3730 3HD1 ILE A 747 0.510 -10.350 4.604 1.00 0.00
ATOM 3731 N GLU A 748 3.284 -13.156 -0.596 1.00 0.00
ATOM 3732 CA GLU A 748 3.436 -13.371 -2.000 1.00 0.00
ATOM 3733 C GLU A 748 2.141 -13.951 -2.449 1.00 0.00
ATOM 3734 O GLU A 748 1.764 -13.859 -3.616 1.00 0.00
ATOM 3735 CB GLU A 748 4.568 -14.372 -2.304 1.00 0.00
ATOM 3736 CG GLU A 748 4.775 -14.670 -3.789 1.00 0.00
ATOM 3737 CD GLU A 748 3.903 -15.864 -4.150 1.00 0.00
ATOM 3738 OE1 GLU A 748 3.323 -16.474 -3.212 1.00 0.00
ATOM 3739 OE2 GLU A 748 3.813 -16.188 -5.363 1.00 0.00
ATOM 3740 HN GLU A 748 3.877 -13.651 0.039 1.00 0.00
ATOM 3741 HA GLU A 748 3.656 -12.402 -2.448 1.00 0.00
ATOM 3742 1HB GLU A 748 4.346 -15.308 -1.793 1.00 0.00
ATOM 3743 2HB GLU A 748 5.497 -13.973 -1.900 1.00 0.00
ATOM 3744 1HG GLU A 748 5.819 -14.911 -3.990 1.00 0.00
ATOM 3745 2HG GLU A 748 4.484 -13.813 -4.397 1.00 0.00
ATOM 3746 N PHE A 749 1.432 -14.561 -1.486 1.00 0.00
ATOM 3747 CA PHE A 749 0.228 -15.295 -1.685 1.00 0.00
ATOM 3748 C PHE A 749 -1.022 -14.586 -2.108 1.00 0.00
ATOM 3749 O PHE A 749 -1.822 -15.245 -2.771 1.00 0.00
ATOM 3750 CB PHE A 749 -0.049 -16.229 -0.502 1.00 0.00
ATOM 3751 CG PHE A 749 1.105 -17.172 -0.580 1.00 0.00
ATOM 3752 CD1 PHE A 749 1.105 -18.179 -1.517 1.00 0.00
ATOM 3753 CD2 PHE A 749 2.252 -16.944 0.145 1.00 0.00
ATOM 3754 CE1 PHE A 749 2.221 -18.959 -1.716 1.00 0.00
ATOM 3755 CE2 PHE A 749 3.369 -17.725 -0.043 1.00 0.00
ATOM 3756 CZ PHE A 749 3.358 -18.730 -0.980 1.00 0.00
ATOM 3757 HN PHE A 749 1.779 -14.494 -0.552 1.00 0.00
ATOM 3758 HA PHE A 749 0.350 -15.868 -2.604 1.00 0.00
ATOM 3759 1HB PHE A 749 -0.995 -16.757 -0.614 1.00 0.00
ATOM 3760 2HB PHE A 749 -0.054 -15.693 0.447 1.00 0.00
ATOM 3761 HD1 PHE A 749 0.216 -18.361 -2.104 1.00 0.00
ATOM 3762 HD2 PHE A 749 2.276 -16.143 0.869 1.00 0.00
ATOM 3763 HE1 PHE A 749 2.203 -19.750 -2.450 1.00 0.00
ATOM 3764 HE2 PHE A 749 4.256 -17.548 0.547 1.00 0.00
ATOM 3765 HZ PHE A 749 4.237 -19.337 -1.137 1.00 0.00
ATOM 3766 N PRO A 750 -1.315 -13.342 -1.805 1.00 0.00
ATOM 3767 CA PRO A 750 -2.560 -12.833 -2.313 1.00 0.00
ATOM 3768 C PRO A 750 -2.536 -12.817 -3.807 1.00 0.00
ATOM 3769 O PRO A 750 -1.746 -12.081 -4.395 1.00 0.00
ATOM 3770 CB PRO A 750 -2.791 -11.502 -1.606 1.00 0.00
ATOM 3771 CG PRO A 750 -2.100 -11.720 -0.244 1.00 0.00
ATOM 3772 CD PRO A 750 -0.975 -12.738 -0.529 1.00 0.00

ATOM 3773 1HD PRO A 750 -0.006 -12.243 -0.593 1.00 0.00
ATOM 3774 2HD PRO A 750 -0.931 -13.501 0.248 1.00 0.00
ATOM 3775 HA PRO A 750 -3.366 -13.534 -2.096 1.00 0.00
ATOM 3776 1HB PRO A 750 -3.854 -11.293 -1.486 1.00 0.00
ATOM 3777 2HB PRO A 750 -2.341 -10.675 -2.155 1.00 0.00
ATOM 3778 1HG PRO A 750 -1.692 -10.785 0.139 1.00 0.00
ATOM 3779 2HG PRO A 750 -2.803 -12.112 0.491 1.00 0.00
ATOM 3780 N GLU A 751 -3.415 -13.633 -4.421 1.00 0.00
ATOM 3781 CA GLU A 751 -3.460 -13.836 -5.840 1.00 0.00
ATOM 3782 C GLU A 751 -3.919 -12.660 -6.642 1.00 0.00
ATOM 3783 O GLU A 751 -3.277 -12.291 -7.623 1.00 0.00
ATOM 3784 CB GLU A 751 -4.349 -15.034 -6.212 1.00 0.00
ATOM 3785 CG GLU A 751 -5.788 -14.904 -5.711 1.00 0.00
ATOM 3786 CD GLU A 751 -6.544 -16.157 -6.130 1.00 0.00
ATOM 3787 OE1 GLU A 751 -6.025 -17.274 -5.868 1.00 0.00
ATOM 3788 OE2 GLU A 751 -7.649 -16.014 -6.717 1.00 0.00
ATOM 3789 HN GLU A 751 -4.073 -14.126 -3.853 1.00 0.00
ATOM 3790 HA GLU A 751 -2.436 -14.006 -6.171 1.00 0.00
ATOM 3791 1HB GLU A 751 -3.912 -15.937 -5.789 1.00 0.00
ATOM 3792 2HB GLU A 751 -4.364 -15.135 -7.296 1.00 0.00
ATOM 3793 1HG GLU A 751 -6.269 -14.030 -6.150 1.00 0.00
ATOM 3794 2HG GLU A 751 -5.810 -14.815 -4.625 1.00 0.00
ATOM 3795 N MET A 752 -5.033 -12.022 -6.240 1.00 0.00
ATOM 3796 CA MET A 752 -5.558 -10.951 -7.036 1.00 0.00
ATOM 3797 C MET A 752 -4.576 -9.828 -7.065 1.00 0.00
ATOM 3798 O MET A 752 -4.358 -9.205 -8.103 1.00 0.00
ATOM 3799 CB MET A 752 -6.887 -10.401 -6.498 1.00 0.00
ATOM 3800 CG MET A 752 -7.528 -9.365 -7.423 1.00 0.00
ATOM 3801 SD MET A 752 -8.234 -10.030 -8.960 1.00 0.00
ATOM 3802 CE MET A 752 -8.804 -8.414 -9.560 1.00 0.00
ATOM 3803 HN MET A 752 -5.491 -12.294 -5.393 1.00 0.00
ATOM 3804 HA MET A 752 -5.697 -11.348 -8.041 1.00 0.00
ATOM 3805 1HB MET A 752 -6.710 -9.942 -5.526 1.00 0.00
ATOM 3806 2HB MET A 752 -7.582 -11.229 -6.364 1.00 0.00
ATOM 3807 1HG MET A 752 -6.772 -8.630 -7.698 1.00 0.00
ATOM 3808 2HG MET A 752 -8.329 -8.863 -6.881 1.00 0.00
ATOM 3809 1HE MET A 752 -7.986 -7.695 -9.501 1.00 0.00
ATOM 3810 2HE MET A 752 -9.627 -8.057 -8.941 1.00 0.00
ATOM 3811 3HE MET A 752 -9.121 -8.495 -10.600 1.00 0.00
ATOM 3812 N LEU A 753 -3.980 -9.571 -5.881 1.00 0.00
ATOM 3813 CA LEU A 753 -3.011 -8.486 -5.797 1.00 0.00
ATOM 3814 C LEU A 753 -1.796 -8.816 -6.679 1.00 0.00
ATOM 3815 O LEU A 753 -1.275 -8.016 -7.411 1.00 0.00
ATOM 3816 CB LEU A 753 -2.612 -8.246 -4.332 1.00 0.00
ATOM 3817 CG LEU A 753 -1.716 -7.009 -4.115 1.00 0.00
ATOM 3818 CD1 LEU A 753 -2.411 -5.703 -4.529 1.00 0.00
ATOM 3819 CD2 LEU A 753 -1.262 -6.929 -2.652 1.00 0.00
ATOM 3820 HN LEU A 753 -4.193 -10.142 -5.091 1.00 0.00
ATOM 3821 HA LEU A 753 -3.510 -7.604 -6.201 1.00 0.00

ATOM 3822 1HB LEU A 753 -2.102 -9.133 -3.950 1.00 0.00
ATOM 3823 2HB LEU A 753 -3.513 -8.138 -3.727 1.00 0.00
ATOM 3824 HG LEU A 753 -0.817 -7.118 -4.725 1.00 0.00
ATOM 3825 1HD1 LEU A 753 -2.614 -5.679 -5.599 1.00 0.00
ATOM 3826 2HD1 LEU A 753 -1.782 -4.841 -4.304 1.00 0.00
ATOM 3827 3HD1 LEU A 753 -3.356 -5.572 -4.002 1.00 0.00
ATOM 3828 1HD2 LEU A 753 -2.112 -6.817 -1.977 1.00 0.00
ATOM 3829 2HD2 LEU A 753 -0.590 -6.087 -2.490 1.00 0.00
ATOM 3830 3HD2 LEU A 753 -0.728 -7.835 -2.364 1.00 0.00
ATOM 3831 N ALA A 754 -1.355 -10.050 -6.651 1.00 0.00
ATOM 3832 CA ALA A 754 -0.204 -10.417 -7.422 1.00 0.00
ATOM 3833 C ALA A 754 -0.537 -10.216 -8.862 1.00 0.00
ATOM 3834 O ALA A 754 0.294 -9.759 -9.649 1.00 0.00
ATOM 3835 CB ALA A 754 0.178 -11.896 -7.250 1.00 0.00
ATOM 3836 HN ALA A 754 -1.817 -10.738 -6.092 1.00 0.00
ATOM 3837 HA ALA A 754 0.613 -9.777 -7.089 1.00 0.00
ATOM 3838 1HB ALA A 754 -0.640 -12.544 -7.564 1.00 0.00
ATOM 3839 2HB ALA A 754 0.394 -12.110 -6.203 1.00 0.00
ATOM 3840 3HB ALA A 754 1.050 -12.133 -7.859 1.00 0.00
ATOM 3841 N GLU A 755 -1.786 -10.545 -9.230 1.00 0.00
ATOM 3842 CA GLU A 755 -2.225 -10.455 -10.588 1.00 0.00
ATOM 3843 C GLU A 755 -2.065 -9.055 -11.070 1.00 0.00
ATOM 3844 O GLU A 755 -1.477 -8.828 -12.127 1.00 0.00
ATOM 3845 CB GLU A 755 -3.715 -10.810 -10.727 1.00 0.00
ATOM 3846 CG GLU A 755 -4.273 -10.739 -12.149 1.00 0.00
ATOM 3847 CD GLU A 755 -5.752 -11.092 -12.056 1.00 0.00
ATOM 3848 OE1 GLU A 755 -6.066 -12.306 -11.925 1.00 0.00
ATOM 3849 OE2 GLU A 755 -6.587 -10.150 -12.100 1.00 0.00
ATOM 3850 HN GLU A 755 -2.427 -10.864 -8.532 1.00 0.00
ATOM 3851 HA GLU A 755 -1.614 -11.147 -11.167 1.00 0.00
ATOM 3852 1HB GLU A 755 -4.288 -10.128 -10.101 1.00 0.00
ATOM 3853 2HB GLU A 755 -3.860 -11.823 -10.353 1.00 0.00
ATOM 3854 1HG GLU A 755 -3.767 -11.451 -12.801 1.00 0.00
ATOM 3855 2HG GLU A 755 -4.161 -9.736 -12.561 1.00 0.00
ATOM 3856 N ILE A 756 -2.558 -8.063 -10.300 1.00 0.00
ATOM 3857 CA ILE A 756 -2.405 -6.729 -10.798 1.00 0.00
ATOM 3858 C ILE A 756 -0.951 -6.435 -10.893 1.00 0.00
ATOM 3859 O ILE A 756 -0.505 -5.902 -11.910 1.00 0.00
ATOM 3860 CB ILE A 756 -3.029 -5.638 -9.952 1.00 0.00
ATOM 3861 CG1 ILE A 756 -2.921 -4.241 -10.627 1.00 0.00
ATOM 3862 CG2 ILE A 756 -2.437 -5.706 -8.536 1.00 0.00
ATOM 3863 CD1 ILE A 756 -1.513 -3.634 -10.808 1.00 0.00
ATOM 3864 HN ILE A 756 -3.006 -8.250 -9.427 1.00 0.00
ATOM 3865 HA ILE A 756 -2.860 -6.726 -11.788 1.00 0.00
ATOM 3866 HB ILE A 756 -4.110 -5.774 -9.909 1.00 0.00
ATOM 3867 1HG2 ILE A 756 -1.356 -5.563 -8.563 1.00 0.00
ATOM 3868 2HG2 ILE A 756 -2.637 -6.680 -8.090 1.00 0.00
ATOM 3869 3HG2 ILE A 756 -2.864 -4.922 -7.911 1.00 0.00
ATOM 3870 1HG1 ILE A 756 -3.504 -3.542 -10.031 1.00 0.00

ATOM 3871 2HG1 ILE A 756 -3.374 -4.317 -11.613 1.00 0.00
ATOM 3872 1HD1 ILE A 756 -1.016 -4.066 -11.676 1.00 0.00
ATOM 3873 2HD1 ILE A 756 -0.898 -3.840 -9.931 1.00 0.00
ATOM 3874 3HD1 ILE A 756 -1.584 -2.557 -10.961 1.00 0.00
ATOM 3875 N ILE A 757 -0.175 -6.762 -9.850 1.00 0.00
ATOM 3876 CA ILE A 757 1.184 -6.312 -9.796 1.00 0.00
ATOM 3877 C ILE A 757 1.931 -6.758 -11.008 1.00 0.00
ATOM 3878 O ILE A 757 2.694 -5.986 -11.586 1.00 0.00
ATOM 3879 CB ILE A 757 1.925 -6.851 -8.613 1.00 0.00
ATOM 3880 CG1 ILE A 757 1.289 -6.331 -7.315 1.00 0.00
ATOM 3881 CG2 ILE A 757 3.410 -6.491 -8.781 1.00 0.00
ATOM 3882 CD1 ILE A 757 1.268 -4.806 -7.228 1.00 0.00
ATOM 3883 HN ILE A 757 -0.547 -7.322 -9.109 1.00 0.00
ATOM 3884 HA ILE A 757 1.151 -5.224 -9.755 1.00 0.00
ATOM 3885 HB ILE A 757 1.805 -7.933 -8.555 1.00 0.00
ATOM 3886 1HG2 ILE A 757 3.519 -5.482 -9.180 1.00 0.00
ATOM 3887 2HG2 ILE A 757 3.889 -7.181 -9.475 1.00 0.00
ATOM 3888 3HG2 ILE A 757 3.917 -6.529 -7.817 1.00 0.00
ATOM 3889 1HG1 ILE A 757 1.849 -6.724 -6.468 1.00 0.00
ATOM 3890 2HG1 ILE A 757 0.267 -6.701 -7.252 1.00 0.00
ATOM 3891 1HD1 ILE A 757 0.559 -4.389 -7.943 1.00 0.00
ATOM 3892 2HD1 ILE A 757 2.254 -4.402 -7.456 1.00 0.00
ATOM 3893 3HD1 ILE A 757 0.965 -4.490 -6.230 1.00 0.00
ATOM 3894 N THR A 758 1.699 -8.009 -11.440 1.00 0.00
ATOM 3895 CA THR A 758 2.403 -8.548 -12.565 1.00 0.00
ATOM 3896 C THR A 758 2.097 -7.753 -13.792 1.00 0.00
ATOM 3897 O THR A 758 2.966 -7.545 -14.637 1.00 0.00
ATOM 3898 CB THR A 758 2.045 -9.979 -12.854 1.00 0.00
ATOM 3899 OG1 THR A 758 2.968 -10.535 -13.779 1.00 0.00
ATOM 3900 CG2 THR A 758 0.620 -10.034 -13.435 1.00 0.00
ATOM 3901 HN THR A 758 1.023 -8.573 -10.967 1.00 0.00
ATOM 3902 HA THR A 758 3.465 -8.468 -12.334 1.00 0.00
ATOM 3903 HB THR A 758 2.079 -10.570 -11.939 1.00 0.00
ATOM 3904 HG1 THR A 758 3.149 -9.862 -14.421 1.00 0.00
ATOM 3905 1HG2 THR A 758 0.650 -10.130 -14.520 1.00 0.00
ATOM 3906 2HG2 THR A 758 0.079 -9.120 -13.192 1.00 0.00
ATOM 3907 3HG2 THR A 758 0.084 -10.895 -13.035 1.00 0.00
ATOM 3908 N ASN A 759 0.852 -7.259 -13.912 1.00 0.00
ATOM 3909 CA ASN A 759 0.449 -6.558 -15.094 1.00 0.00
ATOM 3910 C ASN A 759 1.381 -5.433 -15.388 1.00 0.00
ATOM 3911 O ASN A 759 1.869 -5.304 -16.509 1.00 0.00
ATOM 3912 CB ASN A 759 -0.951 -5.941 -14.956 1.00 0.00
ATOM 3913 CG ASN A 759 -1.259 -5.187 -16.241 1.00 0.00
ATOM 3914 OD1 ASN A 759 -1.632 -4.013 -16.206 1.00 0.00
ATOM 3915 ND2 ASN A 759 -1.094 -5.868 -17.405 1.00 0.00
ATOM 3916 HN ASN A 759 0.199 -7.383 -13.165 1.00 0.00
ATOM 3917 HA ASN A 759 0.464 -7.282 -15.909 1.00 0.00
ATOM 3918 1HB ASN A 759 -0.983 -5.249 -14.115 1.00 0.00
ATOM 3919 2HB ASN A 759 -1.700 -6.719 -14.806 1.00 0.00

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ATOM  3920 1HD2 ASN A 759     -0.784  -6.819 -17.383  1.00  0.00
ATOM  3921 2HD2 ASN A 759     -1.278  -5.437 -18.288  1.00  0.00
ATOM  3922  N   GLN A 760      1.663  -4.583 -14.389  1.00  0.00
ATOM  3923  CA  GLN A 760      2.499  -3.460 -14.673  1.00  0.00
ATOM  3924  C   GLN A 760      3.920  -3.842 -14.935  1.00  0.00
ATOM  3925  O   GLN A 760      4.581  -3.218 -15.763  1.00  0.00
ATOM  3926  CB  GLN A 760      2.341  -2.318 -13.653  1.00  0.00
ATOM  3927  CG  GLN A 760      0.911  -1.764 -13.764  1.00  0.00
ATOM  3928  CD  GLN A 760      0.769  -0.440 -13.032  1.00  0.00
ATOM  3929  OE1 GLN A 760      1.510   0.510 -13.277  1.00  0.00
ATOM  3930  NE2 GLN A 760     -0.221  -0.373 -12.102  1.00  0.00
ATOM  3931  HN  GLN A 760      1.298  -4.733 -13.470  1.00  0.00
ATOM  3932  HA  GLN A 760      2.225  -3.112 -15.669  1.00  0.00
ATOM  3933 1HB  GLN A 760      3.065  -1.530 -13.860  1.00  0.00
ATOM  3934 2HB  GLN A 760      2.521  -2.690 -12.645  1.00  0.00
ATOM  3935 1HG  GLN A 760      0.207  -2.474 -13.330  1.00  0.00
ATOM  3936 2HG  GLN A 760      0.659  -1.606 -14.812  1.00  0.00
ATOM  3937 1HE2 GLN A 760     -0.702  -1.206 -11.828  1.00  0.00
ATOM  3938 2HE2 GLN A 760     -0.480   0.497 -11.683  1.00  0.00
ATOM  3939  N   ILE A 761      4.442  -4.879 -14.248  1.00  0.00
ATOM  3940  CA  ILE A 761      5.781  -5.292 -14.553  1.00  0.00
ATOM  3941  C   ILE A 761      5.742  -6.011 -15.908  1.00  0.00
ATOM  3942 1OCT ILE A 761      5.322  -5.360 -16.902  1.00  0.00
ATOM  3943  CB  ILE A 761      6.385  -6.218 -13.530  1.00  0.00
ATOM  3944  CG1 ILE A 761      7.830  -6.571 -13.928  1.00  0.00
ATOM  3945  CG2 ILE A 761      5.457  -7.428 -13.332  1.00  0.00
ATOM  3946  CD1 ILE A 761      8.597  -7.355 -12.864  1.00  0.00
ATOM  3947 2OCT ILE A 761      6.129  -7.209 -15.978  1.00  0.00
ATOM  3948  HN  ILE A 761      3.908  -5.347 -13.544  1.00  0.00
ATOM  3949  HA  ILE A 761      6.375  -4.381 -14.624  1.00  0.00
ATOM  3950  HB  ILE A 761      6.414  -5.651 -12.601  1.00  0.00
ATOM  3951 1HG2 ILE A 761      4.449  -7.102 -13.075  1.00  0.00
ATOM  3952 2HG2 ILE A 761      5.825  -8.056 -12.520  1.00  0.00
ATOM  3953 3HG2 ILE A 761      5.399  -8.013 -14.250  1.00  0.00
ATOM  3954 1HG1 ILE A 761      8.369  -5.647 -14.132  1.00  0.00
ATOM  3955 2HG1 ILE A 761      7.804  -7.162 -14.842  1.00  0.00
ATOM  3956 1HD1 ILE A 761      8.098  -8.299 -12.647  1.00  0.00
ATOM  3957 2HD1 ILE A 761      8.649  -6.781 -11.939  1.00  0.00
ATOM  3958 3HD1 ILE A 761      9.604  -7.578 -13.214  1.00  0.00
ATOM  3959  HCT ILE A 761      5.361  -4.423 -16.765  1.00  0.00
ATOM  3960  O   HOH W 516     -9.097   2.914   0.913  1.00  0.00
ATOM  3961 1H   HOH W 516     -8.853   3.396   0.115  1.00  0.00
ATOM  3962 2H   HOH W 516     -8.335   2.330   1.052  1.00  0.00
ATOM  3963 NA+  CIP C 206      6.097   8.962  -3.974  1.00  0.00
ATOM  3964 NA+  CIP C 157     -9.340  -4.397 -27.602  1.00  0.00
ATOM  3965 NA+  CIP C 105     -8.364  -4.063  14.059  1.00  0.00
ATOM  3966 NA+  CIP C 184    -23.434  28.968 -12.650  1.00  0.00
ATOM  3967 NA+  CIP C 202      3.261  11.659 -12.120  1.00  0.00
ATOM  3968 NA+  CIP C 166    -15.650   5.434 -32.841  1.00  0.00
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ATOM  3969 NA+  CIP C 234    -7.350 -13.381 -10.083  1.00  0.00
ATOM  3970 NA+  CIP C 120     9.673   4.279  -1.053  1.00  0.00
ATOM  3971 CL-  CIM C  58   -20.663  -6.966 -18.429  1.00  0.00
ATOM  3972 NA+  CIP C 167   -16.694  -0.528 -26.996  1.00  0.00
ATOM  3973 CL-  CIM C 174   -24.680  17.196 -19.047  1.00  0.00
ATOM  3974 NA+  CIP C  16   -22.819  13.330  -4.433  1.00  0.00
ATOM  3975 NA+  CIP C 227     1.631 -16.295  -6.675  1.00  0.00
ATOM  3976 NA+  CIP C 221    11.345  -4.726   2.532  1.00  0.00
ATOM  3977 CL-  CIM C  93   -13.515   6.310   6.654  1.00  0.00
ATOM  3978 CL-  CIM C 160   -10.213  -4.624 -36.213  1.00  0.00
ATOM  3979 CL-  CIM C 178   -24.595  17.570  -9.392  1.00  0.00
ATOM  3980 CL-  CIM C  55   -18.222  -8.698 -11.429  1.00  0.00
ATOM  3981 CL-  CIM C 183   -15.467  17.246 -10.379  1.00  0.00
END
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Fig 13

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REMARK  1 grfromer modeller, no optimisation july 15 1998
ATOM      1  N   GLN 1   1      31.226  -1.970  94.273  1.00  5.90
ATOM      2  CA  GLN 1   1      32.061  -3.185  94.135  1.00  5.90
ATOM      3  C   GLN 1   1      33.238  -2.949  93.251  1.00  5.90
ATOM      4  O   GLN 1   1      33.964  -1.969  93.402  1.00  5.90
ATOM      5  CB  GLN 1   1      31.246  -4.344  93.534  1.00  5.90
ATOM      6  CG  GLN 1   1      30.248  -4.977  94.504  1.00  5.90
ATOM      7  CD  GLN 1   1      31.030  -5.896  95.434  1.00  5.90
ATOM      8  OE1 GLN 1   1      30.460  -6.569  96.291  1.00  5.90
ATOM      9  NE2 GLN 1   1      32.378  -5.931  95.256  1.00  5.90
ATOM     10  N   LEU 1   2      33.462  -3.888  92.314  1.00  0.97
ATOM     11  CA  LEU 1   2      34.556  -3.825  91.394  1.00  0.97
ATOM     12  C   LEU 1   2      34.400  -2.709  90.407  1.00  0.97
ATOM     13  O   LEU 1   2      35.388  -2.108  89.988  1.00  0.97
ATOM     14  CB  LEU 1   2      34.752  -5.124  90.594  1.00  0.97
ATOM     15  CG  LEU 1   2      35.203  -6.310  91.465  1.00  0.97
ATOM     16  CD1 LEU 1   2      35.397  -7.582  90.624  1.00  0.97
ATOM     17  CD2 LEU 1   2      36.445  -5.948  92.295  1.00  0.97
ATOM     18  N   THR 1   3      33.154  -2.414  89.990  1.00  4.97
ATOM     19  CA  THR 1   3      32.946  -1.389  89.006  1.00  4.97
ATOM     20  C   THR 1   3      33.539  -0.098  89.475  1.00  4.97
ATOM     21  O   THR 1   3      33.281   0.370  90.583  1.00  4.97
ATOM     22  CB  THR 1   3      31.496  -1.151  88.687  1.00  4.97
ATOM     23  OG1 THR 1   3      31.375  -0.248  87.598  1.00  4.97
ATOM     24  CG2 THR 1   3      30.792  -0.588  89.932  1.00  4.97
ATOM     25  N   PRO 1   4      34.334   0.496  88.629  1.00  1.53
ATOM     26  CA  PRO 1   4      34.970   1.734  88.985  1.00  1.53
ATOM     27  C   PRO 1   4      33.953   2.822  89.105  1.00  1.53
ATOM     28  O   PRO 1   4      32.935   2.768  88.416  1.00  1.53
ATOM     29  CB  PRO 1   4      36.021   1.984  87.906  1.00  1.53
ATOM     30  CG  PRO 1   4      36.397   0.567  87.435  1.00  1.53
ATOM     31  CD  PRO 1   4      35.129  -0.270  87.682  1.00  1.53
ATOM     32  N   THR 1   5      34.221   3.822  89.966  1.00  4.74
ATOM     33  CA  THR 1   5      33.280   4.873  90.217  1.00  4.74
ATOM     34  C   THR 1   5      32.996   5.653  88.973  1.00  4.74
ATOM     35  O   THR 1   5      31.839   5.946  88.679  1.00  4.74
ATOM     36  CB  THR 1   5      33.749   5.833  91.276  1.00  4.74
ATOM     37  OG1 THR 1   5      32.717   6.755  91.592  1.00  4.74
ATOM     38  CG2 THR 1   5      35.000   6.575  90.777  1.00  4.74
ATOM     39  N   LEU 1   6      34.042   5.976  88.189  1.00  0.89
ATOM     40  CA  LEU 1   6      33.888   6.778  87.008  1.00  0.89
ATOM     41  C   LEU 1   6      33.005   6.068  86.029  1.00  0.89
ATOM     42  O   LEU 1   6      32.203   6.696  85.338  1.00  0.89
ATOM     43  CB  LEU 1   6      35.231   7.060  86.306  1.00  0.89
ATOM     44  CG  LEU 1   6      35.101   7.915  85.031  1.00  0.89
ATOM     45  CD1 LEU 1   6      34.528   9.306  85.351  1.00  0.89
ATOM     46  CD2 LEU 1   6      36.436   7.988  84.273  1.00  0.89
ATOM     47  N   VAL 1   7      33.146   4.733  85.934  1.00  0.63
ATOM     48  CA  VAL 1   7      32.354   3.959  85.021  1.00  0.63
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ATOM   49  C  VAL 1  7    30.930  4.080 85.438  1.00 0.63
ATOM   50  O  VAL 1  7    30.032  4.219 84.610  1.00 0.63
ATOM   51  CB VAL 1  7    32.646  2.485 85.082  1.00 0.63
ATOM   52  CG1 VAL 1  7   31.739  1.778 84.061  1.00 0.63
ATOM   53  CG2 VAL 1  7   34.150  2.232 84.893  1.00 0.63
ATOM   54  N  SER 1  8    30.698  4.024 86.760  1.00 0.66
ATOM   55  CA SER 1  8    29.369  4.077 87.284  1.00 0.66
ATOM   56  C  SER 1  8    28.753  5.387 86.910  1.00 0.66
ATOM   57  O  SER 1  8    27.579  5.432 86.546  1.00 0.66
ATOM   58  CB SER 1  8    29.331  3.967 88.819  1.00 0.66
ATOM   59  OG SER 1  8    29.819  2.698 89.229  1.00 0.66
ATOM   60  N  LEU 1  9    29.523  6.497 86.978  1.00 8.73
ATOM   61  CA LEU 1  9    28.901  7.750 86.646  1.00 8.73
ATOM   62  C  LEU 1  9    28.462  7.675 85.232  1.00 8.73
ATOM   63  O  LEU 1  9    27.335  8.038 84.904  1.00 8.73
ATOM   64  CB LEU 1  9    29.780  9.012 86.517  1.00 8.73
ATOM   65  CG LEU 1  9    30.572  9.500 87.724  1.00 8.73
ATOM   66  CD1 LEU 1  9   29.685  9.772 88.945  1.00 8.73
ATOM   67  CD2 LEU 1  9   31.763  8.586 87.961  1.00 8.73
ATOM   68  N  LEU 1  10   29.363  7.182 84.363  1.00 1.17
ATOM   69  CA LEU 1  10   29.124  7.190 82.952  1.00 1.17
ATOM   70  C  LEU 1  10   27.867  6.438 82.663  1.00 1.17
ATOM   71  O  LEU 1  10   27.061  6.863 81.837  1.00 1.17
ATOM   72  CB LEU 1  10   30.291  6.589 82.144  1.00 1.17
ATOM   73  CG LEU 1  10   31.600  7.406 82.258  1.00 1.17
ATOM   74  CD1 LEU 1  10   32.739  6.781 81.435  1.00 1.17
ATOM   75  CD2 LEU 1  10   31.372  8.887 81.913  1.00 1.17
ATOM   76  N  GLU 1  11   27.653  5.307 83.355  1.00 3.68
ATOM   77  CA GLU 1  11   26.453  4.545 83.160  1.00 3.68
ATOM   78  C  GLU 1  11   25.296  5.429 83.496  1.00 3.68
ATOM   79  O  GLU 1  11   24.319  5.514 82.752  1.00 3.68
ATOM   80  CB GLU 1  11   26.364  3.363 84.145  1.00 3.68
ATOM   81  CG GLU 1  11   27.158  2.110 83.772  1.00 3.68
ATOM   82  CD GLU 1  11   26.140  1.007 83.512  1.00 3.68
ATOM   83  OE1 GLU 1  11   25.188  0.896 84.330  1.00 3.68
ATOM   84  OE2 GLU 1  11   26.293  0.260 82.511  1.00 3.68
ATOM   85  N  VAL 1  12   25.395  6.135 84.635  1.00 0.75
ATOM   86  CA VAL 1  12   24.309  6.939 85.107  1.00 0.75
ATOM   87  C  VAL 1  12   23.970  8.054 84.169  1.00 0.75
ATOM   88  O  VAL 1  12   22.797  8.283 83.880  1.00 0.75
ATOM   89  CB VAL 1  12   24.598  7.561 86.442  1.00 0.75
ATOM   90  CG1 VAL 1  12   23.394  8.424 86.854  1.00 0.75
ATOM   91  CG2 VAL 1  12   24.934  6.439 87.440  1.00 0.75
ATOM   92  N  ILE 1  13   24.984  8.784 83.664  1.00 4.56
ATOM   93  CA ILE 1  13   24.694  9.920 82.836  1.00 4.56
ATOM   94  C  ILE 1  13   24.234  9.610 81.445  1.00 4.56
ATOM   95  O  ILE 1  13   23.698 10.497 80.784  1.00 4.56
ATOM   96  CB ILE 1  13   25.744 11.011 82.766  1.00 4.56
ATOM   97  CG1 ILE 1  13   27.064 10.605 82.098  1.00 4.56
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ATOM 98 CG2 ILE 1 13 25.959 11.490 84.213 1.00 4.56
ATOM 99 CD1 ILE 1 13 28.035 9.910 83.035 1.00 4.56
ATOM 100 N GLU 1 14 24.471 8.384 80.928 1.00 2.30
ATOM 101 CA GLU 1 14 24.078 8.151 79.566 1.00 2.30
ATOM 102 C GLU 1 14 22.611 8.405 79.384 1.00 2.30
ATOM 103 O GLU 1 14 21.774 8.069 80.220 1.00 2.30
ATOM 104 CB GLU 1 14 24.485 6.783 78.994 1.00 2.30
ATOM 105 CG GLU 1 14 24.341 6.743 77.471 1.00 2.30
ATOM 106 CD GLU 1 14 25.404 5.808 76.924 1.00 2.30
ATOM 107 OE1 GLU 1 14 26.589 6.006 77.303 1.00 2.30
ATOM 108 OE2 GLU 1 14 25.060 4.899 76.122 1.00 2.30
ATOM 109 N PRO 1 15 22.304 9.030 78.278 1.00 6.71
ATOM 110 CA PRO 1 15 20.949 9.443 78.025 1.00 6.71
ATOM 111 C PRO 1 15 20.014 8.313 77.771 1.00 6.71
ATOM 112 O PRO 1 15 20.454 7.242 77.356 1.00 6.71
ATOM 113 CB PRO 1 15 21.022 10.438 76.870 1.00 6.71
ATOM 114 CG PRO 1 15 22.432 11.038 76.998 1.00 6.71
ATOM 115 CD PRO 1 15 23.264 9.918 77.643 1.00 6.71
ATOM 116 N GLU 1 16 18.712 8.539 78.032 1.00 3.50
ATOM 117 CA GLU 1 16 17.726 7.533 77.798 1.00 3.50
ATOM 118 C GLU 1 16 17.577 7.447 76.316 1.00 3.50
ATOM 119 O GLU 1 16 18.023 8.329 75.584 1.00 3.50
ATOM 120 CB GLU 1 16 16.348 7.856 78.404 1.00 3.50
ATOM 121 CG GLU 1 16 15.723 9.143 77.862 1.00 3.50
ATOM 122 CD GLU 1 16 14.375 9.333 78.542 1.00 3.50
ATOM 123 OE1 GLU 1 16 14.007 8.465 79.378 1.00 3.50
ATOM 124 OE2 GLU 1 16 13.695 10.348 78.235 1.00 3.50
ATOM 125 N VAL 1 17 16.953 6.359 75.831 1.00 1.33
ATOM 126 CA VAL 1 17 16.815 6.185 74.417 1.00 1.33
ATOM 127 C VAL 1 17 16.046 7.322 73.826 1.00 1.33
ATOM 128 O VAL 1 17 15.108 7.846 74.423 1.00 1.33
ATOM 129 CB VAL 1 17 16.115 4.914 74.029 1.00 1.33
ATOM 130 CG1 VAL 1 17 15.809 4.956 72.526 1.00 1.33
ATOM 131 CG2 VAL 1 17 17.015 3.732 74.408 1.00 1.33
ATOM 132 N LEU 1 18 16.453 7.724 72.607 1.00 6.49
ATOM 133 CA LEU 1 18 15.863 8.817 71.889 1.00 6.49
ATOM 134 C LEU 1 18 15.010 8.266 70.788 1.00 6.49
ATOM 135 O LEU 1 18 15.418 7.345 70.083 1.00 6.49
ATOM 136 CB LEU 1 18 16.940 9.683 71.217 1.00 6.49
ATOM 137 CG LEU 1 18 16.413 10.883 70.418 1.00 6.49
ATOM 138 CD1 LEU 1 18 15.769 11.940 71.329 1.00 6.49
ATOM 139 CD2 LEU 1 18 17.523 11.442 69.514 1.00 6.49
ATOM 140 N TYR 1 19 13.795 8.830 70.609 1.00 0.75
ATOM 141 CA TYR 1 19 12.907 8.372 69.575 1.00 0.75
ATOM 142 C TYR 1 19 12.967 9.322 68.419 1.00 0.75
ATOM 143 O TYR 1 19 13.101 10.533 68.592 1.00 0.75
ATOM 144 CB TYR 1 19 11.432 8.284 70.007 1.00 0.75
ATOM 145 CG TYR 1 19 11.317 7.194 71.016 1.00 0.75
ATOM 146 CD1 TYR 1 19 11.565 7.440 72.347 1.00 0.75

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ATOM  147 CD2 TYR 1 19    10.970  5.920 70.627 1.00 0.75
ATOM  148 CE1 TYR 1 19    11.468  6.431 73.276 1.00 0.75
ATOM  149 CE2 TYR 1 19    10.874  4.907 71.552 1.00 0.75
ATOM  150 CZ  TYR 1 19    11.125  5.162 72.878 1.00 0.75
ATOM  151 OH  TYR 1 19    11.032  4.124 73.830 1.00 0.75
ATOM  152 N   ALA 1 20    12.923  8.766 67.192 1.00 1.03
ATOM  153 CA  ALA 1 20    12.957  9.542 65.982 1.00 1.03
ATOM  154 C   ALA 1 20    11.661 10.258 65.768 1.00 1.03
ATOM  155 O   ALA 1 20    11.626 11.345 65.191 1.00 1.03
ATOM  156 CB  ALA 1 20    13.237  8.691 64.730 1.00 1.03
ATOM  157 N   GLY 1 21    10.549  9.642 66.210 1.00 0.75
ATOM  158 CA  GLY 1 21     9.268 10.244 66.005 1.00 0.75
ATOM  159 C   GLY 1 21     8.897 10.016 64.574 1.00 0.75
ATOM  160 O   GLY 1 21     8.194 10.836 63.983 1.00 0.75
ATOM  161 N   TYR 1 22     9.368  8.905 63.959 1.00 4.21
ATOM  162 CA  TYR 1 22     9.008  8.766 62.577 1.00 4.21
ATOM  163 C   TYR 1 22     7.659  8.129 62.432 1.00 4.21
ATOM  164 O   TYR 1 22     7.187  7.412 63.313 1.00 4.21
ATOM  165 CB  TYR 1 22    10.036  8.080 61.636 1.00 4.21
ATOM  166 CG  TYR 1 22     9.989  6.587 61.596 1.00 4.21
ATOM  167 CD1 TYR 1 22     8.946  5.944 60.960 1.00 4.21
ATOM  168 CD2 TYR 1 22    11.165  5.887 61.738 1.00 4.21
ATOM  169 CE1 TYR 1 22     9.008  4.616 60.613 1.00 4.21
ATOM  170 CE2 TYR 1 22    11.255  4.573 61.345 1.00 4.21
ATOM  171 CZ  TYR 1 22    10.174  3.924 60.806 1.00 4.21
ATOM  172 OH  TYR 1 22    10.274  2.570 60.421 1.00 4.21
ATOM  173 N   ASP 1 23     6.996  8.403 61.290 1.00 3.58
ATOM  174 CA  ASP 1 23     5.649  7.950 61.068 1.00 3.58
ATOM  175 C   ASP 1 23     5.491  6.457 61.014 1.00 3.58
ATOM  176 O   ASP 1 23     4.768  5.874 61.823 1.00 3.58
ATOM  177 CB  ASP 1 23     5.060  8.515 59.762 1.00 3.58
ATOM  178 CG  ASP 1 23     3.559  8.254 59.744 1.00 3.58
ATOM  179 OD1 ASP 1 23     3.041  7.660 60.727 1.00 3.58
ATOM  180 OD2 ASP 1 23     2.909  8.650 58.740 1.00 3.58
ATOM  181 N   SER 1 24     6.185  5.797 60.069 1.00 3.81
ATOM  182 CA  SER 1 24     6.117  4.371 59.899 1.00 3.81
ATOM  183 C   SER 1 24     4.843  3.956 59.222 1.00 3.81
ATOM  184 O   SER 1 24     4.821  2.977 58.478 1.00 3.81
ATOM  185 CB  SER 1 24     6.208  3.608 61.231 1.00 3.81
ATOM  186 OG  SER 1 24     6.138  2.209 60.997 1.00 3.81
ATOM  187 N   SER 1 25     3.760  4.735 59.402 1.00 3.40
ATOM  188 CA  SER 1 25     2.488  4.381 58.834 1.00 3.40
ATOM  189 C   SER 1 25     2.578  4.438 57.345 1.00 3.40
ATOM  190 O   SER 1 25     1.996  3.609 56.647 1.00 3.40
ATOM  191 CB  SER 1 25     1.358  5.334 59.260 1.00 3.40
ATOM  192 OG  SER 1 25     0.131  4.932 58.670 1.00 3.40
ATOM  193 N   VAL 1 26     3.332  5.425 56.826 1.00 1.09
ATOM  194 CA  VAL 1 26     3.411  5.643 55.409 1.00 1.09
ATOM  195 C   VAL 1 26     4.639  4.982 54.864 1.00 1.09
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ATOM  196 O  VAL 1 26    5.579  4.677 55.597 1.00 1.09
ATOM  197 CB VAL 1 26    3.478  7.107 55.066 1.00 1.09
ATOM  198 CG1 VAL 1 26   3.569  7.286 53.541 1.00 1.09
ATOM  199 CG2 VAL 1 26   2.258  7.800 55.694 1.00 1.09
ATOM  200 N  PRO 1 27    4.631  4.714 53.582 1.00 1.62
ATOM  201 CA PRO 1 27    5.779  4.108 52.974 1.00 1.62
ATOM  202 C  PRO 1 27    6.940  5.046 53.001 1.00 1.62
ATOM  203 O  PRO 1 27    6.802  6.193 52.577 1.00 1.62
ATOM  204 CB PRO 1 27    5.336  3.662 51.583 1.00 1.62
ATOM  205 CG PRO 1 27    3.831  3.388 51.767 1.00 1.62
ATOM  206 CD PRO 1 27    3.401  4.330 52.906 1.00 1.62
ATOM  207 N  ASP 1 28    8.104  4.559 53.467 1.00 1.30
ATOM  208 CA ASP 1 28    9.254  5.398 53.617 1.00 1.30
ATOM  209 C  ASP 1 28    9.928  5.629 52.304 1.00 1.30
ATOM  210 O  ASP 1 28   10.293  4.688 51.600 1.00 1.30
ATOM  211 CB ASP 1 28   10.315  4.781 54.543 1.00 1.30
ATOM  212 CG ASP 1 28    9.737  4.660 55.947 1.00 1.30
ATOM  213 OD1 ASP 1 28   8.605  5.166 56.170 1.00 1.30
ATOM  214 OD2 ASP 1 28  10.423  4.057 56.815 1.00 1.30
ATOM  215 N  SER 1 29   10.124  6.911 51.948 1.00 3.54
ATOM  216 CA SER 1 29   10.824  7.216 50.739 1.00 3.54
ATOM  217 C  SER 1 29   12.225  7.538 51.142 1.00 3.54
ATOM  218 O  SER 1 29   12.521  7.686 52.327 1.00 3.54
ATOM  219 CB SER 1 29   10.246  8.412 49.973 1.00 3.54
ATOM  220 OG SER 1 29   11.001  8.632 48.793 1.00 3.54
ATOM  221 N  THR 1 30   13.138  7.644 50.160 1.00 4.86
ATOM  222 CA THR 1 30   14.509  7.906 50.481 1.00 4.86
ATOM  223 C  THR 1 30   14.641  9.237 51.156 1.00 4.86
ATOM  224 O  THR 1 30   15.323  9.357 52.173 1.00 4.86
ATOM  225 CB THR 1 30   15.399  7.895 49.269 1.00 4.86
ATOM  226 OG1 THR 1 30   16.754  8.080 49.653 1.00 4.86
ATOM  227 CG2 THR 1 30   14.956  9.001 48.295 1.00 4.86
ATOM  228 N  TRP 1 31   13.976 10.275 50.616 1.00 6.14
ATOM  229 CA TRP 1 31   14.080 11.589 51.186 1.00 6.14
ATOM  230 C  TRP 1 31   13.464 11.621 52.544 1.00 6.14
ATOM  231 O  TRP 1 31   14.005 12.236 53.461 1.00 6.14
ATOM  232 CB TRP 1 31   13.359 12.670 50.367 1.00 6.14
ATOM  233 CG TRP 1 31   11.901 12.359 50.163 1.00 6.14
ATOM  234 CD1 TRP 1 31   11.320 11.152 49.924 1.00 6.14
ATOM  235 CD2 TRP 1 31   10.830 13.306 50.286 1.00 6.14
ATOM  236 NE1 TRP 1 31    9.956 11.290 49.846 1.00 6.14
ATOM  237 CE2 TRP 1 31    9.639 12.612 50.074 1.00 6.14
ATOM  238 CE3 TRP 1 31   10.836 14.642 50.560 1.00 6.14
ATOM  239 CZ2 TRP 1 31    8.433 13.248 50.122 1.00 6.14
ATOM  240 CZ3 TRP 1 31    9.619 15.283 50.606 1.00 6.14
ATOM  241 CH2 TRP 1 31    8.440 14.600 50.387 1.00 6.14
ATOM  242 N  ARG 1 32   12.303 10.961 52.705 1.00 4.31
ATOM  243 CA ARG 1 32   11.616 10.989 53.964 1.00 4.31
ATOM  244 C  ARG 1 32   12.464 10.336 55.006 1.00 4.31
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ATOM  245  O   ARG 1  32     12.542  10.805  56.141  1.00  4.31
ATOM  246  CB  ARG 1  32     10.270  10.243  53.942  1.00  4.31
ATOM  247  CG  ARG 1  32      9.191  10.930  53.104  1.00  4.31
ATOM  248  CD  ARG 1  32      7.797  10.331  53.305  1.00  4.31
ATOM  249  NE  ARG 1  32      7.321  10.755  54.653  1.00  4.31
ATOM  250  CZ  ARG 1  32      6.177  10.226  55.177  1.00  4.31
ATOM  251  NH1 ARG 1  32      5.742  10.626  56.408  1.00  4.31
ATOM  252  NH2 ARG 1  32      5.469   9.295  54.473  1.00  4.31
ATOM  253  N   ILE 1  33     13.125   9.224  54.644  1.00  3.71
ATOM  254  CA  ILE 1  33     13.940   8.530  55.594  1.00  3.71
ATOM  255  C   ILE 1  33     15.061   9.402  56.059  1.00  3.71
ATOM  256  O   ILE 1  33     15.351   9.472  57.252  1.00  3.71
ATOM  257  CB  ILE 1  33     14.560   7.284  55.032  1.00  3.71
ATOM  258  CG1 ILE 1  33     13.474   6.250  54.703  1.00  3.71
ATOM  259  CG2 ILE 1  33     15.600   6.777  56.045  1.00  3.71
ATOM  260  CD1 ILE 1  33     12.707   5.788  55.940  1.00  3.71
ATOM  261  N   MET 1  34     15.725  10.105  55.129  1.00  6.71
ATOM  262  CA  MET 1  34     16.838  10.910  55.535  1.00  6.71
ATOM  263  C   MET 1  34     16.356  12.005  56.428  1.00  6.71
ATOM  264  O   MET 1  34     17.008  12.349  57.413  1.00  6.71
ATOM  265  CB  MET 1  34     17.596  11.530  54.353  1.00  6.71
ATOM  266  CG  MET 1  34     18.982  12.038  54.748  1.00  6.71
ATOM  267  SD  MET 1  34     20.190  10.734  55.128  1.00  6.71
ATOM  268  CE  MET 1  34     21.536  11.890  55.515  1.00  6.71
ATOM  269  N   THR 1  35     15.182  12.578  56.104  1.00  0.49
ATOM  270  CA  THR 1  35     14.647  13.643  56.897  1.00  0.49
ATOM  271  C   THR 1  35     14.395  13.141  58.285  1.00  0.49
ATOM  272  O   THR 1  35     14.699  13.826  59.260  1.00  0.49
ATOM  273  CB  THR 1  35     13.344  14.164  56.367  1.00  0.49
ATOM  274  OG1 THR 1  35     13.515  14.665  55.049  1.00  0.49
ATOM  275  CG2 THR 1  35     12.845  15.282  57.299  1.00  0.49
ATOM  276  N   THR 1  36     13.835  11.922  58.418  1.00  4.72
ATOM  277  CA  THR 1  36     13.543  11.426  59.732  1.00  4.72
ATOM  278  C   THR 1  36     14.811  11.197  60.490  1.00  4.72
ATOM  279  O   THR 1  36     14.868  11.419  61.698  1.00  4.72
ATOM  280  CB  THR 1  36     12.757  10.144  59.749  1.00  4.72
ATOM  281  OG1 THR 1  36     12.240   9.916  61.052  1.00  4.72
ATOM  282  CG2 THR 1  36     13.674   8.976  59.355  1.00  4.72
ATOM  283  N   LEU 1  37     15.865  10.722  59.805  1.00  6.67
ATOM  284  CA  LEU 1  37     17.095  10.476  60.496  1.00  6.67
ATOM  285  C   LEU 1  37     17.709  11.770  60.945  1.00  6.67
ATOM  286  O   LEU 1  37     18.377  11.827  61.976  1.00  6.67
ATOM  287  CB  LEU 1  37     18.104   9.650  59.689  1.00  6.67
ATOM  288  CG  LEU 1  37     19.264   9.170  60.574  1.00  6.67
ATOM  289  CD1 LEU 1  37     18.732   8.452  61.824  1.00  6.67
ATOM  290  CD2 LEU 1  37     20.215   8.261  59.788  1.00  6.67
ATOM  291  N   ASN 1  38     17.520  12.851  60.164  1.00  0.62
ATOM  292  CA  ASN 1  38     18.044  14.132  60.547  1.00  0.62
ATOM  293  C   ASN 1  38     17.355  14.597  61.793  1.00  0.62
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ATOM 294 O ASN 1 38 17.978 15.197 62.668 1.00 0.62
ATOM 295 CB ASN 1 38 17.840 15.217 59.474 1.00 0.62
ATOM 296 CG ASN 1 38 18.787 14.931 58.315 1.00 0.62
ATOM 297 OD1 ASN 1 38 19.823 14.291 58.486 1.00 0.62
ATOM 298 ND2 ASN 1 38 18.427 15.428 57.101 1.00 0.62
ATOM 299 N MET 1 39 16.036 14.337 61.896 1.00 3.81
ATOM 300 CA MET 1 39 15.265 14.746 63.037 1.00 3.81
ATOM 301 C MET 1 39 15.797 14.033 64.238 1.00 3.81
ATOM 302 O MET 1 39 15.937 14.618 65.312 1.00 3.81
ATOM 303 CB MET 1 39 13.779 14.373 62.907 1.00 3.81
ATOM 304 CG MET 1 39 13.070 15.075 61.746 1.00 3.81
ATOM 305 SD MET 1 39 11.311 14.649 61.572 1.00 3.81
ATOM 306 CE MET 1 39 11.071 15.588 60.036 1.00 3.81
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ATOM 308 CA LEU 1 40 16.635 11.963 65.166 1.00 0.61
ATOM 309 C LEU 1 40 17.956 12.559 65.555 1.00 0.61
ATOM 310 O LEU 1 40 18.264 12.708 66.737 1.00 0.61
ATOM 311 CB LEU 1 40 16.868 10.496 64.762 1.00 0.61
ATOM 312 CG LEU 1 40 17.439 9.607 65.880 1.00 0.61
ATOM 313 CD1 LEU 1 40 16.465 9.504 67.066 1.00 0.61
ATOM 314 CD2 LEU 1 40 17.853 8.232 65.332 1.00 0.61
ATOM 315 N GLY 1 41 18.762 12.947 64.550 1.00 0.41
ATOM 316 CA GLY 1 41 20.063 13.501 64.797 1.00 0.41
ATOM 317 C GLY 1 41 19.947 14.758 65.600 1.00 0.41
ATOM 318 O GLY 1 41 20.773 15.023 66.472 1.00 0.41
ATOM 319 N GLY 1 42 18.926 15.584 65.309 1.00 0.36
ATOM 320 CA GLY 1 42 18.765 16.812 66.031 1.00 0.36
ATOM 321 C GLY 1 42 18.514 16.504 67.473 1.00 0.36
ATOM 322 O GLY 1 42 19.052 17.165 68.359 1.00 0.36
ATOM 323 N ARG 1 43 17.667 15.491 67.742 1.00 3.86
ATOM 324 CA ARG 1 43 17.347 15.134 69.095 1.00 3.86
ATOM 325 C ARG 1 43 18.549 14.575 69.790 1.00 3.86
ATOM 326 O ARG 1 43 18.742 14.794 70.983 1.00 3.86
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ATOM 328 CG ARG 1 43 14.859 14.528 68.756 1.00 3.86
ATOM 329 CD ARG 1 43 13.772 13.521 69.131 1.00 3.86
ATOM 330 NE ARG 1 43 12.525 13.909 68.420 1.00 3.86
ATOM 331 CZ ARG 1 43 12.362 13.517 67.124 1.00 3.86
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ATOM 333 NH2 ARG 1 43 13.380 12.867 66.488 1.00 3.86
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ATOM 335 CA GLN 1 44 20.545 13.211 69.655 1.00 1.14
ATOM 336 C GLN 1 44 21.563 14.265 69.967 1.00 1.14
ATOM 337 O GLN 1 44 22.303 14.153 70.944 1.00 1.14
ATOM 338 CB GLN 1 44 21.202 12.148 68.759 1.00 1.14
ATOM 339 CG GLN 1 44 20.322 10.909 68.574 1.00 1.14
ATOM 340 CD GLN 1 44 21.060 9.924 67.679 1.00 1.14
ATOM 341 OE1 GLN 1 44 20.499 9.396 66.720 1.00 1.14
ATOM 342 NE2 GLN 1 44 22.351 9.655 68.008 1.00 1.14

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ATOM  344 CA VAL 1 45   22.607 16.356 69.340 1.00 0.68
ATOM  345 C  VAL 1 45   22.347 17.012 70.657 1.00 0.68
ATOM  346 O  VAL 1 45   23.276 17.273 71.419 1.00 0.68
ATOM  347 CB VAL 1 45   22.551 17.427 68.290 1.00 0.68
ATOM  348 CG1 VAL 1 45  23.548 18.534 68.669 1.00 0.68
ATOM  349 CG2 VAL 1 45  22.829 16.787 66.919 1.00 0.68
ATOM  350 N  ILE 1 46   21.066 17.292 70.968 1.00 3.68
ATOM  351 CA ILE 1 46   20.767 17.932 72.216 1.00 3.68
ATOM  352 C  ILE 1 46   21.144 16.999 73.323 1.00 3.68
ATOM  353 O  ILE 1 46   21.656 17.416 74.360 1.00 3.68
ATOM  354 CB ILE 1 46   19.320 18.308 72.383 1.00 3.68
ATOM  355 CG1 ILE 1 46  19.163 19.287 73.559 1.00 3.68
ATOM  356 CG2 ILE 1 46  18.487 17.028 72.547 1.00 3.68
ATOM  357 CD1 ILE 1 46  17.789 19.952 73.617 1.00 3.68
ATOM  358 N  ALA 1 47   20.910 15.691 73.123 1.00 0.54
ATOM  359 CA ALA 1 47   21.221 14.727 74.136 1.00 0.54
ATOM  360 C  ALA 1 47   22.695 14.748 74.397 1.00 0.54
ATOM  361 O  ALA 1 47   23.130 14.677 75.546 1.00 0.54
ATOM  362 CB ALA 1 47   20.845 13.293 73.726 1.00 0.54
ATOM  363 N  ALA 1 48   23.505 14.854 73.327 1.00 0.69
ATOM  364 CA ALA 1 48   24.934 14.846 73.450 1.00 0.69
ATOM  365 C  ALA 1 48   25.414 16.025 74.239 1.00 0.69
ATOM  366 O  ALA 1 48   26.303 15.890 75.078 1.00 0.69
ATOM  367 CB ALA 1 48   25.648 14.887 72.089 1.00 0.69
ATOM  368 N  VAL 1 49   24.846 17.222 73.992 1.00 4.14
ATOM  369 CA VAL 1 49   25.308 18.380 74.705 1.00 4.14
ATOM  370 C  VAL 1 49   24.997 18.224 76.160 1.00 4.14
ATOM  371 O  VAL 1 49   25.816 18.556 77.015 1.00 4.14
ATOM  372 CB VAL 1 49   24.685 19.680 74.258 1.00 4.14
ATOM  373 CG1 VAL 1 49  25.020 19.902 72.779 1.00 4.14
ATOM  374 CG2 VAL 1 49  23.180 19.682 74.561 1.00 4.14
ATOM  375 N  LYS 1 50   23.797 17.703 76.478 1.00 4.12
ATOM  376 CA LYS 1 50   23.385 17.556 77.843 1.00 4.12
ATOM  377 C  LYS 1 50   24.303 16.597 78.529 1.00 4.12
ATOM  378 O  LYS 1 50   24.723 16.823 79.663 1.00 4.12
ATOM  379 CB LYS 1 50   21.956 17.000 77.969 1.00 4.12
ATOM  380 CG LYS 1 50   20.885 17.949 77.427 1.00 4.12
ATOM  381 CD LYS 1 50   19.523 17.283 77.219 1.00 4.12
ATOM  382 CE LYS 1 50   18.819 16.903 78.523 1.00 4.12
ATOM  383 NZ LYS 1 50   18.315 18.118 79.200 1.00 4.12
ATOM  384 N  TRP 1 51   24.653 15.500 77.835 1.00 1.08
ATOM  385 CA TRP 1 51   25.499 14.479 78.378 1.00 1.08
ATOM  386 C  TRP 1 51   26.840 15.056 78.713 1.00 1.08
ATOM  387 O  TRP 1 51   27.404 14.777 79.769 1.00 1.08
ATOM  388 CB TRP 1 51   25.696 13.328 77.372 1.00 1.08
ATOM  389 CG TRP 1 51   26.619 12.207 77.794 1.00 1.08
ATOM  390 CD1 TRP 1 51  26.426 11.208 78.703 1.00 1.08
ATOM  391 CD2 TRP 1 51  27.845 11.903 77.112 1.00 1.08
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ATOM 394 CE3 TRP 1 51 28.486 12.539 76.089 1.00 1.08
ATOM 395 CZ2 TRP 1 51 29.515 10.176 77.220 1.00 1.08
ATOM 396 CZ3 TRP 1 51 29.659 11.977 75.634 1.00 1.08
ATOM 397 CH2 TRP 1 51 30.163 10.818 76.187 1.00 1.08
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ATOM 399 CA ALA 1 52 28.672 16.497 78.001 1.00 0.96
ATOM 400 C ALA 1 52 28.739 17.346 79.234 1.00 0.96
ATOM 401 O ALA 1 52 29.788 17.447 79.869 1.00 0.96
ATOM 402 CB ALA 1 52 29.092 17.377 76.811 1.00 0.96
ATOM 403 N LYS 1 53 27.624 18.005 79.593 1.00 1.49
ATOM 404 CA LYS 1 53 27.607 18.862 80.744 1.00 1.49
ATOM 405 C LYS 1 53 27.885 18.038 81.967 1.00 1.49
ATOM 406 O LYS 1 53 28.537 18.496 82.902 1.00 1.49
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ATOM 408 CG LYS 1 53 25.853 20.448 79.763 1.00 1.49
ATOM 409 CD LYS 1 53 24.376 20.846 79.760 1.00 1.49
ATOM 410 CE LYS 1 53 23.985 21.753 78.592 1.00 1.49
ATOM 411 NZ LYS 1 53 22.544 22.086 78.671 1.00 1.49
ATOM 412 N ALA 1 54 27.331 16.813 82.003 1.00 1.47
ATOM 413 CA ALA 1 54 27.477 15.863 83.072 1.00 1.47
ATOM 414 C ALA 1 54 28.807 15.162 83.114 1.00 1.47
ATOM 415 O ALA 1 54 29.223 14.688 84.171 1.00 1.47
ATOM 416 CB ALA 1 54 26.400 14.766 83.028 1.00 1.47
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ATOM 418 CA ILE 1 55 30.697 14.250 81.896 1.00 4.27
ATOM 419 C ILE 1 55 31.835 14.871 82.643 1.00 4.27
ATOM 420 O ILE 1 55 32.224 16.013 82.407 1.00 4.27
ATOM 421 CB ILE 1 55 31.139 13.951 80.492 1.00 4.27
ATOM 422 CG1 ILE 1 55 32.287 12.928 80.492 1.00 4.27
ATOM 423 CG2 ILE 1 55 31.470 15.278 79.796 1.00 4.27
ATOM 424 CD1 ILE 1 55 32.586 12.351 79.109 1.00 4.27
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ATOM 426 CA PRO 1 56 33.455 14.586 84.395 1.00 6.47
ATOM 427 C PRO 1 56 34.624 15.142 83.639 1.00 6.47
ATOM 428 O PRO 1 56 35.175 14.461 82.775 1.00 6.47
ATOM 429 CB PRO 1 56 33.793 13.420 85.332 1.00 6.47
ATOM 430 CG PRO 1 56 33.206 12.179 84.629 1.00 6.47
ATOM 431 CD PRO 1 56 32.028 12.733 83.810 1.00 6.47
ATOM 432 N GLY 1 57 35.005 16.395 83.964 1.00 0.90
ATOM 433 CA GLY 1 57 36.155 17.046 83.406 1.00 0.90
ATOM 434 C GLY 1 57 35.842 17.885 82.201 1.00 0.90
ATOM 435 O GLY 1 57 36.558 18.839 81.906 1.00 0.90
ATOM 436 N PHE 1 58 34.753 17.572 81.480 1.00 1.63
ATOM 437 CA PHE 1 58 34.449 18.259 80.254 1.00 1.63
ATOM 438 C PHE 1 58 34.130 19.708 80.487 1.00 1.63
ATOM 439 O PHE 1 58 34.602 20.583 79.763 1.00 1.63
ATOM 440 CB PHE 1 58 33.255 17.606 79.532 1.00 1.63

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ATOM  441 CG  PHE 1  58    33.258 17.977 78.087 1.00 1.63
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ATOM  443 CD2 PHE 1  58    32.309 18.831 77.576 1.00 1.63
ATOM  444 CE1 PHE 1  58    34.027 17.553 75.860 1.00 1.63
ATOM  445 CE2 PHE 1  58    32.233 19.067 76.223 1.00 1.63
ATOM  446 CZ  PHE 1  58    33.094 18.430 75.363 1.00 1.63
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ATOM  448 CA  ARG 1  59    32.897 21.339 81.821 1.00 3.96
ATOM  449 C   ARG 1  59    34.060 22.230 82.134 1.00 3.96
ATOM  450 O   ARG 1  59    33.975 23.446 81.976 1.00 3.96
ATOM  451 CB  ARG 1  59    31.901 21.413 82.993 1.00 3.96
ATOM  452 CG  ARG 1  59    32.454 20.929 84.335 1.00 3.96
ATOM  453 CD  ARG 1  59    31.399 20.919 85.444 1.00 3.96
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ATOM  462 CB  ASN 1  60    37.373 21.425 83.699 1.00 1.96
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ATOM  465 ND2 ASN 1  60    35.687 21.700 85.455 1.00 1.96
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ATOM  469 O   LEU 1  61    35.922 24.604 79.629 1.00 3.77
ATOM  470 CB  LEU 1  61    36.933 22.006 78.192 1.00 3.77
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ATOM  473 CD2 LEU 1  61    37.318 19.825 79.450 1.00 3.77
ATOM  474 N   HIS 1  62    37.728 24.956 78.323 1.00 0.83
ATOM  475 CA  HIS 1  62    37.312 26.273 77.944 1.00 0.83
ATOM  476 C   HIS 1  62    36.042 26.055 77.181 1.00 0.83
ATOM  477 O   HIS 1  62    35.859 25.014 76.553 1.00 0.83
ATOM  478 CB  HIS 1  62    38.329 26.959 77.014 1.00 0.83
ATOM  479 CG  HIS 1  62    38.028 28.396 76.709 1.00 0.83
ATOM  480 ND1 HIS 1  62    37.075 28.811 75.807 1.00 0.83
ATOM  481 CD2 HIS 1  62    38.621 29.530 77.172 1.00 0.83
ATOM  482 CE1 HIS 1  62    37.135 30.166 75.770 1.00 0.83
ATOM  483 NE2 HIS 1  62    38.059 30.648 76.582 1.00 0.83
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ATOM  485 CA  LEU 1  63    33.841 26.895 76.589 1.00 6.44
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ATOM  487 O   LEU 1  63    33.338 25.838 74.524 1.00 6.44
ATOM  488 CB  LEU 1  63    32.960 28.144 76.769 1.00 6.44
ATOM  489 CG  LEU 1  63    31.576 28.033 76.105 1.00 6.44
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ATOM 490 CD1 LEU 1 63 30.730 26.927 76.756 1.00 6.44
ATOM 491 CD2 LEU 1 63 30.858 29.392 76.080 1.00 6.44
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ATOM 493 CA ASP 1 64 35.142 27.315 73.083 1.00 0.59
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ATOM 539 CD2 LEU 1 69 34.402 16.660 72.377 1.00 4.63
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ATOM 559 C TYR 1 72 33.570 16.343 65.724 1.00 4.09
ATOM 560 O TYR 1 72 33.602 15.594 64.749 1.00 4.09
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ATOM 564 CD2 TYR 1 72 36.860 19.556 67.257 1.00 4.09
ATOM 565 CE1 TYR 1 72 36.796 21.046 64.957 1.00 4.09
ATOM 566 CE2 TYR 1 72 37.529 20.759 67.192 1.00 4.09
ATOM 567 CZ TYR 1 72 37.486 21.514 66.044 1.00 4.09
ATOM 568 OH TYR 1 72 38.169 22.746 65.962 1.00 4.09
ATOM 569 N SER 1 73 33.144 15.947 66.930 1.00 1.90
ATOM 570 CA SER 1 73 32.739 14.620 67.315 1.00 1.90
ATOM 571 C SER 1 73 31.344 14.111 67.096 1.00 1.90
ATOM 572 O SER 1 73 31.133 12.901 67.159 1.00 1.90
ATOM 573 CB SER 1 73 33.055 14.338 68.794 1.00 1.90
ATOM 574 OG SER 1 73 32.243 15.147 69.631 1.00 1.90
ATOM 575 N TRP 1 74 30.348 14.988 66.875 1.00 1.47
ATOM 576 CA TRP 1 74 28.973 14.557 66.922 1.00 1.47
ATOM 577 C TRP 1 74 28.678 13.369 66.047 1.00 1.47
ATOM 578 O TRP 1 74 28.008 12.436 66.488 1.00 1.47
ATOM 579 CB TRP 1 74 27.998 15.678 66.520 1.00 1.47
ATOM 580 CG TRP 1 74 28.085 16.095 65.072 1.00 1.47
ATOM 581 CD1 TRP 1 74 28.924 16.982 64.464 1.00 1.47
ATOM 582 CD2 TRP 1 74 27.155 15.661 64.068 1.00 1.47
ATOM 583 NE1 TRP 1 74 28.588 17.113 63.137 1.00 1.47
ATOM 584 CE2 TRP 1 74 27.496 16.310 62.882 1.00 1.47
ATOM 585 CE3 TRP 1 74 26.098 14.800 64.134 1.00 1.47
ATOM 586 CZ2 TRP 1 74 26.783 16.102 61.737 1.00 1.47
ATOM 587 CZ3 TRP 1 74 25.382 14.591 62.977 1.00 1.47

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ATOM  588 CH2 TRP 1  74    25.719 15.230 61.801 1.00 1.47
ATOM  589 N   MET 1  75    29.179 13.348 64.799 1.00 8.65
ATOM  590 CA  MET 1  75    28.914 12.245 63.909 1.00 8.65
ATOM  591 C   MET 1  75    29.449 10.969 64.476 1.00 8.65
ATOM  592 O   MET 1  75    28.795  9.928 64.442 1.00 8.65
ATOM  593 CB  MET 1  75    29.654 12.355 62.562 1.00 8.65
ATOM  594 CG  MET 1  75    29.113 13.388 61.582 1.00 8.65
ATOM  595 SD  MET 1  75    27.569 12.911 60.754 1.00 8.65
ATOM  596 CE  MET 1  75    27.660 14.291 59.579 1.00 8.65
ATOM  597 N   PHE 1  76    30.680 11.037 65.002 1.00 6.18
ATOM  598 CA  PHE 1  76    31.420  9.914 65.494 1.00 6.18
ATOM  599 C   PHE 1  76    30.657  9.318 66.645 1.00 6.18
ATOM  600 O   PHE 1  76    30.457  8.106 66.712 1.00 6.18
ATOM  601 CB  PHE 1  76    32.777 10.430 66.015 1.00 6.18
ATOM  602 CG  PHE 1  76    33.873  9.429 65.892 1.00 6.18
ATOM  603 CD1 PHE 1  76    34.022  8.395 66.780 1.00 6.18
ATOM  604 CD2 PHE 1  76    34.898  9.693 65.013 1.00 6.18
ATOM  605 CE1 PHE 1  76    35.157  7.616 66.761 1.00 6.18
ATOM  606 CE2 PHE 1  76    36.038  8.926 64.993 1.00 6.18
ATOM  607 CZ  PHE 1  76    36.175  7.890 65.882 1.00 6.18
ATOM  608 N   LEU 1  77    30.188 10.172 67.576 1.00 0.90
ATOM  609 CA  LEU 1  77    29.472  9.716 68.736 1.00 0.90
ATOM  610 C   LEU 1  77    28.177  9.076 68.347 1.00 0.90
ATOM  611 O   LEU 1  77    27.792  8.046 68.902 1.00 0.90
ATOM  612 CB  LEU 1  77    29.124 10.853 69.712 1.00 0.90
ATOM  613 CG  LEU 1  77    30.343 11.484 70.408 1.00 0.90
ATOM  614 CD1 LEU 1  77    29.906 12.608 71.360 1.00 0.90
ATOM  615 CD2 LEU 1  77    31.201 10.420 71.112 1.00 0.90
ATOM  616 N   MET 1  78    27.461  9.682 67.385 1.00 3.39
ATOM  617 CA  MET 1  78    26.169  9.206 66.980 1.00 3.39
ATOM  618 C   MET 1  78    26.256  7.850 66.344 1.00 3.39
ATOM  619 O   MET 1  78    25.462  6.962 66.650 1.00 3.39
ATOM  620 CB  MET 1  78    25.521 10.127 65.931 1.00 3.39
ATOM  621 CG  MET 1  78    25.394 11.589 66.368 1.00 3.39
ATOM  622 SD  MET 1  78    24.325 11.892 67.804 1.00 3.39
ATOM  623 CE  MET 1  78    24.452 13.702 67.722 1.00 3.39
ATOM  624 N   ALA 1  79    27.226  7.663 65.428 1.00 1.42
ATOM  625 CA  ALA 1  79    27.373  6.418 64.725 1.00 1.42
ATOM  626 C   ALA 1  79    27.784  5.339 65.684 1.00 1.42
ATOM  627 O   ALA 1  79    27.378  4.183 65.554 1.00 1.42
ATOM  628 CB  ALA 1  79    28.436  6.484 63.613 1.00 1.42
ATOM  629 N   PHE 1  80    28.630  5.701 66.665 1.00 4.87
ATOM  630 CA  PHE 1  80    29.131  4.776 67.643 1.00 4.87
ATOM  631 C   PHE 1  80    27.961  4.289 68.446 1.00 4.87
ATOM  632 O   PHE 1  80    27.832  3.097 68.731 1.00 4.87
ATOM  633 CB  PHE 1  80    30.128  5.481 68.591 1.00 4.87
ATOM  634 CG  PHE 1  80    31.005  4.494 69.285 1.00 4.87
ATOM  635 CD1 PHE 1  80    30.669  3.929 70.489 1.00 4.87
ATOM  636 CD2 PHE 1  80    32.240  4.204 68.766 1.00 4.87
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ATOM 637 CE1 PHE 1 80 31.541 3.085 71.140 1.00 4.87
ATOM 638 CE2 PHE 1 80 33.110 3.357 69.408 1.00 4.87
ATOM 639 CZ PHE 1 80 32.767 2.789 70.604 1.00 4.87
ATOM 640 N ALA 1 81 27.061 5.221 68.816 1.00 0.63
ATOM 641 CA ALA 1 81 25.899 4.891 69.593 1.00 0.63
ATOM 642 C ALA 1 81 25.013 3.977 68.800 1.00 0.63
ATOM 643 O ALA 1 81 24.439 3.030 69.337 1.00 0.63
ATOM 644 CB ALA 1 81 25.065 6.128 69.966 1.00 0.63
ATOM 645 N LEU 1 82 24.889 4.247 67.486 1.00 4.41
ATOM 646 CA LEU 1 82 24.068 3.458 66.610 1.00 4.41
ATOM 647 C LEU 1 82 24.616 2.070 66.661 1.00 4.41
ATOM 648 O LEU 1 82 23.873 1.092 66.763 1.00 4.41
ATOM 649 CB LEU 1 82 24.174 3.949 65.147 1.00 4.41
ATOM 650 CG LEU 1 82 23.343 3.203 64.072 1.00 4.41
ATOM 651 CD1 LEU 1 82 23.781 1.752 63.854 1.00 4.41
ATOM 652 CD2 LEU 1 82 21.840 3.322 64.339 1.00 4.41
ATOM 653 N GLY 1 83 25.956 1.959 66.610 1.00 0.71
ATOM 654 CA GLY 1 83 26.551 0.656 66.624 1.00 0.71
ATOM 655 C GLY 1 83 26.209 -0.053 67.891 1.00 0.71
ATOM 656 O GLY 1 83 25.846 -1.230 67.875 1.00 0.71
ATOM 657 N TRP 1 84 26.312 0.647 69.036 1.00 5.43
ATOM 658 CA TRP 1 84 26.070 -0.084 70.238 1.00 5.43
ATOM 659 C TRP 1 84 24.644 -0.492 70.371 1.00 5.43
ATOM 660 O TRP 1 84 24.377 -1.570 70.885 1.00 5.43
ATOM 661 CB TRP 1 84 26.530 0.587 71.534 1.00 5.43
ATOM 662 CG TRP 1 84 26.714 -0.487 72.576 1.00 5.43
ATOM 663 CD1 TRP 1 84 27.620 -1.503 72.549 1.00 5.43
ATOM 664 CD2 TRP 1 84 25.993 -0.628 73.804 1.00 5.43
ATOM 665 NE1 TRP 1 84 27.490 -2.282 73.667 1.00 5.43
ATOM 666 CE2 TRP 1 84 26.489 -1.762 74.449 1.00 5.43
ATOM 667 CE3 TRP 1 84 25.004 0.121 74.350 1.00 5.43
ATOM 668 CZ2 TRP 1 84 25.993 -2.175 75.648 1.00 5.43
ATOM 669 CZ3 TRP 1 84 24.521 -0.293 75.566 1.00 5.43
ATOM 670 CH2 TRP 1 84 24.986 -1.424 76.197 1.00 5.43
ATOM 671 N ARG 1 85 23.680 0.347 69.945 1.00 7.10
ATOM 672 CA ARG 1 85 22.302 -0.062 70.044 1.00 7.10
ATOM 673 C ARG 1 85 21.943 -1.219 69.137 1.00 7.10
ATOM 674 O ARG 1 85 21.117 -2.053 69.506 1.00 7.10
ATOM 675 CB ARG 1 85 21.334 1.119 69.846 1.00 7.10
ATOM 676 CG ARG 1 85 21.549 1.909 68.557 1.00 7.10
ATOM 677 CD ARG 1 85 20.961 3.320 68.634 1.00 7.10
ATOM 678 NE ARG 1 85 21.336 4.032 67.380 1.00 7.10
ATOM 679 CZ ARG 1 85 21.148 5.380 67.289 1.00 7.10
ATOM 680 NH1 ARG 1 85 20.612 6.062 68.343 1.00 7.10
ATOM 681 NH2 ARG 1 85 21.491 6.044 66.147 1.00 7.10
ATOM 682 N SER 1 86 22.527 -1.297 67.919 1.00 4.93
ATOM 683 CA SER 1 86 22.239 -2.347 66.954 1.00 4.93
ATOM 684 C SER 1 86 22.731 -3.699 67.418 1.00 4.93
ATOM 685 O SER 1 86 22.118 -4:736 67.201 1.00 4.93

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ATOM  686 CB  SER 1  86    22.780 -2.038 65.543 1.00 4.93
ATOM  687 OG  SER 1  86    24.177 -1.799 65.572 1.00 4.93
ATOM  688 N   TYR 1  87    23.740 -3.599 68.271 1.00 5.71
ATOM  689 CA  TYR 1  87    24.722 -4.268 69.053 1.00 5.71
ATOM  690 C   TYR 1  87    23.797 -4.370 70.201 1.00 5.71
ATOM  691 O   TYR 1  87    22.949 -3.542 70.391 1.00 5.71
ATOM  692 CB  TYR 1  87    25.916 -3.424 69.523 1.00 5.71
ATOM  693 CG  TYR 1  87    26.607 -4.240 70.565 1.00 5.71
ATOM  694 CD1 TYR 1  87    27.507 -5.222 70.215 1.00 5.71
ATOM  695 CD2 TYR 1  87    26.295 -4.074 71.895 1.00 5.71
ATOM  696 CE1 TYR 1  87    28.105 -6.003 71.177 1.00 5.71
ATOM  697 CE2 TYR 1  87    26.876 -4.864 72.860 1.00 5.71
ATOM  698 CZ  TYR 1  87    27.793 -5.821 72.503 1.00 5.71
ATOM  699 OH  TYR 1  87    28.403 -6.622 73.491 1.00 5.71
ATOM  700 N   ARG 1  88    23.651 -5.475 70.882 1.00 11.72
ATOM  701 CA  ARG 1  88    22.545 -6.028 71.589 1.00 11.72
ATOM  702 C   ARG 1  88    21.089 -5.674 71.453 1.00 11.72
ATOM  703 O   ARG 1  88    20.291 -6.542 71.804 1.00 11.72
ATOM  704 CB  ARG 1  88    22.920 -5.950 73.084 1.00 11.72
ATOM  705 CG  ARG 1  88    21.818 -5.469 74.021 1.00 11.72
ATOM  706 CD  ARG 1  88    22.173 -5.588 75.505 1.00 11.72
ATOM  707 NE  ARG 1  88    23.480 -4.919 75.748 1.00 11.72
ATOM  708 CZ  ARG 1  88    24.070 -5.048 76.973 1.00 11.72
ATOM  709 NH1 ARG 1  88    23.453 -5.777 77.949 1.00 11.72
ATOM  710 NH2 ARG 1  88    25.274 -4.457 77.226 1.00 11.72
ATOM  711 N   GLN 1  89    20.621 -4.489 71.058 1.00 4.60
ATOM  712 CA  GLN 1  89    19.203 -4.505 70.793 1.00 4.60
ATOM  713 C   GLN 1  89    18.855 -5.524 69.711 1.00 4.60
ATOM  714 O   GLN 1  89    17.867 -6.245 69.854 1.00 4.60
ATOM  715 CB  GLN 1  89    18.679 -3.141 70.312 1.00 4.60
ATOM  716 CG  GLN 1  89    18.840 -2.013 71.336 1.00 4.60
ATOM  717 CD  GLN 1  89    17.787 -2.169 72.427 1.00 4.60
ATOM  718 OE1 GLN 1  89    17.342 -1.180 73.008 1.00 4.60
ATOM  719 NE2 GLN 1  89    17.378 -3.431 72.722 1.00 4.60
ATOM  720 N   SER 1  90    19.645 -5.639 68.610 1.00 2.81
ATOM  721 CA  SER 1  90    19.280 -6.556 67.551 1.00 2.81
ATOM  722 C   SER 1  90    20.424 -7.420 67.087 1.00 2.81
ATOM  723 O   SER 1  90    20.424 -7.886 65.947 1.00 2.81
ATOM  724 CB  SER 1  90    18.752 -5.830 66.302 1.00 2.81
ATOM  725 OG  SER 1  90    19.785 -5.049 65.718 1.00 2.81
ATOM  726 N   SER 1  91    21.429 -7.669 67.951 1.00 3.74
ATOM  727 CA  SER 1  91    22.507 -8.560 67.595 1.00 3.74
ATOM  728 C   SER 1  91    23.278 -8.110 66.390 1.00 3.74
ATOM  729 O   SER 1  91    23.876 -8.922 65.683 1.00 3.74
ATOM  730 CB  SER 1  91    22.028 -9.999 67.336 1.00 3.74
ATOM  731 OG  SER 1  91    21.476 -10.550 68.522 1.00 3.74
ATOM  732 N   ALA 1  92    23.308 -6.789 66.147 1.00 1.75
ATOM  733 CA  ALA 1  92    24.041 -6.197 65.060 1.00 1.75
ATOM  734 C   ALA 1  92    23.484 -6.566 63.718 1.00 1.75
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ATOM   735 O   ALA 1  92    24.097 -6.277 62.691 1.00 1.75
ATOM   736 CB  ALA 1  92    25.531 -6.580 65.070 1.00 1.75
ATOM   737 N   ASN 1  93    22.299 -7.204 63.703 1.00 1.99
ATOM   738 CA  ASN 1  93    21.631 -7.643 62.505 1.00 1.99
ATOM   739 C   ASN 1  93    21.009 -6.533 61.709 1.00 1.99
ATOM   740 O   ASN 1  93    20.905 -6.627 60.485 1.00 1.99
ATOM   741 CB  ASN 1  93    20.515 -8.661 62.794 1.00 1.99
ATOM   742 CG  ASN 1  93    21.168 -9.945 63.287 1.00 1.99
ATOM   743 OD1 ASN 1  93    20.496 -10.843 63.792 1.00 1.99
ATOM   744 ND2 ASN 1  93    22.517 -10.033 63.144 1.00 1.99
ATOM   745 N   LEU 1  94    20.521 -5.479 62.390 1.00 0.96
ATOM   746 CA  LEU 1  94    19.880 -4.388 61.710 1.00 0.96
ATOM   747 C   LEU 1  94    20.429 -3.134 62.313 1.00 0.96
ATOM   748 O   LEU 1  94    21.133 -3.185 63.320 1.00 0.96
ATOM   749 CB  LEU 1  94    18.355 -4.359 61.899 1.00 0.96
ATOM   750 CG  LEU 1  94    17.639 -5.581 61.295 1.00 0.96
ATOM   751 CD1 LEU 1  94    16.120 -5.501 61.511 1.00 0.96
ATOM   752 CD2 LEU 1  94    18.023 -5.780 59.820 1.00 0.96
ATOM   753 N   LEU 1  95    20.147 -1.967 61.693 1.00 3.62
ATOM   754 CA  LEU 1  95    20.646 -0.735 62.243 1.00 3.62
ATOM   755 C   LEU 1  95    19.565 -0.166 63.102 1.00 3.62
ATOM   756 O   LEU 1  95    18.527  0.265 62.603 1.00 3.62
ATOM   757 CB  LEU 1  95    20.954  0.327 61.172 1.00 3.62
ATOM   758 CG  LEU 1  95    22.168  0.034 60.269 1.00 3.62
ATOM   759 CD1 LEU 1  95    23.490  0.393 60.953 1.00 3.62
ATOM   760 CD2 LEU 1  95    22.162 -1.420 59.788 1.00 3.62
ATOM   761 N   CYS 1  96    19.764 -0.139 64.433 1.00 4.51
ATOM   762 CA  CYS 1  96    18.683  0.408 65.190 1.00 4.51
ATOM   763 C   CYS 1  96    18.976  1.828 65.556 1.00 4.51
ATOM   764 O   CYS 1  96    19.596  2.141 66.571 1.00 4.51
ATOM   765 CB  CYS 1  96    18.219 -0.417 66.413 1.00 4.51
ATOM   766 SG  CYS 1  96    19.291 -0.380 67.867 1.00 4.51
ATOM   767 N   PHE 1  97    18.527  2.749 64.686 1.00 0.88
ATOM   768 CA  PHE 1  97    18.736  4.145 64.915 1.00 0.88
ATOM   769 C   PHE 1  97    17.946  4.578 66.113 1.00 0.88
ATOM   770 O   PHE 1  97    18.428  5.352 66.938 1.00 0.88
ATOM   771 CB  PHE 1  97    18.340  5.023 63.714 1.00 0.88
ATOM   772 CG  PHE 1  97    19.305  4.748 62.607 1.00 0.88
ATOM   773 CD1 PHE 1  97    19.077  3.728 61.712 1.00 0.88
ATOM   774 CD2 PHE 1  97    20.453  5.497 62.477 1.00 0.88
ATOM   775 CE1 PHE 1  97    19.966  3.474 60.695 1.00 0.88
ATOM   776 CE2 PHE 1  97    21.350  5.242 61.466 1.00 0.88
ATOM   777 CZ  PHE 1  97    21.104  4.233 60.568 1.00 0.88
ATOM   778 N   ALA 1  98    16.694  4.094 66.232 1.00 0.99
ATOM   779 CA  ALA 1  98    15.862  4.421 67.357 1.00 0.99
ATOM   780 C   ALA 1  98    14.863  3.309 67.454 1.00 0.99
ATOM   781 O   ALA 1  98    14.773  2.480 66.551 1.00 0.99
ATOM   782 CB  ALA 1  98    15.081  5.735 67.181 1.00 0.99
ATOM   783 N   PRO 1  99    14.113  3.239 68.522 1.00 1.69
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ATOM 784 CA PRO 1 99 13.143 2.183 68.629 1.00 1.69
ATOM 785 C PRO 1 99 12.092 2.311 67.572 1.00 1.69
ATOM 786 O PRO 1 99 11.548 1.296 67.140 1.00 1.69
ATOM 787 CB PRO 1 99 12.632 2.242 70.066 1.00 1.69
ATOM 788 CG PRO 1 99 13.837 2.804 70.847 1.00 1.69
ATOM 789 CD PRO 1 99 14.591 3.674 69.824 1.00 1.69
ATOM 790 N ASP 1 100 11.757 3.555 67.192 1.00 1.75
ATOM 791 CA ASP 1 100 10.802 3.836 66.160 1.00 1.75
ATOM 792 C ASP 1 100 11.387 3.687 64.790 1.00 1.75
ATOM 793 O ASP 1 100 10.637 3.615 63.820 1.00 1.75
ATOM 794 CB ASP 1 100 10.150 5.228 66.271 1.00 1.75
ATOM 795 CG ASP 1 100 11.209 6.304 66.121 1.00 1.75
ATOM 796 OD1 ASP 1 100 12.253 6.218 66.820 1.00 1.75
ATOM 797 OD2 ASP 1 100 10.985 7.228 65.295 1.00 1.75
ATOM 798 N LEU 1 101 12.732 3.746 64.662 1.00 1.92
ATOM 799 CA LEU 1 101 13.358 3.662 63.368 1.00 1.92
ATOM 800 C LEU 1 101 14.440 2.619 63.354 1.00 1.92
ATOM 801 O LEU 1 101 15.581 2.886 63.732 1.00 1.92
ATOM 802 CB LEU 1 101 13.994 5.010 62.969 1.00 1.92
ATOM 803 CG LEU 1 101 14.853 5.009 61.688 1.00 1.92
ATOM 804 CD1 LEU 1 101 14.049 4.622 60.438 1.00 1.92
ATOM 805 CD2 LEU 1 101 15.571 6.358 61.523 1.00 1.92
ATOM 806 N ILE 1 102 14.113 1.399 62.879 1.00 3.39
ATOM 807 CA ILE 1 102 15.094 0.355 62.783 1.00 3.39
ATOM 808 C ILE 1 102 15.201 0.038 61.323 1.00 3.39
ATOM 809 O ILE 1 102 14.186 -0.155 60.656 1.00 3.39
ATOM 810 CB ILE 1 102 14.709 -0.926 63.477 1.00 3.39
ATOM 811 CG1 ILE 1 102 14.529 -0.719 64.991 1.00 3.39
ATOM 812 CG2 ILE 1 102 15.774 -1.979 63.134 1.00 3.39
ATOM 813 CD1 ILE 1 102 13.243 0.008 65.374 1.00 3.39
ATOM 814 N ILE 1 103 16.436 -0.029 60.779 1.00 4.51
ATOM 815 CA ILE 1 103 16.560 -0.283 59.374 1.00 4.51
ATOM 816 C ILE 1 103 17.129 -1.634 59.093 1.00 4.51
ATOM 817 O ILE 1 103 18.055 -2.108 59.748 1.00 4.51
ATOM 818 CB ILE 1 103 17.407 0.716 58.636 1.00 4.51
ATOM 819 CG1 ILE 1 103 18.857 0.673 59.134 1.00 4.51
ATOM 820 CG2 ILE 1 103 16.744 2.096 58.778 1.00 4.51
ATOM 821 CD1 ILE 1 103 19.831 1.443 58.243 1.00 4.51
ATOM 822 N ASN 1 104 16.548 -2.265 58.062 1.00 4.77
ATOM 823 CA ASN 1 104 16.843 -3.577 57.583 1.00 4.77
ATOM 824 C ASN 1 104 17.201 -3.356 56.144 1.00 4.77
ATOM 825 O ASN 1 104 16.881 -2.306 55.592 1.00 4.77
ATOM 826 CB ASN 1 104 15.562 -4.421 57.659 1.00 4.77
ATOM 827 CG ASN 1 104 15.739 -5.726 56.930 1.00 4.77
ATOM 828 OD1 ASN 1 104 15.674 -5.768 55.703 1.00 4.77
ATOM 829 ND2 ASN 1 104 15.945 -6.822 57.703 1.00 4.77
ATOM 830 N GLU 1 105 17.855 -4.338 55.489 1.00 6.85
ATOM 831 CA GLU 1 105 18.307 -4.145 54.137 1.00 6.85
ATOM 832 C GLU 1 105 17.168 -3.846 53.217 1.00 6.85

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ATOM  833 O   GLU 1 105   17.317 -3.074 52.273 1.00 6.85
ATOM  834 CB  GLU 1 105   19.109 -5.319 53.541 1.00 6.85
ATOM  835 CG  GLU 1 105   18.321 -6.616 53.372 1.00 6.85
ATOM  836 CD  GLU 1 105   18.211 -7.282 54.738 1.00 6.85
ATOM  837 OE1 GLU 1 105   18.830 -6.762 55.704 1.00 6.85
ATOM  838 OE2 GLU 1 105   17.507 -8.323 54.832 1.00 6.85
ATOM  839 N   GLN 1 106   15.987 -4.435 53.465 1.00 3.68
ATOM  840 CA  GLN 1 106   14.888 -4.206 52.576 1.00 3.68
ATOM  841 C   GLN 1 106   14.583 -2.741 52.519 1.00 3.68
ATOM  842 O   GLN 1 106   14.276 -2.208 51.456 1.00 3.68
ATOM  843 CB  GLN 1 106   13.615 -4.962 52.999 1.00 3.68
ATOM  844 CG  GLN 1 106   13.061 -4.546 54.363 1.00 3.68
ATOM  845 CD  GLN 1 106   11.816 -5.379 54.632 1.00 3.68
ATOM  846 OE1 GLN 1 106   11.323 -6.085 53.753 1.00 3.68
ATOM  847 NE2 GLN 1 106   11.294 -5.300 55.885 1.00 3.68
ATOM  848 N   ARG 1 107   14.651 -2.051 53.670 1.00 6.71
ATOM  849 CA  ARG 1 107   14.369 -0.647 53.733 1.00 6.71
ATOM  850 C   ARG 1 107   15.397  0.257 53.114 1.00 6.71
ATOM  851 O   ARG 1 107   15.080  1.401 52.795 1.00 6.71
ATOM  852 CB  ARG 1 107   13.931 -0.177 55.129 1.00 6.71
ATOM  853 CG  ARG 1 107   14.838 -0.579 56.282 1.00 6.71
ATOM  854 CD  ARG 1 107   14.205 -0.220 57.627 1.00 6.71
ATOM  855 NE  ARG 1 107   12.773 -0.633 57.597 1.00 6.71
ATOM  856 CZ  ARG 1 107   11.801  0.262 57.252 1.00 6.71
ATOM  857 NH1 ARG 1 107   10.493 -0.128 57.243 1.00 6.71
ATOM  858 NH2 ARG 1 107   12.132  1.546 56.924 1.00 6.71
ATOM  859 N   MET 1 108   16.669 -0.171 52.971 1.00 7.61
ATOM  860 CA  MET 1 108   17.574  0.739 52.321 1.00 7.61
ATOM  861 C   MET 1 108   17.626  0.489 50.841 1.00 7.61
ATOM  862 O   MET 1 108   18.500 -0.215 50.338 1.00 7.61
ATOM  863 CB  MET 1 108   19.014  0.755 52.878 1.00 7.61
ATOM  864 CG  MET 1 108   19.680 -0.604 53.099 1.00 7.61
ATOM  865 SD  MET 1 108   19.434 -1.350 54.736 1.00 7.61
ATOM  866 CE  MET 1 108   20.502 -0.222 55.677 1.00 7.61
ATOM  867 N   THR 1 109   16.653  1.068 50.106 1.00 5.21
ATOM  868 CA  THR 1 109   16.574  0.937 48.678 1.00 5.21
ATOM  869 C   THR 1 109   17.645  1.713 47.974 1.00 5.21
ATOM  870 O   THR 1 109   18.330  1.188 47.097 1.00 5.21
ATOM  871 CB  THR 1 109   15.263  1.422 48.132 1.00 5.21
ATOM  872 OG1 THR 1 109   15.110  2.810 48.390 1.00 5.21
ATOM  873 CG2 THR 1 109   14.127  0.631 48.802 1.00 5.21
ATOM  874 N   LEU 1 110   17.835  2.987 48.372 1.00 6.15
ATOM  875 CA  LEU 1 110   18.754  3.865 47.704 1.00 6.15
ATOM  876 C   LEU 1 110   20.118  3.254 47.804 1.00 6.15
ATOM  877 O   LEU 1 110   20.606  2.945 48.890 1.00 6.15
ATOM  878 CB  LEU 1 110   18.716  5.280 48.323 1.00 6.15
ATOM  879 CG  LEU 1 110   19.494  6.380 47.577 1.00 6.15
ATOM  880 CD1 LEU 1 110   21.006  6.245 47.767 1.00 6.15
ATOM  881 CD2 LEU 1 110   19.081  6.446 46.098 1.00 6.15
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ATOM 882 N PRO 1 111 20.729 3.040 46.668 1.00 5.04
ATOM 883 CA PRO 1 111 22.012 2.390 46.633 1.00 5.04
ATOM 884 C PRO 1 111 23.112 3.146 47.305 1.00 5.04
ATOM 885 O PRO 1 111 23.973 2.516 47.918 1.00 5.04
ATOM 886 CB PRO 1 111 22.274 2.068 45.164 1.00 5.04
ATOM 887 CG PRO 1 111 20.859 1.908 44.576 1.00 5.04
ATOM 888 CD PRO 1 111 19.973 2.815 45.447 1.00 5.04
ATOM 889 N CYS 1 112 23.121 4.484 47.192 1.00 0.66
ATOM 890 CA CYS 1 112 24.142 5.271 47.817 1.00 0.66
ATOM 891 C CYS 1 112 23.989 5.156 49.297 1.00 0.66
ATOM 892 O CYS 1 112 24.966 4.996 50.028 1.00 0.66
ATOM 893 CB CYS 1 112 24.043 6.765 47.466 1.00 0.66
ATOM 894 SG CYS 1 112 24.332 7.087 45.700 1.00 0.66
ATOM 895 N MET 1 113 22.733 5.242 49.769 1.00 3.18
ATOM 896 CA MET 1 113 22.433 5.193 51.167 1.00 3.18
ATOM 897 C MET 1 113 22.748 3.849 51.740 1.00 3.18
ATOM 898 O MET 1 113 23.314 3.754 52.829 1.00 3.18
ATOM 899 CB MET 1 113 20.949 5.478 51.457 1.00 3.18
ATOM 900 CG MET 1 113 20.599 5.458 52.946 1.00 3.18
ATOM 901 SD MET 1 113 18.849 5.795 53.310 1.00 3.18
ATOM 902 CE MET 1 113 18.935 7.557 52.885 1.00 3.18
ATOM 903 N TYR 1 114 22.391 2.751 51.045 1.00 7.80
ATOM 904 CA TYR 1 114 22.695 1.531 51.725 1.00 7.80
ATOM 905 C TYR 1 114 24.163 1.278 51.734 1.00 7.80
ATOM 906 O TYR 1 114 24.678 0.611 52.629 1.00 7.80
ATOM 907 CB TYR 1 114 21.893 0.261 51.375 1.00 7.80
ATOM 908 CG TYR 1 114 22.306 -0.518 50.184 1.00 7.80
ATOM 909 CD1 TYR 1 114 21.577 -0.433 49.024 1.00 7.80
ATOM 910 CD2 TYR 1 114 23.153 -1.587 50.369 1.00 7.80
ATOM 911 CE1 TYR 1 114 21.679 -1.424 48.077 1.00 7.80
ATOM 912 CE2 TYR 1 114 23.282 -2.562 49.412 1.00 7.80
ATOM 913 CZ TYR 1 114 22.517 -2.496 48.275 1.00 7.80
ATOM 914 OH TYR 1 114 22.572 -3.541 47.330 1.00 7.80
ATOM 915 N ASP 1 115 24.887 1.809 50.735 1.00 4.14
ATOM 916 CA ASP 1 115 26.308 1.631 50.732 1.00 4.14
ATOM 917 C ASP 1 115 26.814 2.261 51.992 1.00 4.14
ATOM 918 O ASP 1 115 27.707 1.733 52.653 1.00 4.14
ATOM 919 CB ASP 1 115 26.993 2.331 49.545 1.00 4.14
ATOM 920 CG ASP 1 115 28.461 1.929 49.534 1.00 4.14
ATOM 921 OD1 ASP 1 115 29.180 2.348 48.588 1.00 4.14
ATOM 922 OD2 ASP 1 115 28.882 1.193 50.466 1.00 4.14
ATOM 923 N GLN 1 116 26.238 3.421 52.360 1.00 2.66
ATOM 924 CA GLN 1 116 26.637 4.121 53.546 1.00 2.66
ATOM 925 C GLN 1 116 26.311 3.286 54.750 1.00 2.66
ATOM 926 O GLN 1 116 27.085 3.237 55.705 1.00 2.66
ATOM 927 CB GLN 1 116 25.934 5.487 53.680 1.00 2.66
ATOM 928 CG GLN 1 116 26.323 6.282 54.928 1.00 2.66
ATOM 929 CD GLN 1 116 25.405 5.871 56.069 1.00 2.66
ATOM 930 OE1 GLN 1 116 25.635 6.236 57.220 1.00 2.66

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ATOM   931 NE2 GLN 1 116    24.330  5.104 55.745 1.00 2.66
ATOM   932 N  CYS 1 117    25.151  2.600 54.731 1.00 0.90
ATOM   933 CA CYS 1 117    24.729  1.792 55.843 1.00 0.90
ATOM   934 C  CYS 1 117    25.679  0.662 56.073 1.00 0.90
ATOM   935 O  CYS 1 117    25.979  0.312 57.214 1.00 0.90
ATOM   936 CB CYS 1 117    23.328  1.185 55.654 1.00 0.90
ATOM   937 SG CYS 1 117    22.022  2.449 55.682 1.00 0.90
ATOM   938 N  LYS 1 118    26.185  0.063 54.982 1.00 4.62
ATOM   939 CA LYS 1 118    27.083 -1.046 55.097 1.00 4.62
ATOM   940 C  LYS 1 118    28.284 -0.562 55.835 1.00 4.62
ATOM   941 O  LYS 1 118    28.868 -1.283 56.642 1.00 4.62
ATOM   942 CB LYS 1 118    27.556 -1.566 53.728 1.00 4.62
ATOM   943 CG LYS 1 118    28.508 -2.760 53.815 1.00 4.62
ATOM   944 CD LYS 1 118    28.748 -3.443 52.467 1.00 4.62
ATOM   945 CE LYS 1 118    27.506 -4.136 51.901 1.00 4.62
ATOM   946 NZ LYS 1 118    27.821 -4.746 50.590 1.00 4.62
ATOM   947 N  HIS 1 119    28.687  0.687 55.551 1.00 4.28
ATOM   948 CA HIS 1 119    29.831  1.283 56.167 1.00 4.28
ATOM   949 C  HIS 1 119    29.583  1.420 57.639 1.00 4.28
ATOM   950 O  HIS 1 119    30.446  1.079 58.448 1.00 4.28
ATOM   951 CB HIS 1 119    30.108  2.673 55.569 1.00 4.28
ATOM   952 CG HIS 1 119    31.467  3.225 55.867 1.00 4.28
ATOM   953 ND1 HIS 1 119    32.643  2.608 55.502 1.00 4.28
ATOM   954 CD2 HIS 1 119    31.824  4.440 56.364 1.00 4.28
ATOM   955 CE1 HIS 1 119    33.647  3.468 55.803, 1.00 4.28
ATOM   956 NE2 HIS 1 119    33.197  4.595 56.325 1.00 4.28
ATOM   957 N  MET 1 120    28.391  1.912 58.045 1.00 7.65
ATOM   958 CA MET 1 120    28.194  2.013 59.463 1.00 7.65
ATOM   959 C  MET 1 120    28.060  0.670 60.109 1.00 7.65
ATOM   960 O  MET 1 120    28.397  0.505 61.278 1.00 7.65
ATOM   961 CB MET 1 120    27.096  2.955 60.020 1.00 7.65
ATOM   962 CG MET 1 120    25.636  2.694 59.675 1.00 7.65
ATOM   963 SD MET 1 120    25.017  3.639 58.262 1.00 7.65
ATOM   964 CE MET 1 120    23.295  3.110 58.489 1.00 7.65
ATOM   965 N  LEU 1 121    27.592 -0.333 59.348 1.00 7.58
ATOM   966 CA LEU 1 121    27.347 -1.667 59.827 1.00 7.58
ATOM   967 C  LEU 1 121    28.611 -2.254 60.386 1.00 7.58
ATOM   968 O  LEU 1 121    28.573 -3.128 61.250 1.00 7.58
ATOM   969 CB LEU 1 121    26.815 -2.579 58.700 1.00 7.58
ATOM   970 CG LEU 1 121    26.520 -4.042 59.093 1.00 7.58
ATOM   971 CD1 LEU 1 121    27.803 -4.867 59.280 1.00 7.58
ATOM   972 CD2 LEU 1 121    25.582 -4.108 60.309 1.00 7.58
ATOM   973 N  TYR 1 122    29.777 -1.785 59.913 1.00 0.69
ATOM   974 CA TYR 1 122    31.023 -2.339 60.358 1.00 0.69
ATOM   975 C  TYR 1 122    31.168 -2.246 61.850 1.00 0.69
ATOM   976 O  TYR 1 122    31.742 -3.141 62.468 1.00 0.69
ATOM   977 CB TYR 1 122    32.243 -1.652 59.722 1.00 0.69
ATOM   978 CG TYR 1 122    32.225 -1.982 58.269 1.00 0.69
ATOM   979 CD1 TYR 1 122    32.714 -3.189 57.823 1.00 0.69
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ATOM   980 CD2 TYR 1 122    31.727  -1.087  57.351  1.00  0.69
ATOM   981 CE1 TYR 1 122    32.699  -3.501  56.484  1.00  0.69
ATOM   982 CE2 TYR 1 122    31.710  -1.392  56.010  1.00  0.69
ATOM   983 CZ  TYR 1 122    32.195  -2.602  55.575  1.00  0.69
ATOM   984 OH  TYR 1 122    32.176  -2.919  54.201  1.00  0.69
ATOM   985 N   VAL 1 123    30.676  -1.160  62.477  1.00  3.47
ATOM   986 CA  VAL 1 123    30.837  -1.018  63.900  1.00  3.47
ATOM   987 C   VAL 1 123    30.149  -2.098  64.691  1.00  3.47
ATOM   988 O   VAL 1 123    30.777  -2.759  65.515  1.00  3.47
ATOM   989 CB  VAL 1 123    30.340   0.309  64.404  1.00  3.47
ATOM   990 CG1 VAL 1 123    31.208   1.416  63.783  1.00  3.47
ATOM   991 CG2 VAL 1 123    28.844   0.445  64.075  1.00  3.47
ATOM   992 N   SER 1 124    28.854  -2.356  64.434  1.00  0.91
ATOM   993 CA  SER 1 124    28.133  -3.337  65.201  1.00  0.91
ATOM   994 C   SER 1 124    28.804  -4.660  65.027  1.00  0.91
ATOM   995 O   SER 1 124    28.880  -5.461  65.958  1.00  0.91
ATOM   996 CB  SER 1 124    26.677  -3.501  64.737  1.00  0.91
ATOM   997 OG  SER 1 124    26.642  -4.017  63.415  1.00  0.91
ATOM   998 N   SER 1 125    29.311  -4.921  63.812  1.00  3.19
ATOM   999 CA  SER 1 125    29.950  -6.171  63.518  1.00  3.19
ATOM  1000 C   SER 1 125    31.149  -6.353  64.395  1.00  3.19
ATOM  1001 O   SER 1 125    31.382  -7.440  64.920  1.00  3.19
ATOM  1002 CB  SER 1 125    30.432  -6.263  62.061  1.00  3.19
ATOM  1003 OG  SER 1 125    29.321  -6.233  61.178  1.00  3.19
ATOM  1004 N   GLU 1 126    31.954  -5.289  64.570  1.00  3.11
ATOM  1005 CA  GLU 1 126    33.127  -5.381  65.392  1.00  3.11
ATOM  1006 C   GLU 1 126    32.716  -5.589  66.813  1.00  3.11
ATOM  1007 O   GLU 1 126    33.373  -6.320  67.553  1.00  3.11
ATOM  1008 CB  GLU 1 126    34.006  -4.119  65.341  1.00  3.11
ATOM  1009 CG  GLU 1 126    34.707  -3.940  63.994  1.00  3.11
ATOM  1010 CD  GLU 1 126    35.640  -5.129  63.802  1.00  3.11
ATOM  1011 OE1 GLU 1 126    35.848  -5.885  64.788  1.00  3.11
ATOM  1012 OE2 GLU 1 126    36.156  -5.297  62.665  1.00  3.11
ATOM  1013 N   LEU 1 127    31.616  -4.934  67.235  1.00  3.70
ATOM  1014 CA  LEU 1 127    31.166  -5.078  68.587  1.00  3.70
ATOM  1015 C   LEU 1 127    30.795  -6.497  68.858  1.00  3.70
ATOM  1016 O   LEU 1 127    31.127  -7.029  69.915  1.00  3.70
ATOM  1017 CB  LEU 1 127    29.962  -4.186  68.948  1.00  3.70
ATOM  1018 CG  LEU 1 127    30.327  -2.724  69.279  1.00  3.70
ATOM  1019 CD1 LEU 1 127    31.093  -2.640  70.609  1.00  3.70
ATOM  1020 CD2 LEU 1 127    31.083  -2.036  68.136  1.00  3.70
ATOM  1021 N   HIS 1 128    30.097  -7.152  67.913  1.00  3.09
ATOM  1022 CA  HIS 1 128    29.723  -8.521  68.119  1.00  3.09
ATOM  1023 C   HIS 1 128    30.943  -9.388  68.199  1.00  3.09
ATOM  1024 O   HIS 1 128    31.056 -10.246  69.074  1.00  3.09
ATOM  1025 CB  HIS 1 128    28.840  -9.071  66.986  1.00  3.09
ATOM  1026 CG  HIS 1 128    28.369 -10.473  67.237  1.00  3.09
ATOM  1027 ND1 HIS 1 128    27.246 -10.789  67.969  1.00  3.09
ATOM  1028 CD2 HIS 1 128    28.898 -11.662  66.836  1.00  3.09
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ATOM  1029 CE1 HIS 1 128    27.151 -12.143  67.975  1.00  3.09
ATOM  1030 NE2 HIS 1 128    28.131 -12.716  67.300  1.00  3.09
ATOM  1031 N   ARG 1 129    31.906  -9.176  67.286  1.00  3.04
ATOM  1032 CA  ARG 1 129    33.067 -10.023  67.264  1.00  3.04
ATOM  1033 C   ARG 1 129    33.843  -9.890  68.540  1.00  3.04
ATOM  1034 O   ARG 1 129    34.161 -10.882  69.195  1.00  3.04
ATOM  1035 CB  ARG 1 129    34.023  -9.667  66.112  1.00  3.04
ATOM  1036 CG  ARG 1 129    35.201 -10.632  65.965  1.00  3.04
ATOM  1037 CD  ARG 1 129    36.150 -10.270  64.821  1.00  3.04
ATOM  1038 NE  ARG 1 129    37.233 -11.294  64.801  1.00  3.04
ATOM  1039 CZ  ARG 1 129    38.348 -11.132  65.570  1.00  3.04
ATOM  1040 NH1 ARG 1 129    39.335 -12.075  65.547  1.00  3.04
ATOM  1041 NH2 ARG 1 129    38.478 -10.029  66.365  1.00  3.04
ATOM  1042 N   LEU 1 130    34.148  -8.638  68.924  1.00  1.27
ATOM  1043 CA  LEU 1 130    34.912  -8.315  70.098  1.00  1.27
ATOM  1044 C   LEU 1 130    34.140  -8.585  71.349  1.00  1.27
ATOM  1045 O   LEU 1 130    34.726  -8.841  72.402  1.00  1.27
ATOM  1046 CB  LEU 1 130    35.349  -6.840  70.154  1.00  1.27
ATOM  1047 CG  LEU 1 130    36.357  -6.449  69.058  1.00  1.27
ATOM  1048 CD1 LEU 1 130    36.756  -4.967  69.166  1.00  1.27
ATOM  1049 CD2 LEU 1 130    37.568  -7.395  69.056  1.00  1.27
ATOM  1050 N   GLN 1 131    32.800  -8.512  71.280  1.00  3.66
ATOM  1051 CA  GLN 1 131    32.028  -8.721  72.465  1.00  3.66
ATOM  1052 C   GLN 1 131    32.351  -7.633  73.444  1.00  3.66
ATOM  1053 O   GLN 1 131    32.692  -7.886  74.598  1.00  3.66
ATOM  1054 CB  GLN 1 131    32.317 -10.086  73.107  1.00  3.66
ATOM  1055 CG  GLN 1 131    31.424 -10.404  74.298  1.00  3.66
ATOM  1056 CD  GLN 1 131    31.824 -11.775  74.824  1.00  3.66
ATOM  1057 OE1 GLN 1 131    32.705 -12.433  74.273  1.00  3.66
ATOM  1058 NE2 GLN 1 131    31.157 -12.222  75.922  1.00  3.66
ATOM  1059 N   VAL 1 132    32.242  -6.372  72.973  1.00  1.28
ATOM  1060 CA  VAL 1 132    32.502  -5.198  73.762  1.00  1.28
ATOM  1061 C   VAL 1 132    31.545  -5.125  74.907  1.00  1.28
ATOM  1062 O   VAL 1 132    30.359  -5.417  74.766  1.00  1.28
ATOM  1063 CB  VAL 1 132    32.332  -3.926  72.979  1.00  1.28
ATOM  1064 CG1 VAL 1 132    32.333  -2.726  73.943  1.00  1.28
ATOM  1065 CG2 VAL 1 132    33.438  -3.871  71.912  1.00  1.28
ATOM  1066 N   SER 1 133    32.065  -4.719  76.083  1.00  3.60
ATOM  1067 CA  SER 1 133    31.288  -4.615  77.284  1.00  3.60
ATOM  1068 C   SER 1 133    30.703  -3.246  77.382  1.00  3.60
ATOM  1069 O   SER 1 133    31.171  -2.297  76.754  1.00  3.60
ATOM  1070 CB  SER 1 133    32.135  -4.715  78.559  1.00  3.60
ATOM  1071 OG  SER 1 133    33.062  -5.779  78.468  1.00  3.60
ATOM  1072 N   TYR 1 134    29.669  -3.112  78.231  1.00  3.87
ATOM  1073 CA  TYR 1 134    29.038  -1.843  78.423  1.00  3.87
ATOM  1074 C   TYR 1 134    30.064  -0.924  79.016  1.00  3.87
ATOM  1075 O   TYR 1 134    30.149   0.244  78.643  1.00  3.87
ATOM  1076 CB  TYR 1 134    27.849  -1.915  79.396  1.00  3.87
ATOM  1077 CG  TYR 1 134    27.208  -0.571  79.429  1.00  3.87
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ATOM 1078 CD1 TYR 1 134 27.732 0.446 80.191 1.00 3.87
ATOM 1079 CD2 TYR 1 134 26.052 -0.339 78.721 1.00 3.87
ATOM 1080 CE1 TYR 1 134 27.105 1.667 80.243 1.00 3.87
ATOM 1081 CE2 TYR 1 134 25.432 0.887 78.753 1.00 3.87
ATOM 1082 CZ TYR 1 134 25.961 1.896 79.520 1.00 3.87
ATOM 1083 OH TYR 1 134 25.333 3.159 79.566 1.00 3.87
ATOM 1084 N GLU 1 135 30.883 -1.434 79.957 1.00 5.78
ATOM 1085 CA GLU 1 135 31.859 -0.601 80.599 1.00 5.78
ATOM 1086 C GLU 1 135 32.885 -0.112 79.621 1.00 5.78
ATOM 1087 O GLU 1 135 33.347 1.025 79.700 1.00 5.78
ATOM 1088 CB GLU 1 135 32.589 -1.300 81.763 1.00 5.78
ATOM 1089 CG GLU 1 135 33.356 -2.570 81.385 1.00 5.78
ATOM 1090 CD GLU 1 135 32.391 -3.750 81.391 1.00 5.78
ATOM 1091 OE1 GLU 1 135 31.166 -3.532 81.582 1.00 5.78
ATOM 1092 OE2 GLU 1 135 32.875 -4.896 81.197 1.00 5.78
ATOM 1093 N GLU 1 136 33.286 -0.980 78.682 1.00 3.49
ATOM 1094 CA GLU 1 136 34.276 -0.676 77.692 1.00 3.49
ATOM 1095 C GLU 1 136 33.736 0.366 76.745 1.00 3.49
ATOM 1096 O GLU 1 136 34.420 1.323 76.380 1.00 3.49
ATOM 1097 CB GLU 1 136 34.580 -1.976 76.932 1.00 3.49
ATOM 1098 CG GLU 1 136 36.007 -2.148 76.438 1.00 3.49
ATOM 1099 CD GLU 1 136 36.196 -3.653 76.286 1.00 3.49
ATOM 1100 OE1 GLU 1 136 35.422 -4.270 75.507 1.00 3.49
ATOM 1101 OE2 GLU 1 136 37.102 -4.210 76.963 1.00 3.49
ATOM 1102 N TYR 1 137 32.459 0.208 76.351 1.00 1.07
ATOM 1103 CA TYR 1 137 31.774 1.072 75.425 1.00 1.07
ATOM 1104 C TYR 1 137 31.710 2.476 75.955 1.00 1.07
ATOM 1105 O TYR 1 137 31.964 3.439 75.229 1.00 1.07
ATOM 1106 CB TYR 1 137 30.329 0.568 75.207 1.00 1.07
ATOM 1107 CG TYR 1 137 29.561 1.518 74.358 1.00 1.07
ATOM 1108 CD1 TYR 1 137 29.695 1.512 72.990 1.00 1.07
ATOM 1109 CD2 TYR 1 137 28.597 2.314 74.931 1.00 1.07
ATOM 1110 CE1 TYR 1 137 28.904 2.320 72.209 1.00 1.07
ATOM 1111 CE2 TYR 1 137 27.814 3.134 74.155 1.00 1.07
ATOM 1112 CZ TYR 1 137 27.974 3.144 72.791 1.00 1.07
ATOM 1113 OH TYR 1 137 27.165 3.979 71.990 1.00 1.07
ATOM 1114 N LEU 1 138 31.391 2.624 77.254 1.00 1.14
ATOM 1115 CA LEU 1 138 31.235 3.929 77.836 1.00 1.14
ATOM 1116 C LEU 1 138 32.502 4.725 77.769 1.00 1.14
ATOM 1117 O LEU 1 138 32.474 5.919 77.474 1.00 1.14
ATOM 1118 CB LEU 1 138 30.862 3.910 79.328 1.00 1.14
ATOM 1119 CG LEU 1 138 29.457 3.381 79.651 1.00 1.14
ATOM 1120 CD1 LEU 1 138 29.143 3.587 81.143 1.00 1.14
ATOM 1121 CD2 LEU 1 138 28.393 3.991 78.723 1.00 1.14
ATOM 1122 N CYS 1 139 33.645 4.088 78.084 1.00 1.03
ATOM 1123 CA CYS 1 139 34.923 4.743 78.092 1.00 1.03
ATOM 1124 C CYS 1 139 35.315 5.115 76.696 1.00 1.03
ATOM 1125 O CYS 1 139 35.836 6.200 76.445 1.00 1.03
ATOM 1126 CB CYS 1 139 36.025 3.817 78.627 1.00 1.03

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ATOM  1127 SG  CYS 1 139    35.597  3.111 80.246 1.00 1.03
ATOM  1128 N   MET 1 140    35.070  4.209 75.735 1.00 1.00
ATOM  1129 CA  MET 1 140    35.468  4.495 74.387 1.00 1.00
ATOM  1130 C   MET 1 140    34.720  5.683 73.874 1.00 1.00
ATOM  1131 O   MET 1 140    35.275  6.502 73.150 1.00 1.00
ATOM  1132 CB  MET 1 140    35.236  3.338 73.402 1.00 1.00
ATOM  1133 CG  MET 1 140    36.172  2.154 73.642 1.00 1.00
ATOM  1134 SD  MET 1 140    35.935  0.762 72.499 1.00 1.00
ATOM  1135 CE  MET 1 140    36.614  1.644 71.064 1.00 1.00
ATOM  1136 N   LYS 1 141    33.440  5.821 74.255 1.00 8.36
ATOM  1137 CA  LYS 1 141    32.600  6.896 73.798 1.00 8.36
ATOM  1138 C   LYS 1 141    33.239  8.207 74.142 1.00 8.36
ATOM  1139 O   LYS 1 141    33.265  9.126 73.324 1.00 8.36
ATOM  1140 CB  LYS 1 141    31.266  6.892 74.563 1.00 8.36
ATOM  1141 CG  LYS 1 141    30.210  5.896 74.094 1.00 8.36
ATOM  1142 CD  LYS 1 141    29.337  6.420 72.957 1.00 8.36
ATOM  1143 CE  LYS 1 141    28.021  7.015 73.475 1.00 8.36
ATOM  1144 NZ  LYS 1 141    28.282  7.977 74.575 1.00 8.36
ATOM  1145 N   THR 1 142    33.757  8.333 75.380 1.00 4.68
ATOM  1146 CA  THR 1 142    34.342  9.572 75.806 1.00 4.68
ATOM  1147 C   THR 1 142    35.582  9.858 75.018 1.00 4.68
ATOM  1148 O   THR 1 142    35.838 10.999 74.639 1.00 4.68
ATOM  1149 CB  THR 1 142    34.699  9.614 77.266 1.00 4.68
ATOM  1150 OG1 THR 1 142    34.996 10.947 77.652 1.00 4.68
ATOM  1151 CG2 THR 1 142    35.920  8.717 77.518 1.00 4.68
ATOM  1152 N   LEU 1 143    36.380  8.813 74.733 1.00 1.09
ATOM  1153 CA  LEU 1 143    37.596  8.982 73.995 1.00 1.09
ATOM  1154 C   LEU 1 143    37.268  9.518 72.634 1.00 1.09
ATOM  1155 O   LEU 1 143    38.052 10.264 72.047 1.00 1.09
ATOM  1156 CB  LEU 1 143    38.401  7.680 73.834 1.00 1.09
ATOM  1157 CG  LEU 1 143    39.033  7.181 75.150 1.00 1.09
ATOM  1158 CD1 LEU 1 143    39.825  5.882 74.932 1.00 1.09
ATOM  1159 CD2 LEU 1 143    39.883  8.279 75.812 1.00 1.09
ATOM  1160 N   LEU 1 144    36.107  9.127 72.080 1.00 4.43
ATOM  1161 CA  LEU 1 144    35.669  9.620 70.802 1.00 4.43
ATOM  1162 C   LEU 1 144    35.448 11.105 70.850 1.00 4.43
ATOM  1163 O   LEU 1 144    35.804 11.807 69.905 1.00 4.43
ATOM  1164 CB  LEU 1 144    34.345  8.988 70.331 1.00 4.43
ATOM  1165 CG  LEU 1 144    34.469  7.624 69.623 1.00 4.43
ATOM  1166 CD1 LEU 1 144    35.238  6.580 70.428 1.00 4.43
ATOM  1167 CD2 LEU 1 144    33.083  7.095 69.244 1.00 4.43
ATOM  1168 N   LEU 1 145    34.859 11.633 71.947 1.00 7.68
ATOM  1169 CA  LEU 1 145    34.649 13.060 72.019 1.00 7.68
ATOM  1170 C   LEU 1 145    35.968 13.755 71.901 1.00 7.68
ATOM  1171 O   LEU 1 145    36.092 14.810 71.286 1.00 7.68
ATOM  1172 CB  LEU 1 145    34.168 13.631 73.373 1.00 7.68
ATOM  1173 CG  LEU 1 145    32.665 13.714 73.671 1.00 7.68
ATOM  1174 CD1 LEU 1 145    31.946 14.615 72.655 1.00 7.68
ATOM  1175 CD2 LEU 1 145    32.028 12.343 73.869 1.00 7.68
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ATOM  1176 N   LEU 1 146   36.964 13.187 72.583 1.00 2.09
ATOM  1177 CA  LEU 1 146   38.313 13.644 72.745 1.00 2.09
ATOM  1178 C   LEU 1 146   39.224 13.344 71.590 1.00 2.09
ATOM  1179 O   LEU 1 146   40.428 13.562 71.694 1.00 2.09
ATOM  1180 CB  LEU 1 146   38.957 13.045 74.006 1.00 2.09
ATOM  1181 CG  LEU 1 146   38.174 13.370 75.294 1.00 2.09
ATOM  1182 CD1 LEU 1 146   38.845 12.755 76.532 1.00 2.09
ATOM  1183 CD2 LEU 1 146   37.921 14.879 75.436 1.00 2.09
ATOM  1184 N   SER 1 147   38.702 12.687 70.541 1.00 1.91
ATOM  1185 CA  SER 1 147   39.438 12.173 69.420 1.00 1.91
ATOM  1186 C   SER 1 147   40.101 13.132 68.468 1.00 1.91
ATOM  1187 O   SER 1 147   41.080 12.752 67.830 1.00 1.91
ATOM  1188 CB  SER 1 147   38.556 11.238 68.576 1.00 1.91
ATOM  1189 OG  SER 1 147   39.322 10.657 67.535 1.00 1.91
ATOM  1190 N   SER 1 148   39.570 14.355 68.262 1.00 1.23
ATOM  1191 CA  SER 1 148   40.202 15.238 67.315 1.00 1.23
ATOM  1192 C   SER 1 148   40.247 16.631 67.864 1.00 1.23
ATOM  1193 O   SER 1 148   39.362 17.032 68.619 1.00 1.23
ATOM  1194 CB  SER 1 148   39.460 15.310 65.971 1.00 1.23
ATOM  1195 OG  SER 1 148   39.439 14.026 65.364 1.00 1.23
ATOM  1196 N   VAL 1 149   41.297 17.412 67.515 1.00 2.96
ATOM  1197 CA  VAL 1 149   41.290 18.766 67.989 1.00 2.96
ATOM  1198 C   VAL 1 149   41.865 19.635 66.902 1.00 2.96
ATOM  1199 O   VAL 1 149   42.328 19.128 65.881 1.00 2.96
ATOM  1200 CB  VAL 1 149   42.008 18.984 69.297 1.00 2.96
ATOM  1201 CG1 VAL 1 149   43.323 19.756 69.103 1.00 2.96
ATOM  1202 CG2 VAL 1 149   40.995 19.585 70.278 1.00 2.96
ATOM  1203 N   PRO 1 150   41.840 20.932 67.070 1.00 1.47
ATOM  1204 CA  PRO 1 150   42.293 21.827 66.038 1.00 1.47
ATOM  1205 C   PRO 1 150   43.760 21.693 65.799 1.00 1.47
ATOM  1206 O   PRO 1 150   44.470 21.226 66.687 1.00 1.47
ATOM  1207 CB  PRO 1 150   41.879 23.223 66.496 1.00 1.47
ATOM  1208 CG  PRO 1 150   40.654 22.967 67.394 1.00 1.47
ATOM  1209 CD  PRO 1 150   40.887 21.561 67.969 1.00 1.47
ATOM  1210 N   LYS 1 151   44.233 22.091 64.601 1.00 7.70
ATOM  1211 CA  LYS 1 151   45.627 21.985 64.285 1.00 7.70
ATOM  1212 C   LYS 1 151   46.373 22.845 65.252 1.00 7.70
ATOM  1213 O   LYS 1 151   47.477 22.508 65.674 1.00 7.70
ATOM  1214 CB  LYS 1 151   45.969 22.422 62.847 1.00 7.70
ATOM  1215 CG  LYS 1 151   45.445 23.804 62.455 1.00 7.70
ATOM  1216 CD  LYS 1 151   43.917 23.896 62.448 1.00 7.70
ATOM  1217 CE  LYS 1 151   43.378 25.217 61.895 1.00 7.70
ATOM  1218 NZ  LYS 1 151   43.413 25.197 60.415 1.00 7.70
ATOM  1219 N   ASP 1 152   45.768 23.990 65.613 1.00 4.33
ATOM  1220 CA  ASP 1 152   46.301 24.933 66.553 1.00 4.33
ATOM  1221 C   ASP 1 152   46.338 24.294 67.911 1.00 4.33
ATOM  1222 O   ASP 1 152   47.229 24.555 68.719 1.00 4.33
ATOM  1223 CB  ASP 1 152   45.407 26.180 66.648 1.00 4.33
ATOM  1224 CG  ASP 1 152   46.062 27.198 67.562 1.00 4.33
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ATOM 1225 OD1 ASP 1 152 47.234 26.977 67.967 1.00 4.33
ATOM 1226 OD2 ASP 1 152 45.394 28.222 67.868 1.00 4.33
ATOM 1227 N GLY 1 153 45.359 23.420 68.201 1.00 2.44
ATOM 1228 CA GLY 1 153 45.294 22.834 69.507 1.00 2.44
ATOM 1229 C GLY 1 153 44.183 23.547 70.208 1.00 2.44
ATOM 1230 O GLY 1 153 43.566 24.446 69.639 1.00 2.44
ATOM 1231 N LEU 1 154 43.904 23.152 71.467 1.00 1.42
ATOM 1232 CA LEU 1 154 42.822 23.715 72.225 1.00 1.42
ATOM 1233 C LEU 1 154 43.372 24.737 73.167 1.00 1.42
ATOM 1234 O LEU 1 154 44.554 24.721 73.504 1.00 1.42
ATOM 1235 CB LEU 1 154 42.091 22.689 73.118 1.00 1.42
ATOM 1236 CG LEU 1 154 41.267 21.609 72.388 1.00 1.42
ATOM 1237 CD1 LEU 1 154 40.595 20.649 73.387 1.00 1.42
ATOM 1238 CD2 LEU 1 154 40.227 22.221 71.435 1.00 1.42
ATOM 1239 N LYS 1 155 42.510 25.676 73.602 1.00 1.13
ATOM 1240 CA LYS 1 155 42.936 26.678 74.532 1.00 1.13
ATOM 1241 C LYS 1 155 43.307 25.989 75.804 1.00 1.13
ATOM 1242 O LYS 1 155 44.310 26.323 76.433 1.00 1.13
ATOM 1243 CB LYS 1 155 41.839 27.702 74.866 1.00 1.13
ATOM 1244 CG LYS 1 155 41.486 28.617 73.694 1.00 1.13
ATOM 1245 CD LYS 1 155 40.266 29.502 73.952 1.00 1.13
ATOM 1246 CE LYS 1 155 40.053 30.567 72.876 1.00 1.13
ATOM 1247 NZ LYS 1 155 38.923 31.447 73.249 1.00 1.13
ATOM 1248 N SER 1 156 42.498 24.996 76.214 1.00 4.74
ATOM 1249 CA SER 1 156 42.757 24.284 77.431 1.00 4.74
ATOM 1250 C SER 1 156 43.387 22.972 77.079 1.00 4.74
ATOM 1251 O SER 1 156 42.895 21.908 77.453 1.00 4.74
ATOM 1252 CB SER 1 156 41.469 24.009 78.225 1.00 4.74
ATOM 1253 OG SER 1 156 40.569 23.231 77.451 1.00 4.74
ATOM 1254 N GLN 1 157 44.525 23.021 76.362 1.00 1.05
ATOM 1255 CA GLN 1 157 45.170 21.820 75.920 1.00 1.05
ATOM 1256 C GLN 1 157 45.643 20.998 77.079 1.00 1.05
ATOM 1257 O GLN 1 157 45.504 19.776 77.075 1.00 1.05
ATOM 1258 CB GLN 1 157 46.381 22.086 75.010 1.00 1.05
ATOM 1259 CG GLN 1 157 46.956 20.810 74.392 1.00 1.05
ATOM 1260 CD GLN 1 157 45.943 20.286 73.381 1.00 1.05
ATOM 1261 OE1 GLN 1 157 45.030 21.000 72.969 1.00 1.05
ATOM 1262 NE2 GLN 1 157 46.106 19.000 72.967 1.00 1.05
ATOM 1263 N GLU 1 158 46.212 21.644 78.114 1.00 0.94
ATOM 1264 CA GLU 1 158 46.742 20.891 79.214 1.00 0.94
ATOM 1265 C GLU 1 158 45.659 20.120 79.899 1.00 0.94
ATOM 1266 O GLU 1 158 45.817 18.930 80.171 1.00 0.94
ATOM 1267 CB GLU 1 158 47.424 21.774 80.272 1.00 0.94
ATOM 1268 CG GLU 1 158 48.706 22.437 79.763 1.00 0.94
ATOM 1269 CD GLU 1 158 49.284 23.279 80.891 1.00 0.94
ATOM 1270 OE1 GLU 1 158 48.666 23.303 81.988 1.00 0.94
ATOM 1271 OE2 GLU 1 158 50.354 23.907 80.670 1.00 0.94
ATOM 1272 N LEU 1 159 44.516 20.771 80.183 1.00 6.51
ATOM 1273 CA LEU 1 159 43.458 20.081 80.860 1.00 6.51

ATOM 1274 C LEU 1 159 42.923 19.004 79.972 1.00 6.51
ATOM 1275 O LEU 1 159 42.515 17.943 80.440 1.00 6.51
ATOM 1276 CB LEU 1 159 42.317 21.002 81.343 1.00 6.51
ATOM 1277 CG LEU 1 159 41.671 21.902 80.276 1.00 6.51
ATOM 1278 CD1 LEU 1 159 40.863 21.092 79.254 1.00 6.51
ATOM 1279 CD2 LEU 1 159 40.842 23.018 80.932 1.00 6.51
ATOM 1280 N PHE 1 160 42.914 19.254 78.652 1.00 0.70
ATOM 1281 CA PHE 1 160 42.424 18.300 77.701 1.00 0.70
ATOM 1282 C PHE 1 160 43.261 17.057 77.743 1.00 0.70
ATOM 1283 O PHE 1 160 42.737 15.943 77.743 1.00 0.70
ATOM 1284 CB PHE 1 160 42.463 18.878 76.274 1.00 0.70
ATOM 1285 CG PHE 1 160 42.008 17.861 75.284 1.00 0.70
ATOM 1286 CD1 PHE 1 160 40.669 17.641 75.049 1.00 0.70
ATOM 1287 CD2 PHE 1 160 42.936 17.229 74.489 1.00 0.70
ATOM 1288 CE1 PHE 1 160 40.265 16.779 74.055 1.00 0.70
ATOM 1289 CE2 PHE 1 160 42.539 16.371 73.492 1.00 0.70
ATOM 1290 CZ PHE 1 160 41.202 16.146 73.273 1.00 0.70
ATOM 1291 N ASP 1 161 44.595 17.217 77.804 1.00 2.07
ATOM 1292 CA ASP 1 161 45.471 16.080 77.802 1.00 2.07
ATOM 1293 C ASP 1 161 45.219 15.249 79.018 1.00 2.07
ATOM 1294 O ASP 1 161 45.138 14.024 78.939 1.00 2.07
ATOM 1295 CB ASP 1 161 46.959 16.474 77.823 1.00 2.07
ATOM 1296 CG ASP 1 161 47.307 17.100 76.480 1.00 2.07
ATOM 1297 OD1 ASP 1 161 48.432 17.656 76.361 1.00 2.07
ATOM 1298 OD2 ASP 1 161 46.453 17.035 75.556 1.00 2.07
ATOM 1299 N GLU 1 162 45.075 15.901 80.185 1.00 4.44
ATOM 1300 CA GLU 1 162 44.878 15.164 81.396 1.00 4.44
ATOM 1301 C GLU 1 162 43.575 14.430 81.337 1.00 4.44
ATOM 1302 O GLU 1 162 43.483 13.287 81.782 1.00 4.44
ATOM 1303 CB GLU 1 162 44.905 16.049 82.658 1.00 4.44
ATOM 1304 CG GLU 1 162 43.824 17.129 82.707 1.00 4.44
ATOM 1305 CD GLU 1 162 44.022 17.927 83.987 1.00 4.44
ATOM 1306 OE1 GLU 1 162 43.156 18.792 84.287 1.00 4.44
ATOM 1307 OE2 GLU 1 162 45.045 17.685 84.682 1.00 4.44
ATOM 1308 N ILE 1 163 42.528 15.062 80.774 1.00 0.97
ATOM 1309 CA ILE 1 163 41.251 14.412 80.717 1.00 0.97
ATOM 1310 C ILE 1 163 41.348 13.174 79.880 1.00 0.97
ATOM 1311 O ILE 1 163 40.853 12.117 80.271 1.00 0.97
ATOM 1312 CB ILE 1 163 40.184 15.272 80.104 1.00 0.97
ATOM 1313 CG1 ILE 1 163 39.978 16.548 80.936 1.00 0.97
ATOM 1314 CG2 ILE 1 163 38.913 14.418 79.955 1.00 0.97
ATOM 1315 CD1 ILE 1 163 39.125 17.603 80.233 1.00 0.97
ATOM 1316 N ARG 1 164 42.018 13.266 78.714 1.00 5.11
ATOM 1317 CA ARG 1 164 42.112 12.133 77.835 1.00 5.11
ATOM 1318 C ARG 1 164 42.798 11.013 78.542 1.00 5.11
ATOM 1319 O ARG 1 164 42.361 9.866 78.486 1.00 5.11
ATOM 1320 CB ARG 1 164 42.978 12.373 76.588 1.00 5.11
ATOM 1321 CG ARG 1 164 42.373 13.301 75.545 1.00 5.11
ATOM 1322 CD ARG 1 164 43.195 13.347 74.256 1.00 5.11

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ATOM  1323 NE  ARG 1 164    42.787  12.183  73.419  1.00  5.11
ATOM  1324 CZ  ARG 1 164    43.376  10.963  73.583  1.00  5.11
ATOM  1325 NH1 ARG 1 164    44.321  10.774  74.550  1.00  5.11
ATOM  1326 NH2 ARG 1 164    43.013   9.929  72.770  1.00  5.11
ATOM  1327 N   MET 1 165    43.897  11.331  79.244  1.00  5.20
ATOM  1328 CA  MET 1 165    44.683  10.329  79.900  1.00  5.20
ATOM  1329 C   MET 1 165    43.852   9.624  80.923  1.00  5.20
ATOM  1330 O   MET 1 165    43.925   8.404  81.056  1.00  5.20
ATOM  1331 CB  MET 1 165    45.916  10.942  80.591  1.00  5.20
ATOM  1332 CG  MET 1 165    46.814   9.941  81.318  1.00  5.20
ATOM  1333 SD  MET 1 165    46.178   9.395  82.929  1.00  5.20
ATOM  1334 CE  MET 1 165    47.681   8.484  83.384  1.00  5.20
ATOM  1335 N   THR 1 166    43.020  10.377  81.665  1.00  1.86
ATOM  1336 CA  THR 1 166    42.227   9.776  82.696  1.00  1.86
ATOM  1337 C   THR 1 166    41.281   8.781  82.099  1.00  1.86
ATOM  1338 O   THR 1 166    41.107   7.687  82.633  1.00  1.86
ATOM  1339 CB  THR 1 166    41.409  10.777  83.454  1.00  1.86
ATOM  1340 OG1 THR 1 166    42.256  11.741  84.062  1.00  1.86
ATOM  1341 CG2 THR 1 166    40.597  10.034  84.528  1.00  1.86
ATOM  1342 N   TYR 1 167    40.633   9.138  80.976  1.00  4.58
ATOM  1343 CA  TYR 1 167    39.712   8.236  80.346  1.00  4.58
ATOM  1344 C   TYR 1 167    40.375   7.041  79.745  1.00  4.58
ATOM  1345 O   TYR 1 167    39.795   5.956  79.725  1.00  4.58
ATOM  1346 CB  TYR 1 167    38.807   8.904  79.299  1.00  4.58
ATOM  1347 CG  TYR 1 167    37.739   9.600  80.072  1.00  4.58
ATOM  1348 CD1 TYR 1 167    37.899  10.876  80.557  1.00  4.58
ATOM  1349 CD2 TYR 1 167    36.585   8.922  80.383  1.00  4.58
ATOM  1350 CE1 TYR 1 167    36.903  11.471  81.298  1.00  4.58
ATOM  1351 CE2 TYR 1 167    35.584   9.512  81.117  1.00  4.58
ATOM  1352 CZ  TYR 1 167    35.741  10.796  81.571  1.00  4.58
ATOM  1353 OH  TYR 1 167    34.717  11.422  82.312  1.00  4.58
ATOM  1354 N   ILE 1 168    41.591   7.203  79.193  1.00  4.85
ATOM  1355 CA  ILE 1 168    42.252   6.046  78.673  1.00  4.85
ATOM  1356 C   ILE 1 168    42.607   5.114  79.792  1.00  4.85
ATOM  1357 O   ILE 1 168    42.560   3.896  79.634  1.00  4.85
ATOM  1358 CB  ILE 1 168    43.380   6.367  77.726  1.00  4.85
ATOM  1359 CG1 ILE 1 168    44.398   7.344  78.319  1.00  4.85
ATOM  1360 CG2 ILE 1 168    42.748   6.849  76.412  1.00  4.85
ATOM  1361 CD1 ILE 1 168    45.536   7.660  77.347  1.00  4.85
ATOM  1362 N   LYS 1 169    42.939   5.668  80.973  1.00  6.27
ATOM  1363 CA  LYS 1 169    43.238   4.856  82.121  1.00  6.27
ATOM  1364 C   LYS 1 169    41.992   4.099  82.471  1.00  6.27
ATOM  1365 O   LYS 1 169    42.035   2.915  82.795  1.00  6.27
ATOM  1366 CB  LYS 1 169    43.582   5.704  83.355  1.00  6.27
ATOM  1367 CG  LYS 1 169    44.715   6.703  83.123  1.00  6.27
ATOM  1368 CD  LYS 1 169    46.071   6.077  82.805  1.00  6.27
ATOM  1369 CE  LYS 1 169    46.877   5.725  84.055  1.00  6.27
ATOM  1370 NZ  LYS 1 169    48.286   5.481  83.687  1.00  6.27
ATOM  1371 N   GLU 1 170    40.842   4.792  82.393  1.00  3.71
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ATOM 1372 CA GLU 1 170 39.535 4.287 82.702 1.00 3.71
ATOM 1373 C GLU 1 170 39.184 3.129 81.813 1.00 3.71
ATOM 1374 O GLU 1 170 38.618 2.135 82.266 1.00 3.71
ATOM 1375 CB GLU 1 170 38.514 5.426 82.519 1.00 3.71
ATOM 1376 CG GLU 1 170 37.104 5.005 82.131 1.00 3.71
ATOM 1377 CD GLU 1 170 36.480 4.192 83.241 1.00 3.71
ATOM 1378 OE1 GLU 1 170 37.231 3.606 84.064 1.00 3.71
ATOM 1379 OE2 GLU 1 170 35.223 4.142 83.261 1.00 3.71
ATOM 1380 N LEU 1 171 39.525 3.226 80.517 1.00 0.72
ATOM 1381 CA LEU 1 171 39.238 2.176 79.584 1.00 0.72
ATOM 1382 C LEU 1 171 39.997 0.961 80.009 1.00 0.72
ATOM 1383 O LEU 1 171 39.512 -0.164 79.893 1.00 0.72
ATOM 1384 CB LEU 1 171 39.674 2.534 78.152 1.00 0.72
ATOM 1385 CG LEU 1 171 39.381 1.437 77.112 1.00 0.72
ATOM 1386 CD1 LEU 1 171 37.873 1.178 76.984 1.00 0.72
ATOM 1387 CD2 LEU 1 171 40.040 1.764 75.760 1.00 0.72
ATOM 1388 N GLY 1 172 41.229 1.159 80.511 1.00 0.34
ATOM 1389 CA GLY 1 172 42.030 0.051 80.940 1.00 0.34
ATOM 1390 C GLY 1 172 41.331 -0.658 82.061 1.00 0.34
ATOM 1391 O GLY 1 172 41.312 -1.888 82.100 1.00 0.34
ATOM 1392 N LYS 1 173 40.736 0.098 83.009 1.00 4.65
ATOM 1393 CA LYS 1 173 40.076 -0.530 84.122 1.00 4.65
ATOM 1394 C LYS 1 173 38.922 -1.329 83.607 1.00 4.65
ATOM 1395 O LYS 1 173 38.646 -2.427 84.081 1.00 4.65
ATOM 1396 CB LYS 1 173 39.408 0.418 85.140 1.00 4.65
ATOM 1397 CG LYS 1 173 40.289 1.453 85.840 1.00 4.65
ATOM 1398 CD LYS 1 173 40.465 2.734 85.030 1.00 4.65
ATOM 1399 CE LYS 1 173 41.022 3.903 85.841 1.00 4.65
ATOM 1400 NZ LYS 1 173 42.467 3.709 86.083 1.00 4.65
ATOM 1401 N ALA 1 174 38.194 -0.786 82.618 1.00 0.62
ATOM 1402 CA ALA 1 174 37.042 -1.476 82.119 1.00 0.62
ATOM 1403 C ALA 1 174 37.494 -2.785 81.562 1.00 0.62
ATOM 1404 O ALA 1 174 36.845 -3.812 81.751 1.00 0.62
ATOM 1405 CB ALA 1 174 36.331 -0.715 80.988 1.00 0.62
ATOM 1406 N ILE 1 175 38.640 -2.765 80.862 1.00 4.02
ATOM 1407 CA ILE 1 175 39.217 -3.929 80.253 1.00 4.02
ATOM 1408 C ILE 1 175 39.540 -4.928 81.321 1.00 4.02
ATOM 1409 O ILE 1 175 39.264 -6.119 81.178 1.00 4.02
ATOM 1410 CB ILE 1 175 40.539 -3.616 79.608 1.00 4.02
ATOM 1411 CG1 ILE 1 175 40.398 -2.574 78.486 1.00 4.02
ATOM 1412 CG2 ILE 1 175 41.172 -4.942 79.163 1.00 4.02
ATOM 1413 CD1 ILE 1 175 39.588 -3.060 77.292 1.00 4.02
ATOM 1414 N VAL 1 176 40.121 -4.453 82.440 1.00 1.20
ATOM 1415 CA VAL 1 176 40.587 -5.342 83.465 1.00 1.20
ATOM 1416 C VAL 1 176 39.463 -6.067 84.123 1.00 1.20
ATOM 1417 O VAL 1 176 39.662 -7.154 84.662 1.00 1.20
ATOM 1418 CB VAL 1 176 41.426 -4.700 84.542 1.00 1.20
ATOM 1419 CG1 VAL 1 176 42.626 -4.010 83.872 1.00 1.20
ATOM 1420 CG2 VAL 1 176 40.566 -3.806 85.444 1.00 1.20

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ATOM  1421 N   LYS 1 177    38.252  -5.483  84.122  1.00  9.34
ATOM  1422 CA  LYS 1 177    37.173  -6.140  84.794  1.00  9.34
ATOM  1423 C   LYS 1 177    36.987  -7.509  84.215  1.00  9.34
ATOM  1424 O   LYS 1 177    36.793  -8.474  84.950  1.00  9.34
ATOM  1425 CB  LYS 1 177    35.843  -5.372  84.655  1.00  9.34
ATOM  1426 CG  LYS 1 177    34.706  -5.886  85.546  1.00  9.34
ATOM  1427 CD  LYS 1 177    34.225  -7.301  85.213  1.00  9.34
ATOM  1428 CE  LYS 1 177    33.356  -7.371  83.955  1.00  9.34
ATOM  1429 NZ  LYS 1 177    34.185  -7.132  82.752  1.00  9.34
ATOM  1430 N   ARG 1 178    36.949  -7.602  82.876  1.00  6.15
ATOM  1431 CA  ARG 1 178    36.803  -8.830  82.146  1.00  6.15
ATOM  1432 C   ARG 1 178    38.089  -9.552  81.835  1.00  6.15
ATOM  1433 O   ARG 1 178    38.151 -10.779  81.870  1.00  6.15
ATOM  1434 CB  ARG 1 178    36.100  -8.536  80.816  1.00  6.15
ATOM  1435 CG  ARG 1 178    35.172  -9.641  80.330  1.00  6.15
ATOM  1436 CD  ARG 1 178    33.960  -9.792  81.253  1.00  6.15
ATOM  1437 NE  ARG 1 178    32.797 -10.215  80.427  1.00  6.15
ATOM  1438 CZ  ARG 1 178    31.923  -9.270  79.973  1.00  6.15
ATOM  1439 NH1 ARG 1 178    32.113  -7.958  80.297  1.00  6.15
ATOM  1440 NH2 ARG 1 178    30.855  -9.632  79.205  1.00  6.15
ATOM  1441 N   GLU 1 179    39.160  -8.795  81.512  1.00  5.83
ATOM  1442 CA  GLU 1 179    40.337  -9.414  80.964  1.00  5.83
ATOM  1443 C   GLU 1 179    41.421  -9.588  81.984  1.00  5.83
ATOM  1444 O   GLU 1 179    42.183  -8.665  82.267  1.00  5.83
ATOM  1445 CB  GLU 1 179    40.893  -8.582  79.801  1.00  5.83
ATOM  1446 CG  GLU 1 179    41.573  -9.440  78.749  1.00  5.83
ATOM  1447 CD  GLU 1 179    40.468 -10.276  78.116  1.00  5.83
ATOM  1448 OE1 GLU 1 179    39.682  -9.709  77.312  1.00  5.83
ATOM  1449 OE2 GLU 1 179    40.386 -11.492  78.438  1.00  5.83
ATOM  1450 N   GLY 1 180    41.525 -10.812  82.540  1.00  1.02
ATOM  1451 CA  GLY 1 180    42.476 -11.112  83.571  1.00  1.02
ATOM  1452 C   GLY 1 180    43.910 -11.102  83.135  1.00  1.02
ATOM  1453 O   GLY 1 180    44.758 -10.507  83.798  1.00  1.02
ATOM  1454 N   ASN 1 181    44.232 -11.755  82.001  1.00  3.29
ATOM  1455 CA  ASN 1 181    45.613 -11.860  81.628  1.00  3.29
ATOM  1456 C   ASN 1 181    46.206 -10.515  81.364  1.00  3.29
ATOM  1457 O   ASN 1 181    45.548  -9.582  80.907  1.00  3.29
ATOM  1458 CB  ASN 1 181    45.873 -12.755  80.400  1.00  3.29
ATOM  1459 CG  ASN 1 181    47.344 -13.150  80.358  1.00  3.29
ATOM  1460 OD1 ASN 1 181    48.113 -12.886  81.281  1.00  3.29
ATOM  1461 ND2 ASN 1 181    47.751 -13.816  79.244  1.00  3.29
ATOM  1462 N   SER 1 182    47.498 -10.375  81.696  1.00  0.74
ATOM  1463 CA  SER 1 182    48.172  -9.145  81.442  1.00  0.74
ATOM  1464 C   SER 1 182    48.248  -8.998  79.961  1.00  0.74
ATOM  1465 O   SER 1 182    48.082  -7.904  79.426  1.00  0.74
ATOM  1466 CB  SER 1 182    49.610  -9.127  81.988  1.00  0.74
ATOM  1467 OG  SER 1 182    50.400 -10.094  81.312  1.00  0.74
ATOM  1468 N   SER 1 183    48.541 -10.113  79.266  1.00  3.77
ATOM  1469 CA  SER 1 183    48.669 -10.105  77.840  1.00  3.77
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ATOM 1470 C SER 1 183 47.372 -9.935 77.115 1.00 3.77
ATOM 1471 O SER 1 183 47.274 -9.086 76.229 1.00 3.77
ATOM 1472 CB SER 1 183 49.314 -11.393 77.299 1.00 3.77
ATOM 1473 OG SER 1 183 50.645 -11.510 77.779 1.00 3.77
ATOM 1474 N GLN 1 184 46.325 -10.719 77.460 1.00 7.63
ATOM 1475 CA GLN 1 184 45.186 -10.561 76.607 1.00 7.63
ATOM 1476 C GLN 1 184 44.550 -9.246 76.903 1.00 7.63
ATOM 1477 O GLN 1 184 43.887 -8.663 76.050 1.00 7.63
ATOM 1478 CB GLN 1 184 44.127 -11.695 76.545 1.00 7.63
ATOM 1479 CG GLN 1 184 42.965 -11.733 77.535 1.00 7.63
ATOM 1480 CD GLN 1 184 43.429 -11.922 78.952 1.00 7.63
ATOM 1481 OE1 GLN 1 184 43.982 -10.984 79.514 1.00 7.63
ATOM 1482 NE2 GLN 1 184 43.165 -13.116 79.548 1.00 7.63
ATOM 1483 N ASN 1 185 44.715 -8.751 78.144 1.00 3.79
ATOM 1484 CA ASN 1 185 44.194 -7.463 78.495 1.00 3.79
ATOM 1485 C ASN 1 185 44.890 -6.451 77.637 1.00 3.79
ATOM 1486 O ASN 1 185 44.265 -5.531 77.111 1.00 3.79
ATOM 1487 CB ASN 1 185 44.483 -7.108 79.967 1.00 3.79
ATOM 1488 CG ASN 1 185 43.716 -5.849 80.347 1.00 3.79
ATOM 1489 OD1 ASN 1 185 42.795 -5.901 81.160 1.00 3.79
ATOM 1490 ND2 ASN 1 185 44.101 -4.687 79.754 1.00 3.79
ATOM 1491 N TRP 1 186 46.220 -6.603 77.477 1.00 3.97
ATOM 1492 CA TRP 1 186 46.982 -5.673 76.695 1.00 3.97
ATOM 1493 C TRP 1 186 46.541 -5.785 75.275 1.00 3.97
ATOM 1494 O TRP 1 186 46.382 -4.785 74.577 1.00 3.97
ATOM 1495 CB TRP 1 186 48.496 -5.939 76.727 1.00 3.97
ATOM 1496 CG TRP 1 186 49.305 -4.839 76.079 1.00 3.97
ATOM 1497 CD1 TRP 1 186 49.978 -3.811 76.672 1.00 3.97
ATOM 1498 CD2 TRP 1 186 49.426 -4.640 74.662 1.00 3.97
ATOM 1499 NE1 TRP 1 186 50.528 -2.994 75.713 1.00 3.97
ATOM 1500 CE2 TRP 1 186 50.192 -3.489 74.471 1.00 3.97
ATOM 1501 CE3 TRP 1 186 48.934 -5.351 73.605 1.00 3.97
ATOM 1502 CZ2 TRP 1 186 50.480 -3.032 73.217 1.00 3.97
ATOM 1503 CZ3 TRP 1 186 49.225 -4.887 72.341 1.00 3.97
ATOM 1504 CH2 TRP 1 186 49.983 -3.750 72.151 1.00 3.97
ATOM 1505 N GLN 1 187 46.325 -7.028 74.815 1.00 0.67
ATOM 1506 CA GLN 1 187 45.915 -7.248 73.464 1.00 0.67
ATOM 1507 C GLN 1 187 44.575 -6.618 73.279 1.00 0.67
ATOM 1508 O GLN 1 187 44.315 -6.017 72.237 1.00 0.67
ATOM 1509 CB GLN 1 187 45.782 -8.742 73.124 1.00 0.67
ATOM 1510 CG GLN 1 187 47.108 -9.501 73.209 1.00 0.67
ATOM 1511 CD GLN 1 187 46.844 -10.957 72.853 1.00 0.67
ATOM 1512 OE1 GLN 1 187 45.725 -11.334 72.508 1.00 0.67
ATOM 1513 NE2 GLN 1 187 47.905 -11.804 72.942 1.00 0.67
ATOM 1514 N ARG 1 188 43.674 -6.734 74.277 1.00 7.01
ATOM 1515 CA ARG 1 188 42.393 -6.152 74.025 1.00 7.01
ATOM 1516 C ARG 1 188 42.471 -4.662 73.982 1.00 7.01
ATOM 1517 O ARG 1 188 41.707 -4.025 73.259 1.00 7.01
ATOM 1518 CB ARG 1 188 41.205 -6.560 74.913 1.00 7.01

ATOM 1519 CG ARG 1 188 41.182 -6.124 76.366 1.00 7.01
ATOM 1520 CD ARG 1 188 39.731 -6.059 76.851 1.00 7.01
ATOM 1521 NE ARG 1 188 38.929 -7.004 76.016 1.00 7.01
ATOM 1522 CZ ARG 1 188 38.255 -6.572 74.908 1.00 7.01
ATOM 1523 NH1 ARG 1 188 37.581 -7.464 74.124 1.00 7.01
ATOM 1524 NH2 ARG 1 188 38.254 -5.248 74.577 1.00 7.01
ATOM 1525 N PHE 1 189 43.383 -4.052 74.760 1.00 0.98
ATOM 1526 CA PHE 1 189 43.478 -2.623 74.707 1.00 0.98
ATOM 1527 C PHE 1 189 43.840 -2.264 73.303 1.00 0.98
ATOM 1528 O PHE 1 189 43.277 -1.338 72.727 1.00 0.98
ATOM 1529 CB PHE 1 189 44.545 -2.041 75.652 1.00 0.98
ATOM 1530 CG PHE 1 189 44.534 -0.555 75.493 1.00 0.98
ATOM 1531 CD1 PHE 1 189 43.528 0.202 76.051 1.00 0.98
ATOM 1532 CD2 PHE 1 189 45.574 0.092 74.866 1.00 0.98
ATOM 1533 CE1 PHE 1 189 43.539 1.574 75.949 1.00 0.98
ATOM 1534 CE2 PHE 1 189 45.595 1.465 74.769 1.00 0.98
ATOM 1535 CZ PHE 1 189 44.573 2.210 75.305 1.00 0.98
ATOM 1536 N TYR 1 190 44.766 -3.023 72.695 1.00 0.91
ATOM 1537 CA TYR 1 190 45.206 -2.741 71.360 1.00 0.91
ATOM 1538 C TYR 1 190 44.049 -2.805 70.410 1.00 0.91
ATOM 1539 O TYR 1 190 43.888 -1.932 69.560 1.00 0.91
ATOM 1540 CB TYR 1 190 46.262 -3.757 70.893 1.00 0.91
ATOM 1541 CG TYR 1 190 46.582 -3.521 69.457 1.00 0.91
ATOM 1542 CD1 TYR 1 190 47.439 -2.514 69.079 1.00 0.91
ATOM 1543 CD2 TYR 1 190 46.117 -4.395 68.501 1.00 0.91
ATOM 1544 CE1 TYR 1 190 47.814 -2.374 67.764 1.00 0.91
ATOM 1545 CE2 TYR 1 190 46.490 -4.261 67.185 1.00 0.91
ATOM 1546 CZ TYR 1 190 47.350 -3.257 66.818 1.00 0.91
ATOM 1547 OH TYR 1 190 47.742 -3.121 65.469 1.00 0.91
ATOM 1548 N GLN 1 191 43.200 -3.839 70.545 1.00 1.02
ATOM 1549 CA GLN 1 191 42.095 -4.033 69.649 1.00 1.02
ATOM 1550 C GLN 1 191 41.114 -2.906 69.735 1.00 1.02
ATOM 1551 O GLN 1 191 40.672 -2.376 68.716 1.00 1.02
ATOM 1552 CB GLN 1 191 41.316 -5.320 69.969 1.00 1.02
ATOM 1553 CG GLN 1 191 42.146 -6.595 69.816 1.00 1.02
ATOM 1554 CD GLN 1 191 41.267 -7.774 70.212 1.00 1.02
ATOM 1555 OE1 GLN 1 191 40.666 -7.783 71.285 1.00 1.02
ATOM 1556 NE2 GLN 1 191 41.183 -8.796 69.319 1.00 1.02
ATOM 1557 N LEU 1 192 40.749 -2.506 70.966 1.00 1.00
ATOM 1558 CA LEU 1 192 39.760 -1.485 71.157 1.00 1.00
ATOM 1559 C LEU 1 192 40.237 -0.166 70.656 1.00 1.00
ATOM 1560 O LEU 1 192 39.487 0.592 70.042 1.00 1.00
ATOM 1561 CB LEU 1 192 39.385 -1.308 72.632 1.00 1.00
ATOM 1562 CG LEU 1 192 38.748 -2.573 73.226 1.00 1.00
ATOM 1563 CD1 LEU 1 192 38.380 -2.363 74.698 1.00 1.00
ATOM 1564 CD2 LEU 1 192 37.567 -3.057 72.370 1.00 1.00
ATOM 1565 N THR 1 193 41.512 0.142 70.927 1.00 4.43
ATOM 1566 CA THR 1 193 42.060 1.403 70.562 1.00 4.43
ATOM 1567 C THR 1 193 42.166 1.477 69.075 1.00 4.43

ATOM 1568 O THR 1 193 41.979 2.540 68.488 1.00 4.43
ATOM 1569 CB THR 1 193 43.414 1.596 71.131 1.00 4.43
ATOM 1570 OG1 THR 1 193 43.458 1.208 72.490 1.00 4.43
ATOM 1571 CG2 THR 1 193 43.568 3.091 71.151 1.00 4.43
ATOM 1572 N LYS 1 194 42.494 0.339 68.433 1.00 6.16
ATOM 1573 CA LYS 1 194 42.623 0.290 67.005 1.00 6.16
ATOM 1574 C LYS 1 194 41.296 0.583 66.383 1.00 6.16
ATOM 1575 O LYS 1 194 41.212 1.253 65.356 1.00 6.16
ATOM 1576 CB LYS 1 194 43.111 -1.073 66.484 1.00 6.16
ATOM 1577 CG LYS 1 194 43.248 -1.117 64.961 1.00 6.16
ATOM 1578 CD LYS 1 194 44.290 -0.151 64.396 1.00 6.16
ATOM 1579 CE LYS 1 194 45.715 -0.698 64.418 1.00 6.16
ATOM 1580 NZ LYS 1 194 46.183 -0.792 65.815 1.00 6.16
ATOM 1581 N LEU 1 195 40.215 0.085 67.006 1.00 5.39
ATOM 1582 CA LEU 1 195 38.888 0.303 66.507 1.00 5.39
ATOM 1583 C LEU 1 195 38.613 1.771 66.485 1.00 5.39
ATOM 1584 O LEU 1 195 38.054 2.295 65.522 1.00 5.39
ATOM 1585 CB LEU 1 195 37.836 -0.398 67.397 1.00 5.39
ATOM 1586 CG LEU 1 195 36.356 -0.035 67.146 1.00 5.39
ATOM 1587 CD1 LEU 1 195 35.993 1.320 67.763 1.00 5.39
ATOM 1588 CD2 LEU 1 195 35.993 -0.081 65.660 1.00 5.39
ATOM 1589 N LEU 1 196 39.026 2.480 67.547 1.00 3.85
ATOM 1590 CA LEU 1 196 38.718 3.870 67.649 1.00 3.85
ATOM 1591 C LEU 1 196 39.453 4.591 66.553 1.00 3.85
ATOM 1592 O LEU 1 196 38.899 5.472 65.896 1.00 3.85
ATOM 1593 CB LEU 1 196 39.124 4.424 69.026 1.00 3.85
ATOM 1594 CG LEU 1 196 38.270 5.615 69.496 1.00 3.85
ATOM 1595 CD1 LEU 1 196 38.931 6.355 70.668 1.00 3.85
ATOM 1596 CD2 LEU 1 196 37.816 6.507 68.337 1.00 3.85
ATOM 1597 N ASP 1 197 40.727 4.227 66.300 1.00 5.56
ATOM 1598 CA ASP 1 197 41.420 4.912 65.248 1.00 5.56
ATOM 1599 C ASP 1 197 40.841 4.627 63.891 1.00 5.56
ATOM 1600 O ASP 1 197 40.842 5.491 63.016 1.00 5.56
ATOM 1601 CB ASP 1 197 42.966 4.858 65.312 1.00 5.56
ATOM 1602 CG ASP 1 197 43.553 3.465 65.392 1.00 5.56
ATOM 1603 OD1 ASP 1 197 44.144 3.024 64.378 1.00 5.56
ATOM 1604 OD2 ASP 1 197 43.477 2.844 66.481 1.00 5.56
ATOM 1605 N SER 1 198 40.292 3.417 63.689 1.00 0.90
ATOM 1606 CA SER 1 198 39.691 3.047 62.437 1.00 0.90
ATOM 1607 C SER 1 198 38.489 3.904 62.168 1.00 0.90
ATOM 1608 O SER 1 198 38.138 4.154 61.015 1.00 0.90
ATOM 1609 CB SER 1 198 39.224 1.580 62.412 1.00 0.90
ATOM 1610 OG SER 1 198 40.339 0.709 62.538 1.00 0.90
ATOM 1611 N MET 1 199 37.815 4.380 63.231 1.00 6.77
ATOM 1612 CA MET 1 199 36.599 5.121 63.049 1.00 6.77
ATOM 1613 C MET 1 199 36.816 6.395 62.286 1.00 6.77
ATOM 1614 O MET 1 199 35.907 6.887 61.620 1.00 6.77
ATOM 1615 CB MET 1 199 35.834 5.396 64.355 1.00 6.77
ATOM 1616 CG MET 1 199 34.394 5.851 64.099 1.00 6.77

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ATOM  1617 SD  MET 1 199    33.245  5.583 65.483 1.00 6.77
ATOM  1618 CE  MET 1 199    32.998  3.818 65.128 1.00 6.77
ATOM  1619 N   HIS 1 200    38.025  6.981 62.351 1.00 0.84
ATOM  1620 CA  HIS 1 200    38.228  8.211 61.639 1.00 0.84
ATOM  1621 C   HIS 1 200    37.937  8.046 60.180 1.00 0.84
ATOM  1622 O   HIS 1 200    37.260  8.881 59.582 1.00 0.84
ATOM  1623 CB  HIS 1 200    39.665  8.736 61.742 1.00 0.84
ATOM  1624 CG  HIS 1 200    40.009  9.172 63.128 1.00 0.84
ATOM  1625 ND1 HIS 1 200    40.741  8.424 64.024 1.00 0.84
ATOM  1626 CD2 HIS 1 200    39.683 10.322 63.777 1.00 0.84
ATOM  1627 CE1 HIS 1 200    40.831  9.159 65.160 1.00 0.84
ATOM  1628 NE2 HIS 1 200    40.208 10.319 65.056 1.00 0.84
ATOM  1629 N   GLU 1 201    38.438  6.964 59.560 1.00 5.71
ATOM  1630 CA  GLU 1 201    38.209  6.768 58.158 1.00 5.71
ATOM  1631 C   GLU 1 201    36.749  6.560 57.910 1.00 5.71
ATOM  1632 O   GLU 1 201    36.190  7.104 56.959 1.00 5.71
ATOM  1633 CB  GLU 1 201    38.951  5.541 57.601 1.00 5.71
ATOM  1634 CG  GLU 1 201    38.746  5.331 56.099 1.00 5.71
ATOM  1635 CD  GLU 1 201    39.521  6.414 55.364 1.00 5.71
ATOM  1636 OE1 GLU 1 201    39.482  6.417 54.105 1.00 5.71
ATOM  1637 OE2 GLU 1 201    40.162  7.254 56.051 1.00 5.71
ATOM  1638 N   VAL 1 202    36.085  5.767 58.774 1.00 4.12
ATOM  1639 CA  VAL 1 202    34.702  5.475 58.539 1.00 4.12
ATOM  1640 C   VAL 1 202    33.860  6.711 58.636 1.00 4.12
ATOM  1641 O   VAL 1 202    32.983  6.939 57.805 1.00 4.12
ATOM  1642 CB  VAL 1 202    34.121  4.440 59.465 1.00 4.12
ATOM  1643 CG1 VAL 1 202    34.911  3.132 59.287 1.00 4.12
ATOM  1644 CG2 VAL 1 202    34.084  4.979 60.901 1.00 4.12
ATOM  1645 N   VAL 1 203    34.128  7.562 59.642 1.00 3.85
ATOM  1646 CA  VAL 1 203    33.336  8.742 59.853 1.00 3.85
ATOM  1647 C   VAL 1 203    33.475  9.690 58.699 1.00 3.85
ATOM  1648 O   VAL 1 203    32.552 10.441 58.384 1.00 3.85
ATOM  1649 CB  VAL 1 203    33.684  9.470 61.121 1.00 3.85
ATOM  1650 CG1 VAL 1 203    35.042 10.170 60.960 1.00 3.85
ATOM  1651 CG2 VAL 1 203    32.527 10.419 61.461 1.00 3.85
ATOM  1652 N   GLU 1 204    34.643  9.682 58.032 1.00 3.18
ATOM  1653 CA  GLU 1 204    34.877 10.585 56.942 1.00 3.18
ATOM  1654 C   GLU 1 204    33.848 10.364 55.878 1.00 3.18
ATOM  1655 O   GLU 1 204    33.364 11.319 55.272 1.00 3.18
ATOM  1656 CB  GLU 1 204    36.260 10.392 56.298 1.00 3.18
ATOM  1657 CG  GLU 1 204    36.552 11.380 55.167 1.00 3.18
ATOM  1658 CD  GLU 1 204    37.941 11.076 54.626 1.00 3.18
ATOM  1659 OE1 GLU 1 204    38.216  9.881 54.339 1.00 3.18
ATOM  1660 OE2 GLU 1 204    38.749 12.036 54.497 1.00 3.18
ATOM  1661 N   ASN 1 205    33.491  9.094 55.610 1.00 0.60
ATOM  1662 CA  ASN 1 205    32.509  8.814 54.601 1.00 0.60
ATOM  1663 C   ASN 1 205    31.180  9.372 55.011 1.00 0.60
ATOM  1664 O   ASN 1 205    30.443  9.899 54.180 1.00 0.60
ATOM  1665 CB  ASN 1 205    32.342  7.311 54.324 1.00 0.60
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ATOM  1666 CG  ASN 1 205   33.573  6.857 53.551 1.00 0.60
ATOM  1667 OD1 ASN 1 205   33.971  7.491 52.575 1.00 0.60
ATOM  1668 ND2 ASN 1 205   34.200  5.737 54.000 1.00 0.60
ATOM  1669 N   LEU 1 206   30.833  9.263 56.308 1.00 3.88
ATOM  1670 CA  LEU 1 206   29.590  9.801 56.792 1.00 3.88
ATOM  1671 C   LEU 1 206   29.590 11.288 56.603 1.00 3.88
ATOM  1672 O   LEU 1 206   28.594 11.876 56.185 1.00 3.88
ATOM  1673 CB  LEU 1 206   29.374  9.562 58.302 1.00 3.88
ATOM  1674 CG  LEU 1 206   28.910  8.147 58.708 1.00 3.88
ATOM  1675 CD1 LEU 1 206   27.419  7.956 58.399 1.00 3.88
ATOM  1676 CD2 LEU 1 206   29.780  7.041 58.090 1.00 3.88
ATOM  1677 N   LEU 1 207   30.728 11.935 56.906 1.00 4.19
ATOM  1678 CA  LEU 1 207   30.855 13.361 56.816 1.00 4.19
ATOM  1679 C   LEU 1 207   30.630 13.821 55.409 1.00 4.19
ATOM  1680 O   LEU 1 207   29.925 14.802 55.175 1.00 4.19
ATOM  1681 CB  LEU 1 207   32.253 13.792 57.322 1.00 4.19
ATOM  1682 CG  LEU 1 207   32.675 15.259 57.113 1.00 4.19
ATOM  1683 CD1 LEU 1 207   33.895 15.597 57.985 1.00 4.19
ATOM  1684 CD2 LEU 1 207   33.001 15.538 55.636 1.00 4.19
ATOM  1685 N   ASN 1 208   31.222 13.114 54.431 1.00 1.53
ATOM  1686 CA  ASN 1 208   31.089 13.501 53.056 1.00 1.53
ATOM  1687 C   ASN 1 208   29.664 13.377 52.611 1.00 1.53
ATOM  1688 O   ASN 1 208   29.136 14.262 51.940 1.00 1.53
ATOM  1689 CB  ASN 1 208   31.935 12.625 52.115 1.00 1.53
ATOM  1690 CG  ASN 1 208   33.402 12.887 52.423 1.00 1.53
ATOM  1691 OD1 ASN 1 208   34.144 11.976 52.787 1.00 1.53
ATOM  1692 ND2 ASN 1 208   33.835 14.168 52.275 1.00 1.53
ATOM  1693 N   TYR 1 209   28.999 12.269 52.989 1.00 0.82
ATOM  1694 CA  TYR 1 209   27.651 12.014 52.564 1.00 0.82
ATOM  1695 C   TYR 1 209   26.759 13.093 53.100 1.00 0.82
ATOM  1696 O   TYR 1 209   25.914 13.623 52.379 1.00 0.82
ATOM  1697 CB  TYR 1 209   27.142 10.657 53.088 1.00 0.82
ATOM  1698 CG  TYR 1 209   25.798 10.364 52.512 1.00 0.82
ATOM  1699 CD1 TYR 1 209   24.653 10.876 53.079 1.00 0.82
ATOM  1700 CD2 TYR 1 209   25.682  9.497 51.449 1.00 0.82
ATOM  1701 CE1 TYR 1 209   23.415 10.537 52.584 1.00 0.82
ATOM  1702 CE2 TYR 1 209   24.447  9.155 50.950 1.00 0.82
ATOM  1703 CZ  TYR 1 209   23.310  9.673 51.520 1.00 0.82
ATOM  1704 OH  TYR 1 209   22.042  9.316 51.016 1.00 0.82
ATOM  1705 N   CYS 1 210   26.937 13.457 54.387 1.00 3.72
ATOM  1706 CA  CYS 1 210   26.103 14.462 54.986 1.00 3.72
ATOM  1707 C   CYS 1 210   26.255 15.798 54.337 1.00 3.72
ATOM  1708 O   CYS 1 210   25.267 16.467 54.042 1.00 3.72
ATOM  1709 CB  CYS 1 210   26.370 14.703 56.480 1.00 3.72
ATOM  1710 SG  CYS 1 210   25.473 13.553 57.554 1.00 3.72
ATOM  1711 N   PHE 1 211   27.504 16.221 54.089 1.00 3.96
ATOM  1712 CA  PHE 1 211   27.729 17.524 53.538 1.00 3.96
ATOM  1713 C   PHE 1 211   27.103 17.603 52.183 1.00 3.96
ATOM  1714 O   PHE 1 211   26.519 18.623 51.821 1.00 3.96
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ATOM 1715 CB PHE 1 211 29.226 17.848 53.386 1.00 3.96
ATOM 1716 CG PHE 1 211 29.342 19.260 52.924 1.00 3.96
ATOM 1717 CD1 PHE 1 211 29.233 19.575 51.590 1.00 3.96
ATOM 1718 CD2 PHE 1 211 29.575 20.268 53.831 1.00 3.96
ATOM 1719 CE1 PHE 1 211 29.352 20.879 51.167 1.00 3.96
ATOM 1720 CE2 PHE 1 211 29.695 21.573 53.415 1.00 3.96
ATOM 1721 CZ PHE 1 211 29.584 21.880 52.080 1.00 3.96
ATOM 1722 N GLN 1 212 27.218 16.519 51.393 1.00 0.53
ATOM 1723 CA GLN 1 212 26.678 16.508 50.064 1.00 0.53
ATOM 1724 C GLN 1 212 25.187 16.643 50.107 1.00 0.53
ATOM 1725 O GLN 1 212 24.606 17.437 49.370 1.00 0.53
ATOM 1726 CB GLN 1 212 26.989 15.200 49.317 1.00 0.53
ATOM 1727 CG GLN 1 212 28.483 14.969 49.083 1.00 0.53
ATOM 1728 CD GLN 1 212 28.642 13.649 48.342 1.00 0.53
ATOM 1729 OE1 GLN 1 212 27.660 12.976 48.030 1.00 0.53
ATOM 1730 NE2 GLN 1 212 29.913 13.265 48.052 1.00 0.53
ATOM 1731 N THR 1 213 24.529 15.873 50.993 1.00 0.65
ATOM 1732 CA THR 1 213 23.097 15.882 51.086 1.00 0.65
ATOM 1733 C THR 1 213 22.633 17.223 51.556 1.00 0.65
ATOM 1734 O THR 1 213 21.580 17.711 51.145 1.00 0.65
ATOM 1735 CB THR 1 213 22.573 14.864 52.051 1.00 0.65
ATOM 1736 OG1 THR 1 213 22.993 13.564 51.664 1.00 0.65
ATOM 1737 CG2 THR 1 213 21.039 14.939 52.041 1.00 0.65
ATOM 1738 N PHE 1 214 23.418 17.846 52.452 1.00 0.68
ATOM 1739 CA PHE 1 214 23.086 19.118 53.022 1.00 0.68
ATOM 1740 C PHE 1 214 22.996 20.140 51.926 1.00 0.68
ATOM 1741 O PHE 1 214 22.048 20.921 51.873 1.00 0.68
ATOM 1742 CB PHE 1 214 24.168 19.561 54.028 1.00 0.68
ATOM 1743 CG PHE 1 214 23.759 20.819 54.713 1.00 0.68
ATOM 1744 CD1 PHE 1 214 22.913 20.778 55.798 1.00 0.68
ATOM 1745 CD2 PHE 1 214 24.320 22.023 54.351 1.00 0.68
ATOM 1746 CE1 PHE 1 214 22.605 21.926 56.490 1.00 0.68
ATOM 1747 CE2 PHE 1 214 24.016 23.173 55.039 1.00 0.68
ATOM 1748 CZ PHE 1 214 23.156 23.126 56.110 1.00 0.68
ATOM 1749 N LEU 1 215 23.986 20.159 51.013 1.00 6.34
ATOM 1750 CA LEU 1 215 23.981 21.102 49.927 1.00 6.34
ATOM 1751 C LEU 1 215 22.856 20.758 48.986 1.00 6.34
ATOM 1752 O LEU 1 215 22.184 21.629 48.435 1.00 6.34
ATOM 1753 CB LEU 1 215 25.301 21.078 49.135 1.00 6.34
ATOM 1754 CG LEU 1 215 25.355 22.077 47.965 1.00 6.34
ATOM 1755 CD1 LEU 1 215 25.292 23.529 48.468 1.00 6.34
ATOM 1756 CD2 LEU 1 215 26.579 21.817 47.073 1.00 6.34
ATOM 1757 N ASP 1 216 22.653 19.440 48.808 1.00 3.90
ATOM 1758 CA ASP 1 216 21.725 18.719 47.975 1.00 3.90
ATOM 1759 C ASP 1 216 20.330 18.794 48.524 1.00 3.90
ATOM 1760 O ASP 1 216 19.397 18.265 47.924 1.00 3.90
ATOM 1761 CB ASP 1 216 22.104 17.232 47.855 1.00 3.90
ATOM 1762 CG ASP 1 216 21.375 16.629 46.662 1.00 3.90
ATOM 1763 OD1 ASP 1 216 20.696 17.393 45.926 1.00 3.90

ATOM 1764 OD2 ASP 1 216 21.495 15.389 46.468 1.00 3.90
ATOM 1765 N LYS 1 217 20.165 19.463 49.680 1.00 3.84
ATOM 1766 CA LYS 1 217 18.980 19.529 50.495 1.00 3.84
ATOM 1767 C LYS 1 217 17.745 19.722 49.660 1.00 3.84
ATOM 1768 O LYS 1 217 16.658 19.309 50.062 1.00 3.84
ATOM 1769 CB LYS 1 217 19.089 20.703 51.485 1.00 3.84
ATOM 1770 CG LYS 1 217 17.973 20.790 52.519 1.00 3.84
ATOM 1771 CD LYS 1 217 18.318 21.703 53.696 1.00 3.84
ATOM 1772 CE LYS 1 217 17.234 21.758 54.772 1.00 3.84
ATOM 1773 NZ LYS 1 217 17.690 22.596 55.904 1.00 3.84
ATOM 1774 N THR 1 218 17.873 20.315 48.459 1.00 5.26
ATOM 1775 CA THR 1 218 16.766 20.514 47.558 1.00 5.26
ATOM 1776 C THR 1 218 16.108 19.182 47.278 1.00 5.26
ATOM 1777 O THR 1 218 14.979 19.132 46.791 1.00 5.26
ATOM 1778 CB THR 1 218 17.160 21.119 46.242 1.00 5.26
ATOM 1779 OG1 THR 1 218 16.001 21.528 45.529 1.00 5.26
ATOM 1780 CG2 THR 1 218 17.941 20.077 45.425 1.00 5.26
ATOM 1781 N MET 1 219 16.808 18.067 47.597 1.00 6.69
ATOM 1782 CA MET 1 219 16.430 16.677 47.470 1.00 6.69
ATOM 1783 C MET 1 219 15.188 16.447 48.280 1.00 6.69
ATOM 1784 O MET 1 219 14.613 15.356 48.276 1.00 6.69
ATOM 1785 CB MET 1 219 17.524 15.707 47.938 1.00 6.69
ATOM 1786 CG MET 1 219 17.292 14.281 47.443 1.00 6.69
ATOM 1787 SD MET 1 219 17.338 14.138 45.631 1.00 6.69
ATOM 1788 CE MET 1 219 19.001 14.846 45.455 1.00 6.69
ATOM 1789 N SER 1 220 14.809 17.467 49.072 1.00 4.00
ATOM 1790 CA SER 1 220 13.621 17.455 49.863 1.00 4.00
ATOM 1791 C SER 1 220 13.977 16.815 51.147 1.00 4.00
ATOM 1792 O SER 1 220 13.140 16.226 51.829 1.00 4.00
ATOM 1793 CB SER 1 220 12.434 16.720 49.215 1.00 4.00
ATOM 1794 OG SER 1 220 11.988 17.433 48.070 1.00 4.00
ATOM 1795 N ILE 1 221 15.270 16.937 51.492 1.00 4.77
ATOM 1796 CA ILE 1 221 15.760 16.481 52.750 1.00 4.77
ATOM 1797 C ILE 1 221 15.799 17.683 53.634 1.00 4.77
ATOM 1798 O ILE 1 221 16.357 18.715 53.274 1.00 4.77
ATOM 1799 CB ILE 1 221 17.158 15.938 52.702 1.00 4.77
ATOM 1800 CG1 ILE 1 221 17.582 15.490 54.109 1.00 4.77
ATOM 1801 CG2 ILE 1 221 18.086 16.978 52.051 1.00 4.77
ATOM 1802 CD1 ILE 1 221 18.995 14.921 54.165 1.00 4.77
ATOM 1803 N GLU 1 222 15.194 17.590 54.828 1.00 2.49
ATOM 1804 CA GLU 1 222 15.181 18.727 55.697 1.00 2.49
ATOM 1805 C GLU 1 222 16.154 18.509 56.812 1.00 2.49
ATOM 1806 O GLU 1 222 16.209 17.431 57.400 1.00 2.49
ATOM 1807 CB GLU 1 222 13.785 18.987 56.299 1.00 2.49
ATOM 1808 CG GLU 1 222 13.710 20.127 57.317 1.00 2.49
ATOM 1809 CD GLU 1 222 13.663 19.508 58.708 1.00 2.49
ATOM 1810 OE1 GLU 1 222 14.638 18.802 59.081 1.00 2.49
ATOM 1811 OE2 GLU 1 222 12.643 19.728 59.417 1.00 2.49
ATOM 1812 N PHE 1 223 16.977 19.540 57.101 1.00 0.93

ATOM 1813 CA PHE 1 223 17.919 19.483 58.185 1.00 0.93
ATOM 1814 C PHE 1 223 17.459 20.474 59.211 1.00 0.93
ATOM 1815 O PHE 1 223 17.096 21.603 58.886 1.00 0.93
ATOM 1816 CB PHE 1 223 19.359 19.891 57.805 1.00 0.93
ATOM 1817 CG PHE 1 223 20.012 18.809 57.010 1.00 0.93
ATOM 1818 CD1 PHE 1 223 19.727 18.645 55.674 1.00 0.93
ATOM 1819 CD2 PHE 1 223 21.011 18.046 57.574 1.00 0.93
ATOM 1820 CE1 PHE 1 223 20.394 17.701 54.928 1.00 0.93
ATOM 1821 CE2 PHE 1 223 21.686 17.104 56.833 1.00 0.93
ATOM 1822 CZ PHE 1 223 21.372 16.927 55.507 1.00 0.93
ATOM 1823 N PRO 1 224 17.471 20.069 60.453 1.00 5.86
ATOM 1824 CA PRO 1 224 17.050 20.922 61.534 1.00 5.86
ATOM 1825 C PRO 1 224 18.090 21.970 61.789 1.00 5.86
ATOM 1826 O PRO 1 224 19.202 21.841 61.282 1.00 5.86
ATOM 1827 CB PRO 1 224 16.789 19.996 62.727 1.00 5.86
ATOM 1828 CG PRO 1 224 17.402 18.643 62.320 1.00 5.86
ATOM 1829 CD PRO 1 224 17.344 18.662 60.787 1.00 5.86
ATOM 1830 N GLU 1 225 17.739 23.020 62.559 1.00 2.88
ATOM 1831 CA GLU 1 225 18.615 24.135 62.793 1.00 2.88
ATOM 1832 C GLU 1 225 19.892 23.801 63.507 1.00 2.88
ATOM 1833 O GLU 1 225 20.962 24.232 63.082 1.00 2.88
ATOM 1834 CB GLU 1 225 17.942 25.263 63.597 1.00 2.88
ATOM 1835 CG GLU 1 225 16.853 26.013 62.825 1.00 2.88
ATOM 1836 CD GLU 1 225 15.579 25.180 62.839 1.00 2.88
ATOM 1837 OE1 GLU 1 225 15.375 24.422 63.825 1.00 2.88
ATOM 1838 OE2 GLU 1 225 14.790 25.294 61.863 1.00 2.88
ATOM 1839 N MET 1 226 19.833 23.028 64.608 1.00 6.09
ATOM 1840 CA MET 1 226 21.035 22.758 65.350 1.00 6.09
ATOM 1841 C MET 1 226 22.000 21.956 64.535 1.00 6.09
ATOM 1842 O MET 1 226 23.203 22.213 64.549 1.00 6.09
ATOM 1843 CB MET 1 226 20.783 21.997 66.666 1.00 6.09
ATOM 1844 CG MET 1 226 20.163 20.610 66.483 1.00 6.09
ATOM 1845 SD MET 1 226 18.403 20.624 66.032 1.00 6.09
ATOM 1846 CE MET 1 226 17.830 20.977 67.719 1.00 6.09
ATOM 1847 N LEU 1 227 21.491 20.948 63.806 1.00 0.72
ATOM 1848 CA LEU 1 227 22.336 20.113 63.004 1.00 0.72
ATOM 1849 C LEU 1 227 22.918 20.921 61.894 1.00 0.72
ATOM 1850 O LEU 1 227 24.082 20.756 61.533 1.00 0.72
ATOM 1851 CB LEU 1 227 21.582 18.934 62.364 1.00 0.72
ATOM 1852 CG LEU 1 227 22.481 18.028 61.504 1.00 0.72
ATOM 1853 CD1 LEU 1 227 23.563 17.344 62.352 1.00 0.72
ATOM 1854 CD2 LEU 1 227 21.647 17.030 60.684 1.00 0.72
ATOM 1855 N ALA 1 228 22.109 21.828 61.320 1.00 0.66
ATOM 1856 CA ALA 1 228 22.574 22.629 60.228 1.00 0.66
ATOM 1857 C ALA 1 228 23.726 23.463 60.695 1.00 0.66
ATOM 1858 O ALA 1 228 24.706 23.638 59.972 1.00 0.66
ATOM 1859 CB ALA 1 228 21.497 23.587 59.693 1.00 0.66
ATOM 1860 N GLU 1 229 23.645 24.002 61.925 1.00 4.93
ATOM 1861 CA GLU 1 229 24.691 24.869 62.386 1.00 4.93

ATOM 1862 C GLU 1 229 25.999 24.149 62.529 1.00 4.93
ATOM 1863 O GLU 1 229 27.039 24.667 62.125 1.00 4.93
ATOM 1864 CB GLU 1 229 24.358 25.573 63.719 1.00 4.93
ATOM 1865 CG GLU 1 229 24.354 24.672 64.954 1.00 4.93
ATOM 1866 CD GLU 1 229 25.721 24.784 65.612 1.00 4.93
ATOM 1867 OE1 GLU 1 229 26.063 23.879 66.419 1.00 4.93
ATOM 1868 OE2 GLU 1 229 26.440 25.778 65.321 1.00 4.93
ATOM 1869 N ILE 1 230 25.992 22.927 63.095 1.00 5.97
ATOM 1870 CA ILE 1 230 27.224 22.216 63.298 1.00 5.97
ATOM 1871 C ILE 1 230 27.828 21.845 61.978 1.00 5.97
ATOM 1872 O ILE 1 230 29.046 21.898 61.806 1.00 5.97
ATOM 1873 CB ILE 1 230 27.042 20.975 64.125 1.00 5.97
ATOM 1874 CG1 ILE 1 230 28.399 20.479 64.647 1.00 5.97
ATOM 1875 CG2 ILE 1 230 26.271 19.943 63.286 1.00 5.97
ATOM 1876 CD1 ILE 1 230 28.275 19.512 65.823 1.00 5.97
ATOM 1877 N ILE 1 231 26.982 21.458 61.005 1.00 3.96
ATOM 1878 CA ILE 1 231 27.466 21.066 59.710 1.00 3.96
ATOM 1879 C ILE 1 231 28.172 22.240 59.102 1.00 3.96
ATOM 1880 O ILE 1 231 29.322 22.149 58.675 1.00 3.96
ATOM 1881 CB ILE 1 231 26.339 20.766 58.749 1.00 3.96
ATOM 1882 CG1 ILE 1 231 25.418 19.622 59.220 1.00 3.96
ATOM 1883 CG2 ILE 1 231 26.972 20.489 57.375 1.00 3.96
ATOM 1884 CD1 ILE 1 231 26.017 18.227 59.087 1.00 3.96
ATOM 1885 N THR 1 232 27.496 23.400 59.089 1.00 0.77
ATOM 1886 CA THR 1 232 28.027 24.564 58.444 1.00 0.77
ATOM 1887 C THR 1 232 29.275 25.027 59.109 1.00 0.77
ATOM 1888 O THR 1 232 30.232 25.418 58.442 1.00 0.77
ATOM 1889 CB THR 1 232 27.062 25.713 58.456 1.00 0.77
ATOM 1890 OG1 THR 1 232 25.861 25.351 57.791 1.00 0.77
ATOM 1891 CG2 THR 1 232 27.716 26.913 57.749 1.00 0.77
ATOM 1892 N ASN 1 233 29.303 25.013 60.451 1.00 2.07
ATOM 1893 CA ASN 1 233 30.466 25.538 61.089 1.00 2.07
ATOM 1894 C ASN 1 233 31.704 24.742 60.810 1.00 2.07
ATOM 1895 O ASN 1 233 32.734 25.302 60.450 1.00 2.07
ATOM 1896 CB ASN 1 233 30.309 25.644 62.614 1.00 2.07
ATOM 1897 CG ASN 1 233 29.322 26.763 62.916 1.00 2.07
ATOM 1898 OD1 ASN 1 233 28.277 26.880 62.278 1.00 2.07
ATOM 1899 ND2 ASN 1 233 29.668 27.620 63.914 1.00 2.07
ATOM 1900 N GLN 1 234 31.676 23.431 61.097 1.00 2.81
ATOM 1901 CA GLN 1 234 32.824 22.592 60.914 1.00 2.81
ATOM 1902 C GLN 1 234 33.052 21.633 59.765 1.00 2.81
ATOM 1903 O GLN 1 234 34.201 21.356 59.425 1.00 2.81
ATOM 1904 CB GLN 1 234 33.166 21.915 62.226 1.00 2.81
ATOM 1905 CG GLN 1 234 33.523 22.907 63.332 1.00 2.81
ATOM 1906 CD GLN 1 234 34.798 23.627 62.926 1.00 2.81
ATOM 1907 OE1 GLN 1 234 35.186 24.630 63.522 1.00 2.81
ATOM 1908 NE2 GLN 1 234 35.473 23.099 61.873 1.00 2.81
ATOM 1909 N ILE 1 235 31.996 21.074 59.135 1.00 7.20
ATOM 1910 CA ILE 1 235 32.227 19.974 58.228 1.00 7.20

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ATOM  1911  C   ILE 1 235    33.138  20.265  57.073  1.00  7.20
ATOM  1912  O   ILE 1 235    33.936  19.389  56.735  1.00  7.20
ATOM  1913  CB  ILE 1 235    30.964  19.231  57.793  1.00  7.20
ATOM  1914  CG1 ILE 1 235    31.296  17.943  57.019  1.00  7.20
ATOM  1915  CG2 ILE 1 235    30.038  20.138  56.975  1.00  7.20
ATOM  1916  CD1 ILE 1 235    31.720  18.184  55.569  1.00  7.20
ATOM  1917  N   PRO 1 236    33.124  21.394  56.428  1.00  1.16
ATOM  1918  CA  PRO 1 236    34.020  21.577  55.326  1.00  1.16
ATOM  1919  C   PRO 1 236    35.435  21.530  55.806  1.00  1.16
ATOM  1920  O   PRO 1 236    36.296  21.042  55.076  1.00  1.16
ATOM  1921  CB  PRO 1 236    33.632  22.909  54.688  1.00  1.16
ATOM  1922  CG  PRO 1 236    32.150  23.083  55.073  1.00  1.16
ATOM  1923  CD  PRO 1 236    32.015  22.333  56.408  1.00  1.16
ATOM  1924  N   LYS 1 237    35.698  22.041  57.025  1.00  4.23
ATOM  1925  CA  LYS 1 237    37.028  22.057  57.557  1.00  4.23
ATOM  1926  C   LYS 1 237    37.491  20.659  57.812  1.00  4.23
ATOM  1927  O   LYS 1 237    38.618  20.303  57.473  1.00  4.23
ATOM  1928  CB  LYS 1 237    37.154  22.792  58.903  1.00  4.23
ATOM  1929  CG  LYS 1 237    36.913  24.300  58.836  1.00  4.23
ATOM  1930  CD  LYS 1 237    36.890  24.960  60.217  1.00  4.23
ATOM  1931  CE  LYS 1 237    36.604  26.462  60.190  1.00  4.23
ATOM  1932  NZ  LYS 1 237    35.143  26.695  60.175  1.00  4.23
ATOM  1933  N   TYR 1 238    36.620  19.820  58.410  1.00  1.32
ATOM  1934  CA  TYR 1 238    37.004  18.473  58.743  1.00  1.32
ATOM  1935  C   TYR 1 238    37.385  17.756  57.503  1.00  1.32
ATOM  1936  O   TYR 1 238    38.418  17.094  57.438  1.00  1.32
ATOM  1937  CB  TYR 1 238    35.862  17.534  59.149  1.00  1.32
ATOM  1938  CG  TYR 1 238    35.233  18.013  60.377  1.00  1.32
ATOM  1939  CD1 TYR 1 238    35.842  17.772  61.578  1.00  1.32
ATOM  1940  CD2 TYR 1 238    34.006  18.620  60.309  1.00  1.32
ATOM  1941  CE1 TYR 1 238    35.279  18.269  62.716  1.00  1.32
ATOM  1942  CE2 TYR 1 238    33.436  19.101  61.451  1.00  1.32
ATOM  1943  CZ  TYR 1 238    34.106  18.973  62.640  1.00  1.32
ATOM  1944  OH  TYR 1 238    33.673  19.698  63.760  1.00  1.32
ATOM  1945  N   SER 1 239    36.514  17.867  56.489  1.00  3.15
ATOM  1946  CA  SER 1 239    36.681  17.123  55.279  1.00  3.15
ATOM  1947  C   SER 1 239    37.975  17.507  54.646  1.00  3.15
ATOM  1948  O   SER 1 239    38.677  16.668  54.084  1.00  3.15
ATOM  1949  CB  SER 1 239    35.564  17.398  54.258  1.00  3.15
ATOM  1950  OG  SER 1 239    35.780  16.633  53.081  1.00  3.15
ATOM  1951  N   ASN 1 240    38.318  18.802  54.734  1.00  0.86
ATOM  1952  CA  ASN 1 240    39.522  19.324  54.162  1.00  0.86
ATOM  1953  C   ASN 1 240    40.702  18.696  54.842  1.00  0.86
ATOM  1954  O   ASN 1 240    41.765  18.555  54.242  1.00  0.86
ATOM  1955  CB  ASN 1 240    39.644  20.850  54.319  1.00  0.86
ATOM  1956  CG  ASN 1 240    38.554  21.496  53.475  1.00  0.86
ATOM  1957  OD1 ASN 1 240    38.152  20.962  52.442  1.00  0.86
ATOM  1958  ND2 ASN 1 240    38.059  22.679  53.925  1.00  0.86
ATOM  1959  N   GLY 1 241    40.561  18.294  56.119  1.00  0.83
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ATOM 1960 CA GLY 1 241 41.697 17.718 56.787 1.00 0.83
ATOM 1961 C GLY 1 241 42.399 18.795 57.555 1.00 0.83
ATOM 1962 O GLY 1 241 43.590 18.708 57.850 1.00 0.83
ATOM 1963 N ASN 1 242 41.635 19.849 57.875 1.00 2.92
ATOM 1964 CA ASN 1 242 42.002 21.027 58.606 1.00 2.92
ATOM 1965 C ASN 1 242 42.169 20.756 60.070 1.00 2.92
ATOM 1966 O ASN 1 242 42.453 21.686 60.813 1.00 2.92
ATOM 1967 CB ASN 1 242 40.955 22.145 58.488 1.00 2.92
ATOM 1968 CG ASN 1 242 40.942 22.624 57.046 1.00 2.92
ATOM 1969 OD1 ASN 1 242 40.035 23.340 56.624 1.00 2.92
ATOM 1970 ND2 ASN 1 242 41.975 22.212 56.264 1.00 2.92
ATOM 1971 N ILE 1 243 41.868 19.533 60.551 1.00 9.49
ATOM 1972 CA ILE 1 243 41.910 19.235 61.960 1.00 9.49
ATOM 1973 C ILE 1 243 42.936 18.170 62.206 1.00 9.49
ATOM 1974 O ILE 1 243 43.381 17.497 61.278 1.00 9.49
ATOM 1975 CB ILE 1 243 40.570 18.707 62.420 1.00 9.49
ATOM 1976 CG1 ILE 1 243 39.491 19.762 62.159 1.00 9.49
ATOM 1977 CG2 ILE 1 243 40.625 18.309 63.901 1.00 9.49
ATOM 1978 CD1 ILE 1 243 39.734 21.041 62.954 1.00 9.49
ATOM 1979 N LYS 1 244 43.387 18.011 63.470 1.00 6.69
ATOM 1980 CA LYS 1 244 44.315 16.949 63.696 1.00 6.69
ATOM 1981 C LYS 1 244 43.670 15.828 64.449 1.00 6.69
ATOM 1982 O LYS 1 244 43.232 15.951 65.587 1.00 6.69
ATOM 1983 CB LYS 1 244 45.660 17.380 64.330 1.00 6.69
ATOM 1984 CG LYS 1 244 45.628 18.055 65.702 1.00 6.69
ATOM 1985 CD LYS 1 244 45.487 17.102 66.888 1.00 6.69
ATOM 1986 CE LYS 1 244 44.224 17.349 67.705 1.00 6.69
ATOM 1987 NZ LYS 1 244 44.078 16.337 68.763 1.00 6.69
ATOM 1988 N LYS 1 245 43.565 14.675 63.771 1.00 7.88
ATOM 1989 CA LYS 1 245 42.994 13.498 64.343 1.00 7.88
ATOM 1990 C LYS 1 245 43.983 12.850 65.261 1.00 7.88
ATOM 1991 O LYS 1 245 45.162 12.739 64.936 1.00 7.88
ATOM 1992 CB LYS 1 245 42.480 12.569 63.221 1.00 7.88
ATOM 1993 CG LYS 1 245 42.550 11.058 63.427 1.00 7.88
ATOM 1994 CD LYS 1 245 43.799 10.426 62.802 1.00 7.88
ATOM 1995 CE LYS 1 245 45.020 10.292 63.705 1.00 7.88
ATOM 1996 NZ LYS 1 245 46.153 9.761 62.911 1.00 7.88
ATOM 1997 N LEU 1 246 43.525 12.433 66.461 1.00 1.24
ATOM 1998 CA LEU 1 246 44.406 11.806 67.410 1.00 1.24
ATOM 1999 C LEU 1 246 44.362 10.349 67.118 1.00 1.24
ATOM 2000 O LEU 1 246 43.285 9.777 66.956 1.00 1.24
ATOM 2001 CB LEU 1 246 43.975 11.978 68.876 1.00 1.24
ATOM 2002 CG LEU 1 246 44.138 13.418 69.380 1.00 1.24
ATOM 2003 CD1 LEU 1 246 43.705 13.561 70.848 1.00 1.24
ATOM 2004 CD2 LEU 1 246 45.582 13.893 69.147 1.00 1.24
ATOM 2005 N LEU 1 247 45.546 9.712 67.038 1.00 6.31
ATOM 2006 CA LEU 1 247 45.532 8.332 66.672 1.00 6.31
ATOM 2007 C LEU 1 247 46.366 7.621 67.690 1.00 6.31
ATOM 2008 O LEU 1 247 47.468 8.058 68.016 1.00 6.31

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ATOM  2009 CB  LEU 1 247    46.199  8.117 65.308 1.00 6.31
ATOM  2010 CG  LEU 1 247    45.682  6.894 64.552 1.00 6.31
ATOM  2011 CD1 LEU 1 247    45.821  5.604 65.373 1.00 6.31
ATOM  2012 CD2 LEU 1 247    44.263  7.166 64.025 1.00 6.31
ATOM  2013 N   PHE 1 248    45.836  6.519 68.249 1.00 1.30
ATOM  2014 CA  PHE 1 248    46.539  5.746 69.229 1.00 1.30
ATOM  2015 C   PHE 1 248    47.648  4.947 68.648 1.00 1.30
ATOM  2016 O   PHE 1 248    48.649  4.687 69.313 1.00 1.30
ATOM  2017 CB  PHE 1 248    45.620  4.819 69.985 1.00 1.30
ATOM  2018 CG  PHE 1 248    44.791  5.716 70.834 1.00 1.30
ATOM  2019 CD1 PHE 1 248    45.240  6.092 72.080 1.00 1.30
ATOM  2020 CD2 PHE 1 248    43.504  6.020 70.458 1.00 1.30
ATOM  2021 CE1 PHE 1 248    44.419  6.778 72.942 1.00 1.30
ATOM  2022 CE2 PHE 1 248    42.682  6.713 71.314 1.00 1.30
ATOM  2023 CZ  PHE 1 248    43.133  7.075 72.562 1.00 1.30
ATOM  2024 N   HIS 1 249    47.487  4.497 67.396 1.00 3.57
ATOM  2025 CA  HIS 1 249    48.517  3.689 66.830 1.00 3.57
ATOM  2026 C   HIS 1 249    49.182  4.514 65.786 1.00 3.57
ATOM  2027 O   HIS 1 249    48.535  5.300 65.096 1.00 3.57
ATOM  2028 CB  HIS 1 249    47.959  2.401 66.206 1.00 3.57
ATOM  2029 CG  HIS 1 249    47.126  1.638 67.200 1.00 3.57
ATOM  2030 ND1 HIS 1 249    45.750  1.671 67.235 1.00 3.57
ATOM  2031 CD2 HIS 1 249    47.501  0.877 68.264 1.00 3.57
ATOM  2032 CE1 HIS 1 249    45.364  0.929 68.304 1.00 3.57
ATOM  2033 NE2 HIS 1 249    46.393  0.428 68.961 1.00 3.57
ATOM  2034 N   GLN 1 250    50.513  4.352 65.668 1.00 3.06
ATOM  2035 CA  GLN 1 250    51.307  5.130 64.766 1.00 3.06
ATOM  2036 C   GLN 1 250    50.873  4.894 63.360 1.00 3.06
ATOM  2037 O   GLN 1 250    49.793  4.366 63.101 1.00 3.06
ATOM  2038 CB  GLN 1 250    52.808  4.803 64.849 1.00 3.06
ATOM  2039 CG  GLN 1 250    53.426  5.104 66.217 1.00 3.06
ATOM  2040 CD  GLN 1 250    54.901  4.737 66.158 1.00 3.06
ATOM  2041 OE1 GLN 1 250    54.148  5.443 65.498 1.00 3.06
ATOM  2042 NE2 GLN 1 250    54.829  3.928 67.254 1.00 3.06
ATOM  2043 N   LYS 1 251    51.730  5.314 62.409 1.00 8.59
ATOM  2044 CA  LYS 1 251    51.464  5.195 61.006 1.00 8.59
ATOM  2045 C   LYS 1 251    50.081  5.753 60.685 1.00 8.59
ATOM  2046 O   LYS 1 251    49.467  6.412 61.567 1.00 8.59
ATOM  2047 CB  LYS 1 251    51.578  3.750 60.471 1.00 8.59
ATOM  2048 CG  LYS 1 251    50.546  2.755 61.013 1.00 8.59
ATOM  2049 CD  LYS 1 251    49.124  2.976 60.490 1.00 8.59
ATOM  2050 CE  LYS 1 251    49.003  2.835 58.971 1.00 8.59
ATOM  2051 NZ  LYS 1 251    47.603  3.062 58.549 1.00 8.59
ATOM  2052 OXT LYS 1 251    49.624  5.533 59.532 1.00 8.59
END
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Fig 14

Sequence alignment of ER and GR used for the conformation of the C-terminal -helix (helix 12) in a PR-based GR-model for the study of binding of antagonists.

```
gr_er     522   PATLPQLTPT LVSLLEVIEP EVLYAGYDSS VPDSTWRIMT TLNMLGGRQV
lerr      307     ALSLTADQ MVSALLDAEP PILYSEYDPT RPFSEASMMG LLTNLADREL
                  .*.  .   .** *   **  .**. **..  * *   .*   *  *. *..

gr_er     572   IAAVKWAKAI PGFRNLHLDD QMTLLQYSWM FLMAFALGWR SYRQSSANLL
lerr      355   VHMINWAKRV PGFVDLTLHD QVHLLECAWL EILMIGLVWR SMEHPG--KL
                .  ..*** . *** .* * * *. **. .*.  .. ..* ** *  ...   *

gr_er     622   CFAPDLIINE QRMTLP-CMY DQCKHMLYVS SELHRLQVSY EEYLCMKTLL
lerr      403   LFAPNLLLDR NQGKCVEGMV EIFDMLLATS SRFRMMNLQG EEFVCLKSII
                 ***.*...   .      *  .    .* * * .. . .   **..*.*...

gr_er     671   LLSSVPKDGL KSQELFDEIR MTYIKELGKA IVKREG--NS S-QNWQRFYQ
lerr      453   LLNSGVY--- ---EEKDHIH RVLDKITDTL IHLMAKAGLT LQQQHQRLAQ
                **.*          *  * *.     *      *         .   *  **. *

gr_er     718   LTKLLDSMHE VVENLLNYCF QTFLDKTMSI EFPEMLAEII TNQ
lerr      507   LLLILSHIRH MSNKGMEHLY SM-------P L-YDLLLEML DAH
                *  .*  ..  . .. ..  .              ..* *..   .
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* = identical amino acid residue
. = conservative amino acid substitution

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FIG. 15.

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HEADER   PROTEIN                    28-FEB-100
COMPND   GR_ER_RAL
AUTHOR   GENERATED BY SYBYL, A PRODUCT OF TRIPOS, INC.
SEQRES  1 1  240  PRO ALA THR LEU PRO GLN LEU THR PRO THR LEU VAL SER
SEQRES  2 1  240  LEU LEU GLU VAL ILE GLU PRO GLU VAL LEU TYR ALA GLY
SEQRES  3 1  240  TYR ASP SER SER VAL PRO ASP SER THR TRP ARG ILE MET
SEQRES  4 1  240  THR THR LEU ASN MET LEU GLY GLY ARG GLN VAL ILE ALA
SEQRES  5 1  240  ALA VAL LYS TRP ALA LYS ALA ILE PRO GLY PHE ARG ASN
SEQRES  6 1  240  LEU HIS LEU ASP ASP GLN MET THR LEU LEU GLN TYR SER
SEQRES  7 1  240  TRP MET PHE LEU MET ALA PHE ALA LEU GLY TRP ARG SER
SEQRES  8 1  240  TYR ARG GLN SER SER ALA ASN LEU LEU CYS PHE ALA PRO
SEQRES  9 1  240  ASP LEU ILE ILE ASN GLU GLN ARG MET THR LEU PRO CYS
SEQRES 10 1  240  MET TYR ASP GLN CYS LYS HIS MET LEU TYR VAL SER SER
SEQRES 11 1  240  GLU LEU HIS ARG LEU GLN VAL SER TYR GLU GLU TYR LEU
SEQRES 12 1  240  CYS MET LYS THR LEU LEU LEU LEU SER SER VAL PRO LYS
SEQRES 13 1  240  ASP GLY LEU LYS SER GLN GLU LEU PHE ASP GLU ILE ARG
SEQRES 14 1  240  MET THR TYR ILE LYS GLU LEU GLY LYS ALA ILE VAL LYS
SEQRES 15 1  240  ARG GLU GLY ASN SER SER GLN ASN TRP GLN ARG PHE TYR
SEQRES 16 1  240  GLN LEU THR LYS LEU LEU ASP SER MET HIS GLU VAL VAL
SEQRES 17 1  240  GLU ASN LEU LEU ASN TYR CYS PHE GLN THR PHE LEU ASP
SEQRES 18 1  240  LYS THR MET SER ILE GLU PHE PRO GLU MET LEU ALA GLU
SEQRES 19 1  240  ILE ILE THR ASN GLN ILE
ATOM    1  N   PRO 1 522   -16.028  23.289  -6.590  1.00  0.53
ATOM    2  CA  PRO 1 522   -14.607  22.883  -6.755  1.00  0.53
ATOM    3  C   PRO 1 522   -13.778  23.929  -6.090  1.00  0.53
ATOM    4  O   PRO 1 522   -13.771  25.067  -6.553  1.00  0.53
ATOM    5  CB  PRO 1 522   -14.354  22.795  -8.259  1.00  0.53
ATOM    6  CG  PRO 1 522   -15.411  23.713  -8.885  1.00  0.53
ATOM    7  CD  PRO 1 522   -16.614  23.612  -7.935  1.00  0.53
ATOM    8  N   ALA 1 523   -13.092  23.572  -4.988  1.00  0.45
ATOM    9  CA  ALA 1 523   -12.249  24.517  -4.317  1.00  0.45
ATOM    10 C   ALA 1 523   -11.040  23.762  -3.879  1.00  0.45
ATOM    11 O   ALA 1 523   -10.754  23.666  -2.687  1.00  0.45
ATOM    12 CB  ALA 1 523   -12.896  25.104  -3.051  1.00  0.45
ATOM    13 N   THR 1 524   -10.294  23.202  -4.846  1.00  0.32
ATOM    14 CA  THR 1 524    -9.142  22.418  -4.509  1.00  0.32
ATOM    15 C   THR 1 524    -8.086  23.314  -3.949  1.00  0.32
ATOM    16 O   THR 1 524    -7.626  23.140  -2.823  1.00  0.32
ATOM    17 CB  THR 1 524    -8.553  21.728  -5.703  1.00  0.32
ATOM    18 OG1 THR 1 524    -9.511  20.859  -6.289  1.00  0.32
ATOM    19 CG2 THR 1 524    -7.316  20.931  -5.257  1.00  0.32
ATOM    20 N   LEU 1 525    -7.686  24.309  -4.755  1.00  0.35
ATOM    21 CA  LEU 1 525    -6.691  25.285  -4.414  1.00  0.35
ATOM    22 C   LEU 1 525    -7.181  26.176  -3.307  1.00  0.35
ATOM    23 O   LEU 1 525    -6.374  26.650  -2.509  1.00  0.35
ATOM    24 CB  LEU 1 525    -6.316  26.182  -5.605  1.00  0.35
ATOM    25 CG  LEU 1 525    -5.676  25.395  -6.764  1.00  0.35
ATOM    26 CD1 LEU 1 525    -5.297  26.322  -7.929  1.00  0.35
ATOM    27 CD2 LEU 1 525    -4.502  24.534  -6.267  1.00  0.35
ATOM    28 N   PRO 1 526    -8.450  26.471  -3.226  1.00  0.52
ATOM    29 CA  PRO 1 526    -8.883  27.338  -2.161  1.00  0.52
ATOM    30 C   PRO 1 526    -8.844  26.769  -0.776  1.00  0.52
ATOM    31 O   PRO 1 526    -9.013  27.542   0.166  1.00  0.52
ATOM    32 CB  PRO 1 526   -10.267  27.842  -2.564  1.00  0.52
ATOM    33 CG  PRO 1 526   -10.218  27.841  -4.098  1.00  0.52
ATOM    34 CD  PRO 1 526    -9.224  26.723  -4.438  1.00  0.52
ATOM    35 N   GLN 1 527    -8.645  25.450  -0.600  1.00  0.57
ATOM    36 CA  GLN 1 527    -8.683  24.919   0.734  1.00  0.57
ATOM    37 C   GLN 1 527    -7.482  25.412   1.476  1.00  0.57
ATOM    38 O   GLN 1 527    -6.393  25.495   0.914  1.00  0.57
ATOM    39 CB  GLN 1 527    -8.653  23.380   0.770  1.00  0.57
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ATOM   40 CG  GLN 1 527    -9.756 22.711 -0.059 1.00 0.57
ATOM   41 CD  GLN 1 527   -11.110 22.880  0.620 1.00 0.57
ATOM   42 OE1 GLN 1 527   -12.023 22.093  0.375 1.00 0.57
ATOM   43 NE2 GLN 1 527   -11.257 23.918  1.487 1.00 0.57
ATOM   44 N   LEU 1 528    -7.636 25.784  2.763 1.00 0.58
ATOM   45 CA  LEU 1 528    -6.462 26.195  3.479 1.00 0.58
ATOM   46 C   LEU 1 528    -5.801 24.950  3.965 1.00 0.58
ATOM   47 O   LEU 1 528    -6.331 23.854  3.792 1.00 0.58
ATOM   48 CB  LEU 1 528    -6.675 27.159  4.667 1.00 0.58
ATOM   49 CG  LEU 1 528    -7.694 26.722  5.733 1.00 0.58
ATOM   50 CD1 LEU 1 528    -7.801 27.774  6.850 1.00 0.58
ATOM   51 CD2 LEU 1 528    -9.065 26.444  5.109 1.00 0.58
ATOM   52 N   THR 1 529    -4.612 25.079  4.583 1.00 0.58
ATOM   53 CA  THR 1 529    -3.936 23.879  4.963 1.00 0.58
ATOM   54 C   THR 1 529    -4.770 23.095  5.934 1.00 0.58
ATOM   55 O   THR 1 529    -4.788 21.870  5.819 1.00 0.58
ATOM   56 CB  THR 1 529    -2.501 24.061  5.426 1.00 0.58
ATOM   57 OG1 THR 1 529    -1.946 22.797  5.757 1.00 0.58
ATOM   58 CG2 THR 1 529    -2.363 25.038  6.602 1.00 0.58
ATOM   59 N   PRO 1 530    -5.490 23.667  6.870 1.00 0.40
ATOM   60 CA  PRO 1 530    -6.256 22.847  7.763 1.00 0.40
ATOM   61 C   PRO 1 530    -7.366 22.137  7.055 1.00 0.40
ATOM   62 O   PRO 1 530    -7.691 21.014  7.434 1.00 0.40
ATOM   63 CB  PRO 1 530    -6.764 23.777  8.864 1.00 0.40
ATOM   64 CG  PRO 1 530    -5.753 24.936  8.868 1.00 0.40
ATOM   65 CD  PRO 1 530    -5.255 24.995  7.414 1.00 0.40
ATOM   66 N   THR 1 531    -7.983 22.770  6.042 1.00 0.29
ATOM   67 CA  THR 1 531    -9.075 22.121  5.380 1.00 0.29
ATOM   68 C   THR 1 531    -8.576 20.949  4.613 1.00 0.29
ATOM   69 O   THR 1 531    -9.227 19.906  4.578 1.00 0.29
ATOM   70 CB  THR 1 531    -9.836 22.998  4.432 1.00 0.29
ATOM   71 OG1 THR 1 531   -10.469 24.049  5.145 1.00 0.29
ATOM   72 CG2 THR 1 531   -10.891 22.143  3.711 1.00 0.29
ATOM   73 N   LEU 1 532    -7.401 21.081  3.976 1.00 0.43
ATOM   74 CA  LEU 1 532    -6.959 19.997  3.159 1.00 0.43
ATOM   75 C   LEU 1 532    -6.677 18.816  4.031 1.00 0.43
ATOM   76 O   LEU 1 532    -7.015 17.685  3.683 1.00 0.43
ATOM   77 CB  LEU 1 532    -5.747 20.340  2.265 1.00 0.43
ATOM   78 CG  LEU 1 532    -4.353 20.319  2.913 1.00 0.43
ATOM   79 CD1 LEU 1 532    -3.873 18.879  3.165 1.00 0.43
ATOM   80 CD2 LEU 1 532    -3.361 21.138  2.069 1.00 0.43
ATOM   81 N   VAL 1 533    -6.067 19.049  5.209 1.00 0.49
ATOM   82 CA  VAL 1 533    -5.715 17.947  6.056 1.00 0.49
ATOM   83 C   VAL 1 533    -6.944 17.239  6.527 1.00 0.49
ATOM   84 O   VAL 1 533    -6.973 16.010  6.589 1.00 0.49
ATOM   85 CB  VAL 1 533    -4.900 18.342  7.257 1.00 0.49
ATOM   86 CG1 VAL 1 533    -5.708 19.275  8.167 1.00 0.49
ATOM   87 CG2 VAL 1 533    -4.467 17.053  7.963 1.00 0.49
ATOM   88 N   SER 1 534    -7.991 18.003  6.879 1.00 0.55
ATOM   89 CA  SER 1 534    -9.207 17.441  7.387 1.00 0.55
ATOM   90 C   SER 1 534    -9.854 16.647  6.309 1.00 0.55
ATOM   91 O   SER 1 534   -10.263 15.505  6.523 1.00 0.55
ATOM   92 CB  SER 1 534   -10.207 18.537  7.772 1.00 0.55
ATOM   93 OG  SER 1 534    -9.571 19.462  8.638 1.00 0.55
ATOM   94 N   LEU 1 535    -9.927 17.235  5.100 1.00 0.57
ATOM   95 CA  LEU 1 535   -10.614 16.574  4.038 1.00 0.57
ATOM   96 C   LEU 1 535    -9.930 15.269  3.823 1.00 0.57
ATOM   97 O   LEU 1 535   -10.590 14.235  3.815 1.00 0.57
ATOM   98 CB  LEU 1 535   -10.646 17.394  2.728 1.00 0.57
ATOM   99 CG  LEU 1 535    -9.329 17.490  1.931 1.00 0.57
ATOM  100 CD1 LEU 1 535    -9.023 16.194  1.160 1.00 0.57
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ATOM   101 CD2 LEU 1 535    -9.326  18.725   1.017  1.00  0.57
ATOM   102 N   LEU 1 536    -8.585  15.266   3.780  1.00  0.36
ATOM   103 CA  LEU 1 536    -7.854  14.065   3.497  1.00  0.36
ATOM   104 C   LEU 1 536    -8.202  13.040   4.523  1.00  0.36
ATOM   105 O   LEU 1 536    -8.454  11.880   4.202  1.00  0.36
ATOM   106 CB  LEU 1 536    -6.330  14.267   3.528  1.00  0.36
ATOM   107 CG  LEU 1 536    -5.795  15.178   2.406  1.00  0.36
ATOM   108 CD1 LEU 1 536    -4.268  15.327   2.499  1.00  0.36
ATOM   109 CD2 LEU 1 536    -6.252  14.697   1.019  1.00  0.36
ATOM   110 N   GLU 1 537    -8.286  13.471   5.789  1.00  0.30
ATOM   111 CA  GLU 1 537    -8.523  12.577   6.880  1.00  0.30
ATOM   112 C   GLU 1 537    -9.791  11.829   6.603  1.00  0.30
ATOM   113 O   GLU 1 537    -9.855  10.616   6.795  1.00  0.30
ATOM   114 CB  GLU 1 537    -8.758  13.357   8.187  1.00  0.30
ATOM   115 CG  GLU 1 537    -7.578  14.236   8.617  1.00  0.30
ATOM   116 CD  GLU 1 537    -6.858  13.565   9.776  1.00  0.30
ATOM   117 OE1 GLU 1 537    -7.484  12.693  10.434  1.00  0.30
ATOM   118 OE2 GLU 1 537    -5.676  13.924  10.026  1.00  0.30
ATOM   119 N   VAL 1 538   -10.840  12.536   6.138  1.00  0.42
ATOM   120 CA  VAL 1 538   -12.105  11.892   5.920  1.00  0.42
ATOM   121 C   VAL 1 538   -12.006  10.913   4.790  1.00  0.42
ATOM   122 O   VAL 1 538   -12.638   9.860   4.833  1.00  0.42
ATOM   123 CB  VAL 1 538   -13.248  12.823   5.614  1.00  0.42
ATOM   124 CG1 VAL 1 538   -13.139  13.335   4.172  1.00  0.42
ATOM   125 CG2 VAL 1 538   -14.561  12.066   5.876  1.00  0.42
ATOM   126 N   ILE 1 539   -11.197  11.220   3.755  1.00  0.45
ATOM   127 CA  ILE 1 539   -11.156  10.375   2.592  1.00  0.45
ATOM   128 C   ILE 1 539   -10.713   9.001   2.955  1.00  0.45
ATOM   129 O   ILE 1 539   -11.189   8.053   2.331  1.00  0.45
ATOM   130 CB  ILE 1 539   -10.184  10.755   1.482  1.00  0.45
ATOM   131 CG1 ILE 1 539   -10.455  12.113   0.848  1.00  0.45
ATOM   132 CG2 ILE 1 539   -10.253   9.685   0.381  1.00  0.45
ATOM   133 CD1 ILE 1 539    -9.752  13.325   1.403  1.00  0.45
ATOM   134 N   GLU 1 540    -9.802   8.870   3.950  1.00  0.40
ATOM   135 CA  GLU 1 540    -9.162   7.620   4.284  1.00  0.40
ATOM   136 C   GLU 1 540   -10.111   6.470   4.207  1.00  0.40
ATOM   137 O   GLU 1 540   -11.258   6.517   4.643  1.00  0.40
ATOM   138 CB  GLU 1 540    -8.435   7.601   5.638  1.00  0.40
ATOM   139 CG  GLU 1 540    -7.105   8.365   5.615  1.00  0.40
ATOM   140 CD  GLU 1 540    -6.012   7.490   5.001  1.00  0.40
ATOM   141 OE1 GLU 1 540    -5.911   7.472   3.745  1.00  0.40
ATOM   142 OE2 GLU 1 540    -5.264   6.835   5.776  1.00  0.40
ATOM   143 N   PRO 1 541    -9.627   5.476   3.519  1.00  0.41
ATOM   144 CA  PRO 1 541   -10.361   4.273   3.259  1.00  0.41
ATOM   145 C   PRO 1 541   -10.454   3.492   4.522  1.00  0.41
ATOM   146 O   PRO 1 541    -9.655   3.728   5.426  1.00  0.41
ATOM   147 CB  PRO 1 541    -9.593   3.541   2.157  1.00  0.41
ATOM   148 CG  PRO 1 541    -8.192   4.181   2.174  1.00  0.41
ATOM   149 CD  PRO 1 541    -8.451   5.609   2.679  1.00  0.41
ATOM   150 N   GLU 1 542   -11.438   2.578   4.608  1.00  0.55
ATOM   151 CA  GLU 1 542   -11.611   1.777   5.784  1.00  0.55
ATOM   152 C   GLU 1 542   -10.650   0.635   5.706  1.00  0.55
ATOM   153 O   GLU 1 542   -10.161   0.290   4.632  1.00  0.55
ATOM   154 CB  GLU 1 542   -13.021   1.175   5.913  1.00  0.55
ATOM   155 CG  GLU 1 542   -13.381   0.217   4.774  1.00  0.55
ATOM   156 CD  GLU 1 542   -13.569   1.035   3.503  1.00  0.55
ATOM   157 OE1 GLU 1 542   -13.850   2.258   3.621  1.00  0.55
ATOM   158 OE2 GLU 1 542   -13.435   0.446   2.398  1.00  0.55
ATOM   159 N   VAL 1 543   -10.345   0.019   6.866  1.00  0.62
ATOM   160 CA  VAL 1 543    -9.445  -1.094   6.867  1.00  0.62
ATOM   161 C   VAL 1 543   -10.277  -2.304   6.592  1.00  0.62
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ATOM   162 O   VAL 1 543   -11.280 -2.557  7.257 1.00 0.62
ATOM   163 CB  VAL 1 543    -8.728 -1.292  8.174 1.00 0.62
ATOM   164 CG1 VAL 1 543    -7.825 -0.070  8.417 1.00 0.62
ATOM   165 CG2 VAL 1 543    -9.761 -1.519  9.291 1.00 0.62
ATOM   166 N   LEU 1 544    -9.879 -3.078  5.568 1.00 0.55
ATOM   167 CA  LEU 1 544   -10.688 -4.183  5.156 1.00 0.55
ATOM   168 C   LEU 1 544   -10.086 -5.420  5.775 1.00 0.55
ATOM   169 O   LEU 1 544    -8.950 -5.384  6.242 1.00 0.55
ATOM   170 CB  LEU 1 544   -10.673 -4.279  3.619 1.00 0.55
ATOM   171 CG  LEU 1 544   -11.936 -4.888  2.996 1.00 0.55
ATOM   172 CD1 LEU 1 544   -12.128 -6.370  3.323 1.00 0.55
ATOM   173 CD2 LEU 1 544   -13.153 -4.023  3.367 1.00 0.55
ATOM   174 N   TYR 1 545   -10.839 -6.543  5.819 1.00 0.30
ATOM   175 CA  TYR 1 545   -10.348 -7.774  6.387 1.00 0.30
ATOM   176 C   TYR 1 545   -10.140 -8.792  5.312 1.00 0.30
ATOM   177 O   TYR 1 545   -10.716 -8.721  4.228 1.00 0.30
ATOM   178 CB  TYR 1 545   -11.290 -8.448  7.403 1.00 0.30
ATOM   179 CG  TYR 1 545   -11.220 -7.730  8.701 1.00 0.30
ATOM   180 CD1 TYR 1 545   -11.929 -6.571  8.912 1.00 0.30
ATOM   181 CD2 TYR 1 545   -10.443 -8.236  9.719 1.00 0.30
ATOM   182 CE1 TYR 1 545   -11.858 -5.921 10.122 1.00 0.30
ATOM   183 CE2 TYR 1 545   -10.367 -7.590 10.930 1.00 0.30
ATOM   184 CZ  TYR 1 545   -11.075 -6.429 11.131 1.00 0.30
ATOM   185 OH  TYR 1 545   -11.002 -5.762 12.372 1.00 0.30
ATOM   186 N   ALA 1 546    -9.278 -9.785  5.615 1.00 0.14
ATOM   187 CA  ALA 1 546    -8.982 -10.841  4.694 1.00 0.14
ATOM   188 C   ALA 1 546   -10.145 -11.770  4.684 1.00 0.14
ATOM   189 O   ALA 1 546   -10.982 -11.740  5.587 1.00 0.14
ATOM   190 CB  ALA 1 546    -7.738 -11.662  5.083 1.00 0.14
ATOM   191 N   GLY 1 547   -10.216 -12.613  3.630 1.00 0.34
ATOM   192 CA  GLY 1 547   -11.275 -13.568  3.511 1.00 0.34
ATOM   193 C   GLY 1 547   -11.244 -14.321  4.785 1.00 0.34
ATOM   194 O   GLY 1 547   -10.171 -14.684  5.265 1.00 0.34
ATOM   195 N   TYR 1 548   -12.449 -14.541  5.345 1.00 0.58
ATOM   196 CA  TYR 1 548   -12.684 -15.135  6.626 1.00 0.58
ATOM   197 C   TYR 1 548   -11.775 -16.315  6.726 1.00 0.58
ATOM   198 O   TYR 1 548   -11.435 -16.897  5.699 1.00 0.58
ATOM   199 CB  TYR 1 548   -14.140 -15.607  6.753 1.00 0.58
ATOM   200 CG  TYR 1 548   -14.519 -15.633  8.188 1.00 0.58
ATOM   201 CD1 TYR 1 548   -14.196 -16.688  9.009 1.00 0.58
ATOM   202 CD2 TYR 1 548   -15.222 -14.569  8.705 1.00 0.58
ATOM   203 CE1 TYR 1 548   -14.573 -16.672 10.332 1.00 0.58
ATOM   204 CE2 TYR 1 548   -15.600 -14.550 10.024 1.00 0.58
ATOM   205 CZ  TYR 1 548   -15.276 -15.605 10.840 1.00 0.58
ATOM   206 OH  TYR 1 548   -15.663 -15.589 12.197 1.00 0.58
ATOM   207 N   ASP 1 549   -11.358 -16.651  7.969 1.00 0.54
ATOM   208 CA  ASP 1 549   -10.379 -17.663  8.288 1.00 0.54
ATOM   209 C   ASP 1 549   -10.510 -18.822  7.361 1.00 0.54
ATOM   210 O   ASP 1 549   -11.474 -19.585  7.410 1.00 0.54
ATOM   211 CB  ASP 1 549   -10.504 -18.197  9.724 1.00 0.54
ATOM   212 CG  ASP 1 549    -9.269 -19.029 10.034 1.00 0.54
ATOM   213 OD1 ASP 1 549    -8.168 -18.659  9.548 1.00 0.54
ATOM   214 OD2 ASP 1 549    -9.412 -20.054 10.752 1.00 0.54
ATOM   215 N   SER 1 550    -9.516 -18.955  6.468 1.00 0.52
ATOM   216 CA  SER 1 550    -9.517 -19.997  5.491 1.00 0.52
ATOM   217 C   SER 1 550    -8.795 -21.150  6.105 1.00 0.52
ATOM   218 O   SER 1 550    -9.384 -21.939  6.843 1.00 0.52
ATOM   219 CB  SER 1 550    -8.791 -19.574  4.201 1.00 0.52
ATOM   220 OG  SER 1 550    -9.124 -20.448  3.134 1.00 0.52
ATOM   221 N   SER 1 551    -7.485 -21.273  5.821 1.00 0.82
ATOM   222 CA  SER 1 551    -6.734 -22.361  6.369 1.00 0.82
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ATOM	223	C	SER 1 551	-5.454	-21.817	6.918	1.00	0.82
ATOM	224	O	SER 1 551	-4.927	-20.803	6.454	1.00	0.82
ATOM	225	CB	SER 1 551	-6.370	-23.444	5.341	1.00	0.82
ATOM	226	OG	SER 1 551	-5.631	-24.481	5.968	1.00	0.82
ATOM	227	N	VAL 1 552	-4.895	-22.551	7.898	1.00	1.25
ATOM	228	CA	VAL 1 552	-3.740	-22.163	8.639	1.00	1.25
ATOM	229	C	VAL 1 552	-2.505	-22.265	7.824	1.00	1.25
ATOM	230	O	VAL 1 552	-2.276	-21.246	7.175	1.00	1.25
ATOM	231	CB	VAL 1 552	-3.665	-22.788	10.017	1.00	1.25
ATOM	232	CG1	VAL 1 552	-4.317	-24.185	10.023	1.00	1.25
ATOM	233	CG2	VAL 1 552	-2.212	-22.736	10.521	1.00	1.25
ATOM	234	N	PRO 1 553	-1.656	-23.294	7.852	1.00	1.24
ATOM	235	CA	PRO 1 553	-0.494	-23.299	7.002	1.00	1.24
ATOM	236	C	PRO 1 553	-1.006	-23.041	5.633	1.00	1.24
ATOM	237	O	PRO 1 553	-1.720	-23.877	5.077	1.00	1.24
ATOM	238	CB	PRO 1 553	0.109	-24.700	7.080	1.00	1.24
ATOM	239	CG	PRO 1 553	-0.775	-25.455	8.087	1.00	1.24
ATOM	240	CD	PRO 1 553	-2.092	-24.663	8.072	1.00	1.24
ATOM	241	N	ASP 1 554	-0.651	-21.875	5.086	1.00	0.74
ATOM	242	CA	ASP 1 554	-1.205	-21.454	3.852	1.00	0.74
ATOM	243	C	ASP 1 554	-0.299	-22.024	2.812	1.00	0.74
ATOM	244	O	ASP 1 554	0.819	-22.433	3.122	1.00	0.74
ATOM	245	CB	ASP 1 554	-1.198	-19.915	3.772	1.00	0.74
ATOM	246	CG	ASP 1 554	-2.288	-19.460	2.829	1.00	0.74
ATOM	247	OD1	ASP 1 554	-2.369	-20.056	1.729	1.00	0.74
ATOM	248	OD2	ASP 1 554	-3.047	-18.523	3.186	1.00	0.74
ATOM	249	N	SER 1 555	-0.788	-22.127	1.566	1.00	0.52
ATOM	250	CA	SER 1 555	0.017	-22.585	0.482	1.00	0.52
ATOM	251	C	SER 1 555	0.411	-21.346	-0.245	1.00	0.52
ATOM	252	O	SER 1 555	-0.037	-20.255	0.102	1.00	0.52
ATOM	253	CB	SER 1 555	-0.745	-23.477	-0.511	1.00	0.52
ATOM	254	OG	SER 1 555	0.119	-23.884	-1.560	1.00	0.52
ATOM	255	N	THR 1 556	1.283	-21.469	-1.261	1.00	0.67
ATOM	256	CA	THR 1 556	1.635	-20.279	-1.968	1.00	0.67
ATOM	257	C	THR 1 556	0.398	-19.746	-2.613	1.00	0.67
ATOM	258	O	THR 1 556	0.010	-18.605	-2.377	1.00	0.67
ATOM	259	CB	THR 1 556	2.656	-20.525	-3.041	1.00	0.67
ATOM	260	OG1	THR 1 556	2.149	-21.432	-4.009	1.00	0.67
ATOM	261	CG2	THR 1 556	3.923	-21.104	-2.388	1.00	0.67
ATOM	262	N	TRP 1 557	-0.301	-20.612	-3.368	1.00	0.70
ATOM	263	CA	TRP 1 557	-1.440	-20.245	-4.162	1.00	0.70
ATOM	264	C	TRP 1 557	-2.526	-19.719	-3.283	1.00	0.70
ATOM	265	O	TRP 1 557	-3.155	-18.706	-3.583	1.00	0.70
ATOM	266	CB	TRP 1 557	-1.997	-21.469	-4.910	1.00	0.70
ATOM	267	CG	TRP 1 557	-3.196	-21.218	-5.788	1.00	0.70
ATOM	268	CD1	TRP 1 557	-4.524	-21.206	-5.474	1.00	0.70
ATOM	269	CD2	TRP 1 557	-3.109	-20.981	-7.202	1.00	0.70
ATOM	270	NE1	TRP 1 557	-5.270	-20.973	-6.604	1.00	0.70
ATOM	271	CE2	TRP 1 557	-4.412	-20.834	-7.676	1.00	0.70
ATOM	272	CE3	TRP 1 557	-2.032	-20.898	-8.037	1.00	0.70
ATOM	273	CZ2	TRP 1 557	-4.659	-20.602	-8.999	1.00	0.70
ATOM	274	CZ3	TRP 1 557	-2.284	-20.658	-9.369	1.00	0.70
ATOM	275	CH2	TRP 1 557	-3.572	-20.513	-9.841	1.00	0.70
ATOM	276	N	ARG 1 558	-2.761	-20.403	-2.156	1.00	0.62
ATOM	277	CA	ARG 1 558	-3.840	-20.090	-1.271	1.00	0.62
ATOM	278	C	ARG 1 558	-3.595	-18.732	-0.674	1.00	0.62
ATOM	279	O	ARG 1 558	-4.516	-17.927	-0.531	1.00	0.62
ATOM	280	CB	ARG 1 558	-3.922	-21.191	-0.201	1.00	0.62
ATOM	281	CG	ARG 1 558	-5.283	-21.459	0.429	1.00	0.62
ATOM	282	CD	ARG 1 558	-5.232	-22.749	1.249	1.00	0.62
ATOM	283	NE	ARG 1 558	-6.617	-23.150	1.607	1.00	0.62

ATOM 284 CZ ARG 1 558 -7.220 -22.547 2.666 1.00 0.62
ATOM 285 NH1 ARG 1 558 -6.619 -21.461 3.233 1.00 0.62
ATOM 286 NH2 ARG 1 558 -8.394 -23.043 3.159 1.00 0.62
ATOM 287 N ILE 1 559 -2.328 -18.441 -0.319 1.00 0.68
ATOM 288 CA ILE 1 559 -1.993 -17.195 0.305 1.00 0.68
ATOM 289 C ILE 1 559 -2.140 -16.110 -0.727 1.00 0.68
ATOM 290 O ILE 1 559 -2.665 -15.035 -0.434 1.00 0.68
ATOM 291 CB ILE 1 559 -0.591 -17.232 0.870 1.00 0.68
ATOM 292 CG1 ILE 1 559 -0.472 -16.357 2.130 1.00 0.68
ATOM 293 CG2 ILE 1 559 0.421 -16.889 -0.235 1.00 0.68
ATOM 294 CD1 ILE 1 559 -0.907 -14.910 1.959 1.00 0.68
ATOM 295 N MET 1 560 -1.714 -16.347 -1.989 1.00 0.55
ATOM 296 CA MET 1 560 -1.890 -15.270 -2.919 1.00 0.55
ATOM 297 C MET 1 560 -3.342 -15.050 -3.136 1.00 0.55
ATOM 298 O MET 1 560 -3.758 -13.942 -3.463 1.00 0.55
ATOM 299 CB MET 1 560 -1.182 -15.317 -4.293 1.00 0.55
ATOM 300 CG MET 1 560 -1.169 -16.608 -5.100 1.00 0.55
ATOM 301 SD MET 1 560 0.410 -17.486 -4.965 1.00 0.55
ATOM 302 CE MET 1 560 1.404 -15.974 -5.136 1.00 0.55
ATOM 303 N THR 1 561 -4.159 -16.104 -2.982 1.00 0.35
ATOM 304 CA THR 1 561 -5.567 -15.934 -3.165 1.00 0.35
ATOM 305 C THR 1 561 -6.036 -14.922 -2.169 1.00 0.35
ATOM 306 O THR 1 561 -6.763 -13.993 -2.519 1.00 0.35
ATOM 307 CB THR 1 561 -6.332 -17.202 -2.922 1.00 0.35
ATOM 308 OG1 THR 1 561 -5.891 -18.216 -3.812 1.00 0.35
ATOM 309 CG2 THR 1 561 -7.829 -16.923 -3.138 1.00 0.35
ATOM 310 N THR 1 562 -5.616 -15.058 -0.897 1.00 0.42
ATOM 311 CA THR 1 562 -6.088 -14.116 0.072 1.00 0.42
ATOM 312 C THR 1 562 -5.571 -12.755 -0.281 1.00 0.42
ATOM 313 O THR 1 562 -6.331 -11.790 -0.291 1.00 0.42
ATOM 314 CB THR 1 562 -5.697 -14.444 1.491 1.00 0.42
ATOM 315 OG1 THR 1 562 -6.420 -13.617 2.390 1.00 0.42
ATOM 316 CG2 THR 1 562 -4.189 -14.233 1.693 1.00 0.42
ATOM 317 N LEU 1 563 -4.274 -12.628 -0.630 1.00 0.48
ATOM 318 CA LEU 1 563 -3.812 -11.295 -0.893 1.00 0.48
ATOM 319 C LEU 1 563 -4.507 -10.730 -2.086 1.00 0.48
ATOM 320 O LEU 1 563 -4.833 -9.546 -2.102 1.00 0.48
ATOM 321 CB LEU 1 563 -2.312 -11.103 -1.184 1.00 0.48
ATOM 322 CG LEU 1 563 -1.359 -11.510 -0.054 1.00 0.48
ATOM 323 CD1 LEU 1 563 -0.892 -12.955 -0.232 1.00 0.48
ATOM 324 CD2 LEU 1 563 -0.222 -10.500 0.130 1.00 0.48
ATOM 325 N ASN 1 564 -4.738 -11.543 -3.133 1.00 0.45
ATOM 326 CA ASN 1 564 -5.334 -10.982 -4.308 1.00 0.45
ATOM 327 C ASN 1 564 -6.723 -10.530 -3.997 1.00 0.45
ATOM 328 O ASN 1 564 -7.157 -9.479 -4.468 1.00 0.45
ATOM 329 CB ASN 1 564 -5.342 -11.908 -5.547 1.00 0.45
ATOM 330 CG ASN 1 564 -6.153 -13.175 -5.323 1.00 0.45
ATOM 331 OD1 ASN 1 564 -7.341 -13.161 -5.012 1.00 0.45
ATOM 332 ND2 ASN 1 564 -5.478 -14.336 -5.537 1.00 0.45
ATOM 333 N MET 1 565 -7.457 -11.302 -3.178 1.00 0.57
ATOM 334 CA MET 1 565 -8.801 -10.924 -2.869 1.00 0.57
ATOM 335 C MET 1 565 -8.751 -9.606 -2.162 1.00 0.57
ATOM 336 O MET 1 565 -9.518 -8.697 -2.478 1.00 0.57
ATOM 337 CB MET 1 565 -9.497 -11.922 -1.926 1.00 0.57
ATOM 338 CG MET 1 565 -9.752 -13.294 -2.552 1.00 0.57
ATOM 339 SD MET 1 565 -11.044 -13.308 -3.832 1.00 0.57
ATOM 340 CE MET 1 565 -12.418 -13.115 -2.659 1.00 0.57
ATOM 341 N LEU 1 566 -7.810 -9.457 -1.207 1.00 0.62
ATOM 342 CA LEU 1 566 -7.746 -8.253 -0.424 1.00 0.62
ATOM 343 C LEU 1 566 -7.560 -7.082 -1.330 1.00 0.62
ATOM 344 O LEU 1 566 -8.369 -6.156 -1.346 1.00 0.62

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ATOM  345  CB  LEU 1 566     -6.494  -8.156   0.468  1.00  0.62
ATOM  346  CG  LEU 1 566     -6.327  -9.185   1.593  1.00  0.62
ATOM  347  CD1 LEU 1 566     -5.025  -8.912   2.356  1.00  0.62
ATOM  348  CD2 LEU 1 566     -7.526  -9.206   2.544  1.00  0.62
ATOM  349  N   GLY 1 567     -6.508  -7.138  -2.163  1.00  0.32
ATOM  350  CA  GLY 1 567     -6.125  -6.004  -2.951  1.00  0.32
ATOM  351  C   GLY 1 567     -7.264  -5.586  -3.817  1.00  0.32
ATOM  352  O   GLY 1 567     -7.508  -4.391  -3.993  1.00  0.32
ATOM  353  N   GLY 1 568     -7.985  -6.561  -4.396  1.00  0.15
ATOM  354  CA  GLY 1 568     -9.067  -6.225  -5.273  1.00  0.15
ATOM  355  C   GLY 1 568    -10.115  -5.496  -4.497  1.00  0.15
ATOM  356  O   GLY 1 568    -10.693  -4.518  -4.966  1.00  0.15
ATOM  357  N   ARG 1 569    -10.416  -5.965  -3.279  1.00  0.29
ATOM  358  CA  ARG 1 569    -11.425  -5.314  -2.501  1.00  0.29
ATOM  359  C   ARG 1 569    -10.953  -3.935  -2.166  1.00  0.29
ATOM  360  O   ARG 1 569    -11.705  -2.966  -2.267  1.00  0.29
ATOM  361  CB  ARG 1 569    -11.706  -6.079  -1.199  1.00  0.29
ATOM  362  CG  ARG 1 569    -12.507  -7.367  -1.421  1.00  0.29
ATOM  363  CD  ARG 1 569    -12.352  -8.380  -0.287  1.00  0.29
ATOM  364  NE  ARG 1 569    -11.653  -7.671   0.816  1.00  0.29
ATOM  365  CZ  ARG 1 569    -10.466  -8.155   1.286  1.00  0.29
ATOM  366  NH1 ARG 1 569    -10.029  -9.385   0.889  1.00  0.29
ATOM  367  NH2 ARG 1 569     -9.718  -7.402   2.145  1.00  0.29
ATOM  368  N   GLN 1 570     -9.673  -3.797  -1.780  1.00  0.39
ATOM  369  CA  GLN 1 570     -9.166  -2.514  -1.394  1.00  0.39
ATOM  370  C   GLN 1 570     -9.169  -1.588  -2.572  1.00  0.39
ATOM  371  O   GLN 1 570     -9.385  -0.387  -2.413  1.00  0.39
ATOM  372  CB  GLN 1 570     -7.741  -2.554  -0.795  1.00  0.39
ATOM  373  CG  GLN 1 570     -7.646  -3.202   0.597  1.00  0.39
ATOM  374  CD  GLN 1 570     -6.226  -3.075   1.130  1.00  0.39
ATOM  375  OE1 GLN 1 570     -5.984  -2.404   2.132  1.00  0.39
ATOM  376  NE2 GLN 1 570     -5.255  -3.728   0.438  1.00  0.39
ATOM  377  N   VAL 1 571     -8.955  -2.114  -3.796  1.00  0.43
ATOM  378  CA  VAL 1 571     -8.860  -1.235  -4.928  1.00  0.43
ATOM  379  C   VAL 1 571    -10.133  -0.455  -5.052  1.00  0.43
ATOM  380  O   VAL 1 571    -10.111   0.714  -5.429  1.00  0.43
ATOM  381  CB  VAL 1 571     -8.624  -1.921  -6.244  1.00  0.43
ATOM  382  CG1 VAL 1 571     -9.932  -2.569  -6.721  1.00  0.43
ATOM  383  CG2 VAL 1 571     -8.070  -0.884  -7.233  1.00  0.43
ATOM  384  N   ILE 1 572    -11.286  -1.072  -4.735  1.00  0.36
ATOM  385  CA  ILE 1 572    -12.526  -0.363  -4.890  1.00  0.36
ATOM  386  C   ILE 1 572    -12.559   0.843  -3.992  1.00  0.36
ATOM  387  O   ILE 1 572    -12.992   1.917  -4.407  1.00  0.36
ATOM  388  CB  ILE 1 572    -13.750  -1.197  -4.607  1.00  0.36
ATOM  389  CG1 ILE 1 572    -15.002  -0.501  -5.160  1.00  0.36
ATOM  390  CG2 ILE 1 572    -13.842  -1.473  -3.099  1.00  0.36
ATOM  391  CD1 ILE 1 572    -16.238  -1.400  -5.177  1.00  0.36
ATOM  392  N   ALA 1 573    -12.095   0.712  -2.737  1.00  0.18
ATOM  393  CA  ALA 1 573    -12.146   1.810  -1.808  1.00  0.18
ATOM  394  C   ALA 1 573    -11.235   2.896  -2.281  1.00  0.18
ATOM  395  O   ALA 1 573    -11.529   4.080  -2.128  1.00  0.18
ATOM  396  CB  ALA 1 573    -11.693   1.413  -0.393  1.00  0.18
ATOM  397  N   ALA 1 574    -10.102   2.505  -2.886  1.00  0.10
ATOM  398  CA  ALA 1 574     -9.103   3.437  -3.319  1.00  0.10
ATOM  399  C   ALA 1 574     -9.701   4.372  -4.319  1.00  0.10
ATOM  400  O   ALA 1 574     -9.374   5.557  -4.339  1.00  0.10
ATOM  401  CB  ALA 1 574     -7.897   2.757  -3.989  1.00  0.10
ATOM  402  N   VAL 1 575    -10.594   3.861  -5.186  1.00  0.13
ATOM  403  CA  VAL 1 575    -11.188   4.703  -6.181  1.00  0.13
ATOM  404  C   VAL 1 575    -11.953   5.790  -5.492  1.00  0.13
ATOM  405  O   VAL 1 575    -11.871   6.956  -5.876  1.00  0.13
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ATOM 406 CB VAL 1 575 -12.150 3.966 -7.066 1.00 0.13
ATOM 407 CG1 VAL 1 575 -12.748 4.963 -8.073 1.00 0.13
ATOM 408 CG2 VAL 1 575 -11.410 2.787 -7.721 1.00 0.13
ATOM 409 N LYS 1 576 -12.708 5.434 -4.434 1.00 0.27
ATOM 410 CA LYS 1 576 -13.506 6.397 -3.726 1.00 0.27
ATOM 411 C LYS 1 576 -12.598 7.442 -3.153 1.00 0.27
ATOM 412 O LYS 1 576 -12.867 8.637 -3.244 1.00 0.27
ATOM 413 CB LYS 1 576 -14.254 5.786 -2.530 1.00 0.27
ATOM 414 CG LYS 1 576 -15.304 4.736 -2.900 1.00 0.27
ATOM 415 CD LYS 1 576 -15.768 3.912 -1.697 1.00 0.27
ATOM 416 CE LYS 1 576 -16.829 2.861 -2.034 1.00 0.27
ATOM 417 NZ LYS 1 576 -18.125 3.522 -2.303 1.00 0.27
ATOM 418 N TRP 1 577 -11.490 6.999 -2.532 1.00 0.34
ATOM 419 CA TRP 1 577 -10.507 7.863 -1.941 1.00 0.34
ATOM 420 C TRP 1 577 -9.883 8.746 -2.973 1.00 0.34
ATOM 421 O TRP 1 577 -9.815 9.963 -2.800 1.00 0.34
ATOM 422 CB TRP 1 577 -9.498 7.010 -1.129 1.00 0.34
ATOM 423 CG TRP 1 577 -8.000 7.274 -1.103 1.00 0.34
ATOM 424 CD1 TRP 1 577 -7.050 6.298 -1.185 1.00 0.34
ATOM 425 CD2 TRP 1 577 -7.281 8.520 -1.094 1.00 0.34
ATOM 426 NE1 TRP 1 577 -5.795 6.847 -1.172 1.00 0.34
ATOM 427 CE2 TRP 1 577 -5.919 8.214 -1.134 1.00 0.34
ATOM 428 CE3 TRP 1 577 -7.705 9.813 -1.069 1.00 0.34
ATOM 429 CZ2 TRP 1 577 -4.970 9.194 -1.145 1.00 0.34
ATOM 430 CZ3 TRP 1 577 -6.746 10.801 -1.073 1.00 0.34
ATOM 431 CH2 TRP 1 577 -5.403 10.498 -1.108 1.00 0.34
ATOM 432 N ALA 1 578 -9.500 8.184 -4.123 1.00 0.38
ATOM 433 CA ALA 1 578 -8.844 8.981 -5.119 1.00 0.38
ATOM 434 C ALA 1 578 -9.740 10.111 -5.529 1.00 0.38
ATOM 435 O ALA 1 578 -9.284 11.234 -5.737 1.00 0.38
ATOM 436 CB ALA 1 578 -8.500 8.174 -6.382 1.00 0.38
ATOM 437 N LYS 1 579 -11.054 9.855 -5.618 1.00 0.46
ATOM 438 CA LYS 1 579 -11.975 10.855 -6.081 1.00 0.46
ATOM 439 C LYS 1 579 -11.960 12.028 -5.153 1.00 0.46
ATOM 440 O LYS 1 579 -12.185 13.160 -5.567 1.00 0.46
ATOM 441 CB LYS 1 579 -13.420 10.341 -6.175 1.00 0.46
ATOM 442 CG LYS 1 579 -13.604 9.242 -7.225 1.00 0.46
ATOM 443 CD LYS 1 579 -13.276 9.676 -8.658 1.00 0.46
ATOM 444 CE LYS 1 579 -14.392 10.474 -9.336 1.00 0.46
ATOM 445 NZ LYS 1 579 -14.077 10.676 -10.769 1.00 0.46
ATOM 446 N ALA 1 580 -11.758 11.774 -3.855 1.00 0.43
ATOM 447 CA ALA 1 580 -11.760 12.785 -2.845 1.00 0.43
ATOM 448 C ALA 1 580 -10.472 13.579 -2.782 1.00 0.43
ATOM 449 O ALA 1 580 -10.416 14.609 -2.111 1.00 0.43
ATOM 450 CB ALA 1 580 -12.158 12.208 -1.493 1.00 0.43
ATOM 451 N ILE 1 581 -9.379 13.106 -3.418 1.00 0.38
ATOM 452 CA ILE 1 581 -8.121 13.804 -3.321 1.00 0.38
ATOM 453 C ILE 1 581 -8.170 15.059 -4.148 1.00 0.38
ATOM 454 O ILE 1 581 -8.457 15.055 -5.344 1.00 0.38
ATOM 455 CB ILE 1 581 -6.970 12.914 -3.708 1.00 0.38
ATOM 456 CG1 ILE 1 581 -5.622 13.452 -3.247 1.00 0.38
ATOM 457 CG2 ILE 1 581 -7.005 12.663 -5.211 1.00 0.38
ATOM 458 CD1 ILE 1 581 -4.559 12.380 -3.445 1.00 0.38
ATOM 459 N PRO 1 582 -7.861 16.159 -3.513 1.00 0.28
ATOM 460 CA PRO 1 582 -8.000 17.439 -4.147 1.00 0.28
ATOM 461 C PRO 1 582 -7.240 17.551 -5.426 1.00 0.28
ATOM 462 O PRO 1 582 -6.035 17.309 -5.439 1.00 0.28
ATOM 463 CB PRO 1 582 -7.651 18.469 -3.077 1.00 0.28
ATOM 464 CG PRO 1 582 -8.048 17.760 -1.764 1.00 0.28
ATOM 465 CD PRO 1 582 -7.884 16.257 -2.063 1.00 0.28
ATOM 466 N GLY 1 583 -7.948 17.938 -6.507 1.00 0.17

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ATOM   467  CA  GLY 1 583     -7.365  18.131  -7.802  1.00  0.17
ATOM   468  C   GLY 1 583     -7.628  16.926  -8.654  1.00  0.17
ATOM   469  O   GLY 1 583     -7.624  17.002  -9.880  1.00  0.17
ATOM   470  N   PHE 1 584     -7.905  15.780  -8.015  1.00  0.34
ATOM   471  CA  PHE 1 584     -8.062  14.534  -8.710  1.00  0.34
ATOM   472  C   PHE 1 584     -9.230  14.603  -9.654  1.00  0.34
ATOM   473  O   PHE 1 584     -9.114  14.236 -10.823  1.00  0.34
ATOM   474  CB  PHE 1 584     -8.349  13.418  -7.697  1.00  0.34
ATOM   475  CG  PHE 1 584     -7.943  12.078  -8.200  1.00  0.34
ATOM   476  CD1 PHE 1 584     -6.610  11.776  -8.364  1.00  0.34
ATOM   477  CD2 PHE 1 584     -8.882  11.106  -8.446  1.00  0.34
ATOM   478  CE1 PHE 1 584     -6.221  10.535  -8.807  1.00  0.34
ATOM   479  CE2 PHE 1 584     -8.498   9.865  -8.885  1.00  0.34
ATOM   480  CZ  PHE 1 584     -7.168   9.577  -9.072  1.00  0.34
ATOM   481  N   ARG 1 585    -10.384  15.099  -9.174  1.00  0.46
ATOM   482  CA  ARG 1 585    -11.600  15.107  -9.947  1.00  0.46
ATOM   483  C   ARG 1 585    -11.539  16.089 -11.077  1.00  0.46
ATOM   484  O   ARG 1 585    -12.288  15.959 -12.041  1.00  0.46
ATOM   485  CB  ARG 1 585    -12.877  15.408  -9.147  1.00  0.46
ATOM   486  CG  ARG 1 585    -12.958  16.807  -8.540  1.00  0.46
ATOM   487  CD  ARG 1 585    -14.368  17.134  -8.044  1.00  0.46
ATOM   488  NE  ARG 1 585    -15.276  17.029  -9.224  1.00  0.46
ATOM   489  CZ  ARG 1 585    -16.560  16.590  -9.074  1.00  0.46
ATOM   490  NH1 ARG 1 585    -17.032  16.261  -7.836  1.00  0.46
ATOM   491  NH2 ARG 1 585    -17.373  16.476 -10.166  1.00  0.46
ATOM   492  N   ASN 1 586    -10.706  17.139 -10.973  1.00  0.45
ATOM   493  CA  ASN 1 586    -10.634  18.120 -12.021  1.00  0.45
ATOM   494  C   ASN 1 586    -10.111  17.463 -13.259  1.00  0.45
ATOM   495  O   ASN 1 586    -10.475  17.821 -14.380  1.00  0.45
ATOM   496  CB  ASN 1 586     -9.703  19.293 -11.678  1.00  0.45
ATOM   497  CG  ASN 1 586    -10.385  20.101 -10.584  1.00  0.45
ATOM   498  OD1 ASN 1 586    -11.610  20.195 -10.547  1.00  0.45
ATOM   499  ND2 ASN 1 586     -9.575  20.697  -9.668  1.00  0.45
ATOM   500  N   LEU 1 587     -9.231  16.473 -13.068  1.00  0.55
ATOM   501  CA  LEU 1 587     -8.562  15.751 -14.107  1.00  0.55
ATOM   502  C   LEU 1 587     -9.618  15.063 -14.928  1.00  0.55
ATOM   503  O   LEU 1 587    -10.739  14.850 -14.466  1.00  0.55
ATOM   504  CB  LEU 1 587     -7.668  14.679 -13.445  1.00  0.55
ATOM   505  CG  LEU 1 587     -6.461  14.146 -14.232  1.00  0.55
ATOM   506  CD1 LEU 1 587     -5.335  15.186 -14.287  1.00  0.55
ATOM   507  CD2 LEU 1 587     -5.960  12.826 -13.636  1.00  0.55
ATOM   508  N   HIS 1 588     -9.286  14.733 -16.194  1.00  0.46
ATOM   509  CA  HIS 1 588    -10.187  14.045 -17.076  1.00  0.46
ATOM   510  C   HIS 1 588    -10.210  12.614 -16.641  1.00  0.46
ATOM   511  O   HIS 1 588     -9.337  12.160 -15.904  1.00  0.46
ATOM   512  CB  HIS 1 588     -9.735  14.093 -18.548  1.00  0.46
ATOM   513  CG  HIS 1 588    -10.650  13.385 -19.503  1.00  0.46
ATOM   514  ND1 HIS 1 588    -10.514  12.066 -19.867  1.00  0.46
ATOM   515  CD2 HIS 1 588    -11.733  13.848 -20.188  1.00  0.46
ATOM   516  CE1 HIS 1 588    -11.511  11.795 -20.748  1.00  0.46
ATOM   517  NE2 HIS 1 588    -12.276  12.848 -20.974  1.00  0.46
ATOM   518  N   LEU 1 589    -11.222  11.856 -17.102  1.00  0.27
ATOM   519  CA  LEU 1 589    -11.395  10.496 -16.683  1.00  0.27
ATOM   520  C   LEU 1 589    -10.182   9.706 -17.062  1.00  0.27
ATOM   521  O   LEU 1 589     -9.646   8.945 -16.259  1.00  0.27
ATOM   522  CB  LEU 1 589    -12.588   9.823 -17.381  1.00  0.27
ATOM   523  CG  LEU 1 589    -12.792   8.365 -16.941  1.00  0.27
ATOM   524  CD1 LEU 1 589    -13.192   8.310 -15.463  1.00  0.27
ATOM   525  CD2 LEU 1 589    -13.781   7.624 -17.853  1.00  0.27
ATOM   526  N   ASP 1 590     -9.705   9.894 -18.303  1.00  0.25
ATOM   527  CA  ASP 1 590     -8.603   9.138 -18.816  1.00  0.25
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ATOM    528  C   ASP 1 590     -7.387   9.404 -17.984  1.00  0.25
ATOM    529  O   ASP 1 590     -6.620   8.491 -17.685  1.00  0.25
ATOM    530  CB  ASP 1 590     -8.266   9.512 -20.271  1.00  0.25
ATOM    531  CG  ASP 1 590     -7.255   8.515 -20.817  1.00  0.25
ATOM    532  OD1 ASP 1 590     -6.868   7.583 -20.062  1.00  0.25
ATOM    533  OD2 ASP 1 590     -6.854   8.676 -22.000  1.00  0.25
ATOM    534  N   ASP 1 591     -7.173  10.673 -17.597  1.00  0.27
ATOM    535  CA  ASP 1 591     -6.010  11.033 -16.832  1.00  0.27
ATOM    536  C   ASP 1 591     -6.104  10.438 -15.472  1.00  0.27
ATOM    537  O   ASP 1 591     -5.102  10.074 -14.858  1.00  0.27
ATOM    538  CB  ASP 1 591     -5.840  12.551 -16.683  1.00  0.27
ATOM    539  CG  ASP 1 591     -5.433  13.097 -18.043  1.00  0.27
ATOM    540  OD1 ASP 1 591     -5.096  12.274 -18.935  1.00  0.27
ATOM    541  OD2 ASP 1 591     -5.449  14.346 -18.205  1.00  0.27
ATOM    542  N   GLN 1 592     -7.329  10.349 -14.945  1.00  0.31
ATOM    543  CA  GLN 1 592     -7.504   9.815 -13.638  1.00  0.31
ATOM    544  C   GLN 1 592     -7.058   8.389 -13.686  1.00  0.31
ATOM    545  O   GLN 1 592     -6.317   7.920 -12.824  1.00  0.31
ATOM    546  CB  GLN 1 592     -8.975   9.908 -13.238  1.00  0.31
ATOM    547  CG  GLN 1 592     -9.192   9.833 -11.742  1.00  0.31
ATOM    548  CD  GLN 1 592    -10.516  10.522 -11.463  1.00  0.31
ATOM    549  OE1 GLN 1 592    -11.571   9.893 -11.437  1.00  0.31
ATOM    550  NE2 GLN 1 592    -10.464  11.865 -11.264  1.00  0.31
ATOM    551  N   MET 1 593     -7.452   7.680 -14.758  1.00  0.38
ATOM    552  CA  MET 1 593     -7.117   6.295 -14.927  1.00  0.38
ATOM    553  C   MET 1 593     -5.622   6.167 -14.920  1.00  0.38
ATOM    554  O   MET 1 593     -5.081   5.268 -14.279  1.00  0.38
ATOM    555  CB  MET 1 593     -7.537   5.763 -16.303  1.00  0.38
ATOM    556  CG  MET 1 593     -9.038   5.737 -16.573  1.00  0.38
ATOM    557  SD  MET 1 593     -9.425   5.580 -18.341  1.00  0.38
ATOM    558  CE  MET 1 593     -8.466   4.055 -18.571  1.00  0.38
ATOM    559  N   THR 1 594     -4.908   7.070 -15.631  1.00  0.56
ATOM    560  CA  THR 1 594     -3.485   6.913 -15.743  1.00  0.56
ATOM    561  C   THR 1 594     -2.854   7.055 -14.395  1.00  0.56
ATOM    562  O   THR 1 594     -1.938   6.317 -14.040  1.00  0.56
ATOM    563  CB  THR 1 594     -2.822   7.881 -16.689  1.00  0.56
ATOM    564  OG1 THR 1 594     -1.494   7.455 -16.954  1.00  0.56
ATOM    565  CG2 THR 1 594     -2.784   9.284 -16.069  1.00  0.56
ATOM    566  N   LEU 1 595     -3.351   8.014 -13.606  1.00  0.67
ATOM    567  CA  LEU 1 595     -2.873   8.315 -12.298  1.00  0.67
ATOM    568  C   LEU 1 595     -3.015   7.054 -11.476  1.00  0.67
ATOM    569  O   LEU 1 595     -2.042   6.553 -10.914  1.00  0.67
ATOM    570  CB  LEU 1 595     -3.808   9.433 -11.781  1.00  0.67
ATOM    571  CG  LEU 1 595     -3.358  10.276 -10.593  1.00  0.67
ATOM    572  CD1 LEU 1 595     -3.379   9.462  -9.298  1.00  0.67
ATOM    573  CD2 LEU 1 595     -2.040  10.998 -10.916  1.00  0.67
ATOM    574  N   LEU 1 596     -4.221   6.451 -11.441  1.00  0.48
ATOM    575  CA  LEU 1 596     -4.421   5.274 -10.631  1.00  0.48
ATOM    576  C   LEU 1 596     -3.625   4.118 -11.126  1.00  0.48
ATOM    577  O   LEU 1 596     -3.050   3.384 -10.328  1.00  0.48
ATOM    578  CB  LEU 1 596     -5.871   4.749 -10.534  1.00  0.48
ATOM    579  CG  LEU 1 596     -6.844   5.622  -9.720  1.00  0.48
ATOM    580  CD1 LEU 1 596     -7.309   6.853 -10.504  1.00  0.48
ATOM    581  CD2 LEU 1 596     -8.006   4.788  -9.167  1.00  0.48
ATOM    582  N   GLN 1 597     -3.549   3.933 -12.453  1.00  0.43
ATOM    583  CA  GLN 1 597     -2.931   2.746 -12.967  1.00  0.43
ATOM    584  C   GLN 1 597     -1.514   2.677 -12.471  1.00  0.43
ATOM    585  O   GLN 1 597     -1.040   1.603 -12.105  1.00  0.43
ATOM    586  CB  GLN 1 597     -2.919   2.701 -14.499  1.00  0.43
ATOM    587  CG  GLN 1 597     -2.335   1.403 -15.054  1.00  0.43
ATOM    588  CD  GLN 1 597     -2.383   1.487 -16.570  1.00  0.43
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ATOM  589 OE1 GLN 1 597   -2.999  2.391 -17.132 1.00 0.43
ATOM  590 NE2 GLN 1 597   -1.718  0.519 -17.255 1.00 0.43
ATOM  591 N  TYR 1 598    -0.805  3.822 -12.449 1.00 0.63
ATOM  592 CA TYR 1 598     0.575  3.879 -12.039 1.00 0.63
ATOM  593 C  TYR 1 598     0.754  3.705 -10.541 1.00 0.63
ATOM  594 O  TYR 1 598     1.622  2.956 -10.095 1.00 0.63
ATOM  595 CB TYR 1 598     1.202  5.233 -12.413 1.00 0.63
ATOM  596 CG TYR 1 598     2.682  5.140 -12.280 1.00 0.63
ATOM  597 CD1 TYR 1 598    3.287  5.130 -11.044 1.00 0.63
ATOM  598 CD2 TYR 1 598    3.471  5.079 -13.406 1.00 0.63
ATOM  599 CE1 TYR 1 598    4.655  5.052 -10.936 1.00 0.63
ATOM  600 CE2 TYR 1 598    4.838  5.000 -13.304 1.00 0.63
ATOM  601 CZ  TYR 1 598    5.433  4.983 -12.066 1.00 0.63
ATOM  602 OH  TYR 1 598    6.837  4.903 -11.956 1.00 0.63
ATOM  603 N  SER 1 599    -0.058  4.423  -9.734 1.00 0.57
ATOM  604 CA SER 1 599     0.007  4.569  -8.295 1.00 0.57
ATOM  605 C  SER 1 599    -0.481  3.412  -7.472 1.00 0.57
ATOM  606 O  SER 1 599    -0.041  3.263  -6.333 1.00 0.57
ATOM  607 CB SER 1 599    -0.841  5.750  -7.781 1.00 0.57
ATOM  608 OG SER 1 599    -0.367  6.985  -8.291 1.00 0.57
ATOM  609 N  TRP 1 600    -1.382  2.566  -8.001 1.00 0.39
ATOM  610 CA TRP 1 600    -2.151  1.642  -7.200 1.00 0.39
ATOM  611 C  TRP 1 600    -1.310  0.848  -6.233 1.00 0.39
ATOM  612 O  TRP 1 600    -1.618  0.807  -5.043 1.00 0.39
ATOM  613 CB TRP 1 600    -2.900  0.632  -8.088 1.00 0.39
ATOM  614 CG TRP 1 600    -1.988 -0.338  -8.803 1.00 0.39
ATOM  615 CD1 TRP 1 600   -1.190 -0.146  -9.895 1.00 0.39
ATOM  616 CD2 TRP 1 600   -1.834 -1.714  -8.423 1.00 0.39
ATOM  617 NE1 TRP 1 600   -0.553 -1.321 -10.220 1.00 0.39
ATOM  618 CE2 TRP 1 600   -0.938 -2.293  -9.321 1.00 0.39
ATOM  619 CE3 TRP 1 600   -2.392 -2.436  -7.406 1.00 0.39
ATOM  620 CZ2 TRP 1 600   -0.589 -3.611  -9.217 1.00 0.39
ATOM  621 CZ3 TRP 1 600   -2.036 -3.763  -7.303 1.00 0.39
ATOM  622 CH2 TRP 1 600   -1.152 -4.338  -8.192 1.00 0.39
ATOM  623 N  MET 1 601    -0.216  0.219  -6.690 1.00 0.53
ATOM  624 CA MET 1 601     0.564 -0.617  -5.819 1.00 0.53
ATOM  625 C  MET 1 601     1.217  0.228  -4.766 1.00 0.53
ATOM  626 O  MET 1 601     1.278 -0.154  -3.600 1.00 0.53
ATOM  627 CB MET 1 601     1.661 -1.370  -6.587 1.00 0.53
ATOM  628 CG MET 1 601     2.274 -2.606  -5.910 1.00 0.53
ATOM  629 SD MET 1 601     3.005 -2.371  -4.261 1.00 0.53
ATOM  630 CE MET 1 601     1.511 -2.869  -3.358 1.00 0.53
ATOM  631 N  PHE 1 602     1.716  1.419  -5.147 1.00 0.69
ATOM  632 CA PHE 1 602     2.386  2.277  -4.208 1.00 0.69
ATOM  633 C  PHE 1 602     1.406  2.538  -3.102 1.00 0.69
ATOM  634 O  PHE 1 602     1.709  2.405  -1.917 1.00 0.69
ATOM  635 CB PHE 1 602     2.653  3.682  -4.783 1.00 0.69
ATOM  636 CG PHE 1 602     3.515  3.647  -5.996 1.00 0.69
ATOM  637 CD1 PHE 1 602    2.987  3.225  -7.192 1.00 0.69
ATOM  638 CD2 PHE 1 602    4.825  4.072  -5.957 1.00 0.69
ATOM  639 CE1 PHE 1 602    3.754  3.200  -8.331 1.00 0.69
ATOM  640 CE2 PHE 1 602    5.597  4.050  -7.096 1.00 0.69
ATOM  641 CZ  PHE 1 602    5.062  3.615  -8.285 1.00 0.69
ATOM  642 N  LEU 1 603     0.168  2.892  -3.473 1.00 0.63
ATOM  643 CA LEU 1 603    -0.807  3.239  -2.483 1.00 0.63
ATOM  644 C  LEU 1 603    -1.101  2.078  -1.589 1.00 0.63
ATOM  645 O  LEU 1 603    -1.198  2.243  -0.376 1.00 0.63
ATOM  646 CB LEU 1 603    -2.148  3.718  -3.063 1.00 0.63
ATOM  647 CG LEU 1 603    -2.117  5.146  -3.640 1.00 0.63
ATOM  648 CD1 LEU 1 603   -1.172  5.264  -4.843 1.00 0.63
ATOM  649 CD2 LEU 1 603   -3.536  5.648  -3.942 1.00 0.63
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ATOM  650 N   MET 1 604   -1.252  0.867 -2.148 1.00 0.49
ATOM  651 CA  MET 1 604   -1.562 -0.244 -1.299 1.00 0.49
ATOM  652 C   MET 1 604   -0.425 -0.409 -0.343 1.00 0.49
ATOM  653 O   MET 1 604   -0.629 -0.699  0.835 1.00 0.49
ATOM  654 CB  MET 1 604   -1.713 -1.566 -2.070 1.00 0.49
ATOM  655 CG  MET 1 604   -2.928 -1.602 -2.999 1.00 0.49
ATOM  656 SD  MET 1 604   -3.371 -3.261 -3.593 1.00 0.49
ATOM  657 CE  MET 1 604   -4.703 -2.693 -4.687 1.00 0.49
ATOM  658 N   ALA 1 605    0.813 -0.234 -0.842 1.00 0.46
ATOM  659 CA  ALA 1 605    1.973 -0.428 -0.025 1.00 0.46
ATOM  660 C   ALA 1 605    2.080  0.598  1.060 1.00 0.46
ATOM  661 O   ALA 1 605    2.354  0.234  2.202 1.00 0.46
ATOM  662 CB  ALA 1 605    3.284 -0.438 -0.820 1.00 0.46
ATOM  663 N   PHE 1 606    1.856  1.899  0.761 1.00 0.53
ATOM  664 CA  PHE 1 606    1.972  2.853  1.833 1.00 0.53
ATOM  665 C   PHE 1 606    0.986  2.488  2.897 1.00 0.53
ATOM  666 O   PHE 1 606    1.304  2.529  4.080 1.00 0.53
ATOM  667 CB  PHE 1 606    1.665  4.323  1.489 1.00 0.53
ATOM  668 CG  PHE 1 606    2.879  4.986  0.949 1.00 0.53
ATOM  669 CD1 PHE 1 606    4.053  4.947  1.664 1.00 0.53
ATOM  670 CD2 PHE 1 606    2.835  5.709 -0.220 1.00 0.53
ATOM  671 CE1 PHE 1 606    5.185  5.570  1.198 1.00 0.53
ATOM  672 CE2 PHE 1 606    3.965  6.340 -0.684 1.00 0.53
ATOM  673 CZ  PHE 1 606    5.143  6.262  0.015 1.00 0.53
ATOM  674 N   ALA 1 607   -0.235  2.084  2.531 1.00 0.30
ATOM  675 CA  ALA 1 607   -1.186  1.776  3.560 1.00 0.30
ATOM  676 C   ALA 1 607   -0.664  0.648  4.398 1.00 0.30
ATOM  677 O   ALA 1 607   -0.782  0.671  5.624 1.00 0.30
ATOM  678 CB  ALA 1 607   -2.548  1.336  2.997 1.00 0.30
ATOM  679 N   LEU 1 608   -0.062 -0.373  3.759 1.00 0.08
ATOM  680 CA  LEU 1 608    0.419 -1.510  4.492 1.00 0.08
ATOM  681 C   LEU 1 608    1.488 -1.092  5.451 1.00 0.08
ATOM  682 O   LEU 1 608    1.457 -1.456  6.626 1.00 0.08
ATOM  683 CB  LEU 1 608    1.031 -2.598  3.589 1.00 0.08
ATOM  684 CG  LEU 1 608    1.572 -3.821  4.364 1.00 0.08
ATOM  685 CD1 LEU 1 608    0.457 -4.567  5.110 1.00 0.08
ATOM  686 CD2 LEU 1 608    2.388 -4.743  3.445 1.00 0.08
ATOM  687 N   GLY 1 609    2.461 -0.290  4.986 1.00 0.10
ATOM  688 CA  GLY 1 609    3.544  0.074  5.850 1.00 0.10
ATOM  689 C   GLY 1 609    3.006  0.831  7.024 1.00 0.10
ATOM  690 O   GLY 1 609    3.383  0.583  8.169 1.00 0.10
ATOM  691 N   TRP 1 610    2.087  1.776  6.766 1.00 0.19
ATOM  692 CA  TRP 1 610    1.563  2.603  7.814 1.00 0.19
ATOM  693 C   TRP 1 610    0.869  1.794  8.865 1.00 0.19
ATOM  694 O   TRP 1 610    1.122  1.963 10.058 1.00 0.19
ATOM  695 CB  TRP 1 610    0.576  3.658  7.279 1.00 0.19
ATOM  696 CG  TRP 1 610   -0.277  4.343  8.322 1.00 0.19
ATOM  697 CD1 TRP 1 610   -1.553  4.017  8.665 1.00 0.19
ATOM  698 CD2 TRP 1 610    0.088  5.465  9.148 1.00 0.19
ATOM  699 NE1 TRP 1 610   -2.010  4.864  9.645 1.00 0.19
ATOM  700 CE2 TRP 1 610   -1.011  5.758  9.955 1.00 0.19
ATOM  701 CE3 TRP 1 610    1.237  6.195  9.234 1.00 0.19
ATOM  702 CZ2 TRP 1 610   -0.976  6.783 10.855 1.00 0.19
ATOM  703 CZ3 TRP 1 610    1.272  7.227 10.145 1.00 0.19
ATOM  704 CH2 TRP 1 610    0.185  7.517 10.942 1.00 0.19
ATOM  705 N   ARG 1 611   -0.018  0.874  8.461 1.00 0.36
ATOM  706 CA  ARG 1 611   -0.765  0.113  9.420 1.00 0.36
ATOM  707 C   ARG 1 611    0.129 -0.825 10.166 1.00 0.36
ATOM  708 O   ARG 1 611   -0.172 -1.222 11.290 1.00 0.36
ATOM  709 CB  ARG 1 611   -1.947 -0.656  8.795 1.00 0.36
ATOM  710 CG  ARG 1 611   -1.594 -1.605  7.649 1.00 0.36
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ATOM   711  CD  ARG 1 611     -2.843  -2.052   6.878  1.00  0.36
ATOM   712  NE  ARG 1 611     -2.414  -2.804   5.665  1.00  0.36
ATOM   713  CZ  ARG 1 611     -3.338  -3.131   4.715  1.00  0.36
ATOM   714  NH1 ARG 1 611     -4.631  -2.718   4.857  1.00  0.36
ATOM   715  NH2 ARG 1 611     -2.979  -3.868   3.623  1.00  0.36
ATOM   716  N   SER 1 612      1.225  -1.249   9.522  1.00  0.43
ATOM   717  CA  SER 1 612      2.174  -2.186  10.050  1.00  0.43
ATOM   718  C   SER 1 612      3.117  -1.602  11.065  1.00  0.43
ATOM   719  O   SER 1 612      3.787  -2.381  11.742  1.00  0.43
ATOM   720  CB  SER 1 612      2.991  -2.907   8.960  1.00  0.43
ATOM   721  OG  SER 1 612      3.707  -1.977   8.165  1.00  0.43
ATOM   722  N   TYR 1 613      3.223  -0.256  11.197  1.00  0.36
ATOM   723  CA  TYR 1 613      4.276   0.291  12.022  1.00  0.36
ATOM   724  C   TYR 1 613      4.237  -0.287  13.399  1.00  0.36
ATOM   725  O   TYR 1 613      5.247  -0.796  13.878  1.00  0.36
ATOM   726  CB  TYR 1 613      4.256   1.814  12.241  1.00  0.36
ATOM   727  CG  TYR 1 613      4.256   2.505  10.930  1.00  0.36
ATOM   728  CD1 TYR 1 613      5.079   2.095   9.908  1.00  0.36
ATOM   729  CD2 TYR 1 613      3.376   3.534  10.714  1.00  0.36
ATOM   730  CE1 TYR 1 613      5.053   2.732   8.690  1.00  0.36
ATOM   731  CE2 TYR 1 613      3.354   4.176   9.505  1.00  0.36
ATOM   732  CZ  TYR 1 613      4.189   3.781   8.489  1.00  0.36
ATOM   733  OH  TYR 1 613      4.146   4.451   7.248  1.00  0.36
ATOM   734  N   ARG 1 614      3.061  -0.308  14.042  1.00  0.35
ATOM   735  CA  ARG 1 614      3.003  -0.756  15.402  1.00  0.35
ATOM   736  C   ARG 1 614      3.435  -2.187  15.518  1.00  0.35
ATOM   737  O   ARG 1 614      4.107  -2.550  16.482  1.00  0.35
ATOM   738  CB  ARG 1 614      1.608  -0.581  16.027  1.00  0.35
ATOM   739  CG  ARG 1 614      1.273   0.899  16.238  1.00  0.35
ATOM   740  CD  ARG 1 614      0.000   1.165  17.044  1.00  0.35
ATOM   741  NE  ARG 1 614     -0.083   2.640  17.244  1.00  0.35
ATOM   742  CZ  ARG 1 614     -1.118   3.186  17.948  1.00  0.35
ATOM   743  NH1 ARG 1 614     -2.094   2.383  18.461  1.00  0.35
ATOM   744  NH2 ARG 1 614     -1.175   4.536  18.139  1.00  0.35
ATOM   745  N   GLN 1 615      3.075  -3.054  14.552  1.00  0.40
ATOM   746  CA  GLN 1 615      3.466  -4.428  14.697  1.00  0.40
ATOM   747  C   GLN 1 615      4.811  -4.597  14.072  1.00  0.40
ATOM   748  O   GLN 1 615      4.927  -4.855  12.876  1.00  0.40
ATOM   749  CB  GLN 1 615      2.505  -5.418  14.012  1.00  0.40
ATOM   750  CG  GLN 1 615      1.105  -5.450  14.637  1.00  0.40
ATOM   751  CD  GLN 1 615      0.327  -4.230  14.160  1.00  0.40
ATOM   752  OE1 GLN 1 615     -0.699  -3.875  14.736  1.00  0.40
ATOM   753  NE2 GLN 1 615      0.820  -3.575  13.076  1.00  0.40
ATOM   754  N   SER 1 616      5.871  -4.490  14.893  1.00  0.38
ATOM   755  CA  SER 1 616      7.205  -4.567  14.381  1.00  0.38
ATOM   756  C   SER 1 616      7.603  -5.993  14.244  1.00  0.38
ATOM   757  O   SER 1 616      7.004  -6.872  14.861  1.00  0.38
ATOM   758  CB  SER 1 616      8.246  -3.885  15.283  1.00  0.38
ATOM   759  OG  SER 1 616      8.331  -4.563  16.528  1.00  0.38
ATOM   760  N   SER 1 617      8.618  -6.216  13.380  1.00  0.34
ATOM   761  CA  SER 1 617      9.277  -7.462  13.112  1.00  0.34
ATOM   762  C   SER 1 617      9.101  -7.783  11.679  1.00  0.34
ATOM   763  O   SER 1 617      8.136  -7.370  11.044  1.00  0.34
ATOM   764  CB  SER 1 617      8.794  -8.691  13.909  1.00  0.34
ATOM   765  OG  SER 1 617      9.025  -8.493  15.296  1.00  0.34
ATOM   766  N   ALA 1 618     10.038  -8.574  11.133  1.00  0.31
ATOM   767  CA  ALA 1 618      9.912  -8.986   9.772  1.00  0.31
ATOM   768  C   ALA 1 618      8.631  -9.736   9.743  1.00  0.31
ATOM   769  O   ALA 1 618      7.901  -9.753   8.753  1.00  0.31
ATOM   770  CB  ALA 1 618     11.029  -9.947   9.330  1.00  0.31
ATOM   771  N   ASN 1 619      8.349 -10.365  10.891  1.00  0.35
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ATOM   772 CA  ASN 1 619     7.190 -11.142  11.140 1.00 0.35
ATOM   773 C   ASN 1 619     5.960 -10.277  11.190 1.00 0.35
ATOM   774 O   ASN 1 619     4.845 -10.793  11.173 1.00 0.35
ATOM   775 CB  ASN 1 619     7.280 -11.924  12.461 1.00 0.35
ATOM   776 CG  ASN 1 619     8.427 -12.924  12.335 1.00 0.35
ATOM   777 OD1 ASN 1 619     9.382 -12.881  13.109 1.00 0.35
ATOM   778 ND2 ASN 1 619     8.339 -13.845  11.338 1.00 0.35
ATOM   779 N   LEU 1 620     6.076  -8.940  11.292 1.00 0.39
ATOM   780 CA  LEU 1 620     4.804  -8.298  11.401 1.00 0.39
ATOM   781 C   LEU 1 620     4.526  -7.328  10.294 1.00 0.39
ATOM   782 O   LEU 1 620     5.102  -6.243  10.228 1.00 0.39
ATOM   783 CB  LEU 1 620     4.612  -7.574  12.743 1.00 0.39
ATOM   784 CG  LEU 1 620     4.585  -8.531  13.951 1.00 0.39
ATOM   785 CD1 LEU 1 620     3.372  -9.470  13.893 1.00 0.39
ATOM   786 CD2 LEU 1 620     5.911  -9.294  14.094 1.00 0.39
ATOM   787 N   LEU 1 621     3.606  -7.728   9.391 1.00 0.36
ATOM   788 CA  LEU 1 621     3.051  -6.876   8.378 1.00 0.36
ATOM   789 C   LEU 1 621     1.576  -7.096   8.477 1.00 0.36
ATOM   790 O   LEU 1 621     1.109  -8.233   8.431 1.00 0.36
ATOM   791 CB  LEU 1 621     3.454  -7.225   6.936 1.00 0.36
ATOM   792 CG  LEU 1 621     4.927  -6.933   6.605 1.00 0.36
ATOM   793 CD1 LEU 1 621     5.248  -7.307   5.150 1.00 0.36
ATOM   794 CD2 LEU 1 621     5.296  -5.479   6.940 1.00 0.36
ATOM   795 N   CYS 1 622     0.790  -6.014   8.626 1.00 0.33
ATOM   796 CA  CYS 1 622    -0.619  -6.208   8.778 1.00 0.33
ATOM   797 C   CYS 1 622    -1.297  -6.000   7.469 1.00 0.33
ATOM   798 O   CYS 1 622    -1.742  -4.897   7.161 1.00 0.33
ATOM   799 CB  CYS 1 622    -1.277  -5.221   9.753 1.00 0.33
ATOM   800 SG  CYS 1 622    -0.819  -5.533  11.478 1.00 0.33
ATOM   801 N   PHE 1 623    -1.427  -7.066   6.663 1.00 0.23
ATOM   802 CA  PHE 1 623    -2.157  -6.892   5.446 1.00 0.23
ATOM   803 C   PHE 1 623    -3.554  -6.558   5.847 1.00 0.23
ATOM   804 O   PHE 1 623    -4.206  -5.711   5.237 1.00 0.23
ATOM   805 CB  PHE 1 623    -2.223  -8.146   4.554 1.00 0.23
ATOM   806 CG  PHE 1 623    -0.889  -8.312   3.914 1.00 0.23
ATOM   807 CD1 PHE 1 623    -0.599  -7.645   2.748 1.00 0.23
ATOM   808 CD2 PHE 1 623     0.077  -9.109   4.477 1.00 0.23
ATOM   809 CE1 PHE 1 623     0.627  -7.783   2.141 1.00 0.23
ATOM   810 CE2 PHE 1 623     1.304  -9.251   3.874 1.00 0.23
ATOM   811 CZ  PHE 1 623     1.586  -8.588   2.704 1.00 0.23
ATOM   812 N   ALA 1 624    -4.046  -7.248   6.892 1.00 0.28
ATOM   813 CA  ALA 1 624    -5.351  -7.021   7.439 1.00 0.28
ATOM   814 C   ALA 1 624    -5.229  -7.359   8.890 1.00 0.28
ATOM   815 O   ALA 1 624    -4.285  -8.041   9.285 1.00 0.28
ATOM   816 CB  ALA 1 624    -6.438  -7.938   6.848 1.00 0.28
ATOM   817 N   PRO 1 625    -6.130  -6.898   9.714 1.00 0.58
ATOM   818 CA  PRO 1 625    -6.054  -7.227  11.107 1.00 0.58
ATOM   819 C   PRO 1 625    -6.288  -8.688  11.219 1.00 0.58
ATOM   820 O   PRO 1 625    -5.817  -9.328  12.159 1.00 0.58
ATOM   821 CB  PRO 1 625    -7.083  -6.329  11.806 1.00 0.58
ATOM   822 CG  PRO 1 625    -7.869  -5.658  10.659 1.00 0.58
ATOM   823 CD  PRO 1 625    -6.896  -5.691   9.471 1.00 0.58
ATOM   824 N   ASP 1 626    -7.035  -9.206  10.241 1.00 0.59
ATOM   825 CA  ASP 1 626    -7.416 -10.568  10.093 1.00 0.59
ATOM   826 C   ASP 1 626    -6.220 -11.387   9.713 1.00 0.59
ATOM   827 O   ASP 1 626    -6.154 -12.571  10.037 1.00 0.59
ATOM   828 CB  ASP 1 626    -8.458 -10.697   8.972 1.00 0.59
ATOM   829 CG  ASP 1 626    -9.119 -12.035   9.151 1.00 0.59
ATOM   830 OD1 ASP 1 626    -8.700 -12.723  10.116 1.00 0.59
ATOM   831 OD2 ASP 1 626   -10.033 -12.389   8.359 1.00 0.59
ATOM   832 N   LEU 1 627    -5.262 -10.799   8.959 1.00 0.40
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ATOM   833 CA  LEU 1 627    -4.156 -11.601   8.517  1.00  0.40
ATOM   834 C   LEU 1 627    -2.873 -10.863   8.760  1.00  0.40
ATOM   835 O   LEU 1 627    -2.474 -10.015   7.967  1.00  0.40
ATOM   836 CB  LEU 1 627    -4.237 -11.897   7.006  1.00  0.40
ATOM   837 CG  LEU 1 627    -3.086 -12.752   6.449  1.00  0.40
ATOM   838 CD1 LEU 1 627    -3.121 -14.176   7.031  1.00  0.40
ATOM   839 CD2 LEU 1 627    -3.074 -12.736   4.911  1.00  0.40
ATOM   840 N   ILE 1 628    -2.165 -11.203   9.856  1.00  0.54
ATOM   841 CA  ILE 1 628    -0.900 -10.585  10.128  1.00  0.54
ATOM   842 C   ILE 1 628     0.130 -11.549   9.617  1.00  0.54
ATOM   843 O   ILE 1 628     0.138 -12.727   9.968  1.00  0.54
ATOM   844 CB  ILE 1 628    -0.685 -10.303  11.591  1.00  0.54
ATOM   845 CG1 ILE 1 628     0.537  -9.397  11.795  1.00  0.54
ATOM   846 CG2 ILE 1 628    -0.632 -11.634  12.360  1.00  0.54
ATOM   847 CD1 ILE 1 628     0.594  -8.779  13.191  1.00  0.54
ATOM   848 N   ILE 1 629     1.027 -11.047   8.752  1.00  0.64
ATOM   849 CA  ILE 1 629     1.979 -11.834   8.023  1.00  0.64
ATOM   850 C   ILE 1 629     3.342 -11.573   8.573  1.00  0.64
ATOM   851 O   ILE 1 629     3.671 -10.449   8.948  1.00  0.64
ATOM   852 CB  ILE 1 629     1.927 -11.403   6.579  1.00  0.64
ATOM   853 CG1 ILE 1 629     2.792 -12.233   5.626  1.00  0.64
ATOM   854 CG2 ILE 1 629     2.287  -9.911   6.572  1.00  0.64
ATOM   855 CD1 ILE 1 629     4.281 -11.955   5.781  1.00  0.64
ATOM   856 N   ASN 1 630     4.169 -12.635   8.633  1.00  0.41
ATOM   857 CA  ASN 1 630     5.482 -12.552   9.194  1.00  0.41
ATOM   858 C   ASN 1 630     6.475 -12.894   8.133  1.00  0.41
ATOM   859 O   ASN 1 630     6.129 -13.466   7.103  1.00  0.41
ATOM   860 CB  ASN 1 630     5.654 -13.509  10.396  1.00  0.41
ATOM   861 CG  ASN 1 630     5.480 -14.950   9.969  1.00  0.41
ATOM   862 OD1 ASN 1 630     5.193 -15.240   8.812  1.00  0.41
ATOM   863 ND2 ASN 1 630     5.644 -15.888  10.938  1.00  0.41
ATOM   864 N   GLU 1 631     7.758 -12.570   8.376  1.00  0.35
ATOM   865 CA  GLU 1 631     8.759 -12.772   7.371  1.00  0.35
ATOM   866 C   GLU 1 631     8.763 -14.218   6.985  1.00  0.35
ATOM   867 O   GLU 1 631     8.946 -14.556   5.819  1.00  0.35
ATOM   868 CB  GLU 1 631    10.186 -12.437   7.834  1.00  0.35
ATOM   869 CG  GLU 1 631    10.707 -13.352   8.945  1.00  0.35
ATOM   870 CD  GLU 1 631    12.203 -13.111   9.077  1.00  0.35
ATOM   871 OE1 GLU 1 631    12.733 -12.257   8.317  1.00  0.35
ATOM   872 OE2 GLU 1 631    12.839 -13.780   9.934  1.00  0.35
ATOM   873 N   GLN 1 632     8.557 -15.133   7.941  1.00  0.52
ATOM   874 CA  GLN 1 632     8.618 -16.517   7.571  1.00  0.52
ATOM   875 C   GLN 1 632     7.574 -16.821   6.535  1.00  0.52
ATOM   876 O   GLN 1 632     7.866 -17.470   5.531  1.00  0.52
ATOM   877 CB  GLN 1 632     8.368 -17.464   8.756  1.00  0.52
ATOM   878 CG  GLN 1 632     9.510 -17.490   9.774  1.00  0.52
ATOM   879 CD  GLN 1 632    10.662 -18.261   9.145  1.00  0.52
ATOM   880 OE1 GLN 1 632    11.721 -18.428   9.747  1.00  0.52
ATOM   881 NE2 GLN 1 632    10.448 -18.754   7.895  1.00  0.52
ATOM   882 N   ARG 1 633     6.333 -16.344   6.737  1.00  0.65
ATOM   883 CA  ARG 1 633     5.256 -16.668   5.845  1.00  0.65
ATOM   884 C   ARG 1 633     5.429 -16.003   4.512  1.00  0.65
ATOM   885 O   ARG 1 633     4.965 -16.513   3.496  1.00  0.65
ATOM   886 CB  ARG 1 633     3.849 -16.355   6.388  1.00  0.65
ATOM   887 CG  ARG 1 633     3.556 -14.883   6.649  1.00  0.65
ATOM   888 CD  ARG 1 633     2.143 -14.652   7.187  1.00  0.65
ATOM   889 NE  ARG 1 633     2.200 -14.773   8.672  1.00  0.65
ATOM   890 CZ  ARG 1 633     2.009 -15.985   9.271  1.00  0.65
ATOM   891 NH1 ARG 1 633     1.776 -17.093   8.509  1.00  0.65
ATOM   892 NH2 ARG 1 633     2.050 -16.087  10.631  1.00  0.65
ATOM   893 N   MET 1 634     6.112 -14.849   4.465  1.00  0.68
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ATOM 894 CA MET 1 634 6.269 -14.113 3.239 1.00 0.68
ATOM 895 C MET 1 634 6.987 -14.978 2.246 1.00 0.68
ATOM 896 O MET 1 634 6.900 -14.757 1.039 1.00 0.68
ATOM 897 CB MET 1 634 7.101 -12.828 3.408 1.00 0.68
ATOM 898 CG MET 1 634 8.600 -13.100 3.547 1.00 0.68
ATOM 899 SD MET 1 634 9.560 -11.763 4.321 1.00 0.68
ATOM 900 CE MET 1 634 10.886 -12.819 4.967 1.00 0.68
ATOM 901 N THR 1 635 7.711 -15.993 2.745 1.00 0.73
ATOM 902 CA THR 1 635 8.559 -16.864 1.977 1.00 0.73
ATOM 903 C THR 1 635 7.806 -17.553 0.873 1.00 0.73
ATOM 904 O THR 1 635 8.424 -17.994 -0.094 1.00 0.73
ATOM 905 CB THR 1 635 9.194 -17.939 2.807 1.00 0.73
ATOM 906 OG1 THR 1 635 10.204 -18.603 2.060 1.00 0.73
ATOM 907 CG2 THR 1 635 8.106 -18.942 3.230 1.00 0.73
ATOM 908 N LEU 1 636 6.469 -17.684 0.969 1.00 0.86
ATOM 909 CA LEU 1 636 5.751 -18.430 -0.032 1.00 0.86
ATOM 910 C LEU 1 636 6.039 -17.924 -1.433 1.00 0.86
ATOM 911 O LEU 1 636 6.092 -18.772 -2.322 1.00 0.86
ATOM 912 CB LEU 1 636 4.229 -18.455 0.191 1.00 0.86
ATOM 913 CG LEU 1 636 3.802 -19.425 1.312 1.00 0.86
ATOM 914 CD1 LEU 1 636 4.438 -19.066 2.661 1.00 0.86
ATOM 915 CD2 LEU 1 636 2.275 -19.537 1.396 1.00 0.86
ATOM 916 N PRO 1 637 6.111 -16.634 -1.719 1.00 0.89
ATOM 917 CA PRO 1 637 6.582 -16.193 -3.029 1.00 0.89
ATOM 918 C PRO 1 637 7.954 -15.629 -2.840 1.00 0.89
ATOM 919 O PRO 1 637 8.410 -15.566 -1.705 1.00 0.89
ATOM 920 CB PRO 1 637 5.629 -15.087 -3.481 1.00 0.89
ATOM 921 CG PRO 1 637 4.391 -15.244 -2.588 1.00 0.89
ATOM 922 CD PRO 1 637 4.954 -15.859 -1.299 1.00 0.89
ATOM 923 N CYS 1 638 8.632 -15.137 -3.899 1.00 0.83
ATOM 924 CA CYS 1 638 9.892 -14.475 -3.665 1.00 0.83
ATOM 925 C CYS 1 638 9.581 -13.084 -3.175 1.00 0.83
ATOM 926 O CYS 1 638 10.144 -12.095 -3.645 1.00 0.83
ATOM 927 CB CYS 1 638 10.749 -14.344 -4.937 1.00 0.83
ATOM 928 SG CYS 1 638 9.943 -13.342 -6.223 1.00 0.83
ATOM 929 N MET 1 639 8.647 -13.005 -2.208 1.00 0.83
ATOM 930 CA MET 1 639 8.116 -11.864 -1.524 1.00 0.83
ATOM 931 C MET 1 639 9.159 -11.384 -0.570 1.00 0.83
ATOM 932 O MET 1 639 9.200 -10.210 -0.221 1.00 0.83
ATOM 933 CB MET 1 639 6.911 -12.243 -0.642 1.00 0.83
ATOM 934 CG MET 1 639 5.951 -11.093 -0.332 1.00 0.83
ATOM 935 SD MET 1 639 4.622 -10.856 -1.556 1.00 0.83
ATOM 936 CE MET 1 639 5.572 -11.366 -3.016 1.00 0.83
ATOM 937 N TYR 1 640 10.041 -12.301 -0.142 1.00 0.81
ATOM 938 CA TYR 1 640 10.993 -12.101 0.914 1.00 0.81
ATOM 939 C TYR 1 640 11.701 -10.796 0.742 1.00 0.81
ATOM 940 O TYR 1 640 11.752 -9.991 1.673 1.00 0.81
ATOM 941 CB TYR 1 640 12.046 -13.227 0.874 1.00 0.81
ATOM 942 CG TYR 1 640 13.176 -12.967 1.810 1.00 0.81
ATOM 943 CD1 TYR 1 640 13.113 -13.365 3.122 1.00 0.81
ATOM 944 CD2 TYR 1 640 14.316 -12.340 1.361 1.00 0.81
ATOM 945 CE1 TYR 1 640 14.160 -13.132 3.982 1.00 0.81
ATOM 946 CE2 TYR 1 640 15.367 -12.103 2.213 1.00 0.81
ATOM 947 CZ TYR 1 640 15.290 -12.500 3.526 1.00 0.81
ATOM 948 OH TYR 1 640 16.369 -12.260 4.403 1.00 0.81
ATOM 949 N ASP 1 641 12.237 -10.525 -0.455 1.00 0.63
ATOM 950 CA ASP 1 641 12.986 -9.314 -0.604 1.00 0.63
ATOM 951 C ASP 1 641 12.114 -8.124 -0.342 1.00 0.63
ATOM 952 O ASP 1 641 12.479 -7.252 0.444 1.00 0.63
ATOM 953 CB ASP 1 641 13.614 -9.163 -2.002 1.00 0.63
ATOM 954 CG ASP 1 641 12.512 -9.127 -3.054 1.00 0.63

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ATOM   955 OD1 ASP 1 641    11.468 -9.804 -2.855 1.00 0.63
ATOM   956 OD2 ASP 1 641    12.702 -8.415 -4.077 1.00 0.63
ATOM   957 N  GLN 1 642    10.927 -8.061 -0.971 1.00 0.38
ATOM   958 CA GLN 1 642    10.081 -6.911 -0.818 1.00 0.38
ATOM   959 C  GLN 1 642     9.535 -6.842  0.573 1.00 0.38
ATOM   960 O  GLN 1 642     9.455 -5.769  1.166 1.00 0.38
ATOM   961 CB GLN 1 642     8.901 -6.886 -1.805 1.00 0.38
ATOM   962 CG GLN 1 642     7.900 -8.030 -1.641 1.00 0.38
ATOM   963 CD GLN 1 642     6.823 -7.829 -2.700 1.00 0.38
ATOM   964 OE1 GLN 1 642    5.800 -8.511 -2.711 1.00 0.38
ATOM   965 NE2 GLN 1 642    7.061 -6.858 -3.622 1.00 0.38
ATOM   966 N  CYS 1 643     9.164 -7.995  1.145 1.00 0.24
ATOM   967 CA CYS 1 643     8.557 -7.993  2.439 1.00 0.24
ATOM   968 C  CYS 1 643     9.519 -7.380  3.393 1.00 0.24
ATOM   969 O  CYS 1 643     9.125 -6.579  4.239 1.00 0.24
ATOM   970 CB CYS 1 643     8.202 -9.401  2.928 1.00 0.24
ATOM   971 SG CYS 1 643     7.433 -9.392  4.575 1.00 0.24
ATOM   972 N  LYS 1 644    10.814 -7.727  3.277 1.00 0.26
ATOM   973 CA LYS 1 644    11.765 -7.146  4.177 1.00 0.26
ATOM   974 C  LYS 1 644    11.804 -5.669  3.942 1.00 0.26
ATOM   975 O  LYS 1 644    11.795 -4.888  4.892 1.00 0.26
ATOM   976 CB LYS 1 644    13.197 -7.679  4.004 1.00 0.26
ATOM   977 CG LYS 1 644    13.377 -9.124  4.470 1.00 0.26
ATOM   978 CD LYS 1 644    14.778 -9.673  4.194 1.00 0.26
ATOM   979 CE LYS 1 644    15.843 -9.093  5.128 1.00 0.26
ATOM   980 NZ LYS 1 644    17.170 -9.665  4.809 1.00 0.26
ATOM   981 N  HIS 1 645    11.820 -5.237  2.665 1.00 0.33
ATOM   982 CA HIS 1 645    11.905 -3.827  2.417 1.00 0.33
ATOM   983 C  HIS 1 645    10.707 -3.166  3.024 1.00 0.33
ATOM   984 O  HIS 1 645    10.823 -2.137  3.686 1.00 0.33
ATOM   985 CB HIS 1 645    11.985 -3.468  0.924 1.00 0.33
ATOM   986 CG HIS 1 645    13.330 -3.796  0.341 1.00 0.33
ATOM   987 ND1 HIS 1 645    13.639 -4.977 -0.296 1.00 0.33
ATOM   988 CD2 HIS 1 645    14.477 -3.062  0.333 1.00 0.33
ATOM   989 CE1 HIS 1 645    14.945 -4.899 -0.655 1.00 0.33
ATOM   990 NE2 HIS 1 645    15.497 -3.754 -0.293 1.00 0.33
ATOM   991 N  MET 1 646     9.522 -3.770  2.850 1.00 0.28
ATOM   992 CA MET 1 646     8.324 -3.212  3.401 1.00 0.28
ATOM   993 C  MET 1 646     8.498 -3.168  4.887 1.00 0.28
ATOM   994 O  MET 1 646     8.093 -2.216  5.553 1.00 0.28
ATOM   995 CB MET 1 646     7.085 -4.072  3.102 1.00 0.28
ATOM   996 CG MET 1 646     6.769 -4.179  1.609 1.00 0.28
ATOM   997 SD MET 1 646     5.313 -5.191  1.211 1.00 0.28
ATOM   998 CE MET 1 646     5.515 -5.055 -0.588 1.00 0.28
ATOM   999 N  LEU 1 647     9.135 -4.203  5.453 1.00 0.37
ATOM  1000 CA LEU 1 647     9.302 -4.259  6.877 1.00 0.37
ATOM  1001 C  LEU 1 647    10.067 -3.044  7.293 1.00 0.37
ATOM  1002 O  LEU 1 647     9.695 -2.348  8.239 1.00 0.37
ATOM  1003 CB LEU 1 647    10.155 -5.470  7.283 1.00 0.37
ATOM  1004 CG LEU 1 647     9.510 -6.823  6.937 1.00 0.37
ATOM  1005 CD1 LEU 1 647    10.517 -7.972  7.083 1.00 0.37
ATOM  1006 CD2 LEU 1 647     8.221 -7.048  7.744 1.00 0.37
ATOM  1007 N  TYR 1 648    11.150 -2.750  6.552 1.00 0.59
ATOM  1008 CA TYR 1 648    12.029 -1.671  6.883 1.00 0.59
ATOM  1009 C  TYR 1 648    11.295 -0.372  6.764 1.00 0.59
ATOM  1010 O  TYR 1 648    11.471  0.520  7.593 1.00 0.59
ATOM  1011 CB TYR 1 648    13.257 -1.613  5.958 1.00 0.59
ATOM  1012 CG TYR 1 648    14.105 -0.469  6.394 1.00 0.59
ATOM  1013 CD1 TYR 1 648    13.869  0.806  5.932 1.00 0.59
ATOM  1014 CD2 TYR 1 648    15.140 -0.677  7.274 1.00 0.59
ATOM  1015 CE1 TYR 1 648    14.656  1.855  6.342 1.00 0.59
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ATOM  1016  CE2 TYR 1 648     15.932   0.368   7.689  1.00  0.59
ATOM  1017  CZ  TYR 1 648     15.689   1.636   7.222  1.00  0.59
ATOM  1018  OH  TYR 1 648     16.499   2.713   7.644  1.00  0.59
ATOM  1019  N   VAL 1 649     10.440  -0.215   5.737  1.00  0.47
ATOM  1020  CA  VAL 1 649      9.815   1.070   5.594  1.00  0.47
ATOM  1021  C   VAL 1 649      8.989   1.394   6.805  1.00  0.47
ATOM  1022  O   VAL 1 649      9.124   2.473   7.373  1.00  0.47
ATOM  1023  CB  VAL 1 649      8.949   1.194   4.368  1.00  0.47
ATOM  1024  CG1 VAL 1 649      7.719   0.283   4.498  1.00  0.47
ATOM  1025  CG2 VAL 1 649      8.591   2.680   4.187  1.00  0.47
ATOM  1026  N   SER 1 650      8.143   0.468   7.285  1.00  0.27
ATOM  1027  CA  SER 1 650      7.306   0.811   8.402  1.00  0.27
ATOM  1028  C   SER 1 650      8.180   1.111   9.573  1.00  0.27
ATOM  1029  O   SER 1 650      7.870   1.984  10.385  1.00  0.27
ATOM  1030  CB  SER 1 650      6.341  -0.324   8.797  1.00  0.27
ATOM  1031  OG  SER 1 650      7.061  -1.448   9.279  1.00  0.27
ATOM  1032  N   SER 1 651      9.308   0.391   9.701  1.00  0.27
ATOM  1033  CA  SER 1 651     10.133   0.627  10.846  1.00  0.27
ATOM  1034  C   SER 1 651     10.635   2.032  10.785  1.00  0.27
ATOM  1035  O   SER 1 651     10.673   2.728  11.799  1.00  0.27
ATOM  1036  CB  SER 1 651     11.336  -0.332  10.964  1.00  0.27
ATOM  1037  OG  SER 1 651     12.300  -0.081   9.954  1.00  0.27
ATOM  1038  N   GLU 1 652     11.015   2.499   9.582  1.00  0.28
ATOM  1039  CA  GLU 1 652     11.531   3.830   9.462  1.00  0.28
ATOM  1040  C   GLU 1 652     10.443   4.785   9.825  1.00  0.28
ATOM  1041  O   GLU 1 652     10.691   5.801  10.469  1.00  0.28
ATOM  1042  CB  GLU 1 652     12.038   4.159   8.047  1.00  0.28
ATOM  1043  CG  GLU 1 652     12.859   5.451   7.989  1.00  0.28
ATOM  1044  CD  GLU 1 652     13.572   5.497   6.646  1.00  0.28
ATOM  1045  OE1 GLU 1 652     13.370   4.553   5.836  1.00  0.28
ATOM  1046  OE2 GLU 1 652     14.332   6.475   6.413  1.00  0.28
ATOM  1047  N   LEU 1 653      9.192   4.485   9.431  1.00  0.34
ATOM  1048  CA  LEU 1 653      8.137   5.394   9.768  1.00  0.34
ATOM  1049  C   LEU 1 653      7.999   5.464  11.253  1.00  0.34
ATOM  1050  O   LEU 1 653      7.721   6.536  11.790  1.00  0.34
ATOM  1051  CB  LEU 1 653      6.785   5.063   9.134  1.00  0.34
ATOM  1052  CG  LEU 1 653      6.705   5.465   7.648  1.00  0.34
ATOM  1053  CD1 LEU 1 653      6.707   6.993   7.496  1.00  0.34
ATOM  1054  CD2 LEU 1 653      7.799   4.799   6.804  1.00  0.34
ATOM  1055  N   HIS 1 654      8.171   4.335  11.973  1.00  0.45
ATOM  1056  CA  HIS 1 654      8.119   4.466  13.401  1.00  0.45
ATOM  1057  C   HIS 1 654      9.228   5.343  13.852  1.00  0.45
ATOM  1058  O   HIS 1 654      9.014   6.248  14.656  1.00  0.45
ATOM  1059  CB  HIS 1 654      8.345   3.192  14.220  1.00  0.45
ATOM  1060  CG  HIS 1 654      7.108   2.675  14.865  1.00  0.45
ATOM  1061  ND1 HIS 1 654      6.329   3.395  15.744  1.00  0.45
ATOM  1062  CD2 HIS 1 654      6.539   1.451  14.785  1.00  0.45
ATOM  1063  CE1 HIS 1 654      5.330   2.571  16.148  1.00  0.45
ATOM  1064  NE2 HIS 1 654      5.416   1.377  15.590  1.00  0.45
ATOM  1065  N   ARG 1 655     10.440   5.109  13.317  1.00  0.58
ATOM  1066  CA  ARG 1 655     11.582   5.841  13.780  1.00  0.58
ATOM  1067  C   ARG 1 655     11.304   7.297  13.588  1.00  0.58
ATOM  1068  O   ARG 1 655     11.511   8.106  14.489  1.00  0.58
ATOM  1069  CB  ARG 1 655     12.862   5.497  13.001  1.00  0.58
ATOM  1070  CG  ARG 1 655     13.315   4.046  13.187  1.00  0.58
ATOM  1071  CD  ARG 1 655     14.588   3.696  12.415  1.00  0.58
ATOM  1072  NE  ARG 1 655     15.730   4.359  13.105  1.00  0.58
ATOM  1073  CZ  ARG 1 655     16.357   3.731  14.141  1.00  0.58
ATOM  1074  NH1 ARG 1 655     15.945   2.493  14.540  1.00  0.58
ATOM  1075  NH2 ARG 1 655     17.400   4.340  14.778  1.00  0.58
ATOM  1076  N   LEU 1 656     10.783   7.659  12.406  1.00  0.65
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ATOM  1077  CA  LEU 1 656      10.457   9.023  12.107  1.00  0.65
ATOM  1078  C   LEU 1 656       9.298   9.465  12.943  1.00  0.65
ATOM  1079  O   LEU 1 656       9.103  10.663  13.143  1.00  0.65
ATOM  1080  CB  LEU 1 656      10.115   9.278  10.627  1.00  0.65
ATOM  1081  CG  LEU 1 656      11.347   9.325   9.698  1.00  0.65
ATOM  1082  CD1 LEU 1 656      12.123   8.001   9.689  1.00  0.65
ATOM  1083  CD2 LEU 1 656      10.954   9.789   8.287  1.00  0.65
ATOM  1084  N   GLN 1 657       8.485   8.516  13.445  1.00  0.65
ATOM  1085  CA  GLN 1 657       7.319   8.910  14.179  1.00  0.65
ATOM  1086  C   GLN 1 657       6.418   9.589  13.207  1.00  0.65
ATOM  1087  O   GLN 1 657       5.896  10.673  13.462  1.00  0.65
ATOM  1088  CB  GLN 1 657       7.620   9.893  15.324  1.00  0.65
ATOM  1089  CG  GLN 1 657       8.497   9.301  16.429  1.00  0.65
ATOM  1090  CD  GLN 1 657       8.712  10.375  17.486  1.00  0.65
ATOM  1091  OE1 GLN 1 657       9.386  10.151  18.490  1.00  0.65
ATOM  1092  NE2 GLN 1 657       8.124  11.582  17.257  1.00  0.65
ATOM  1093  N   VAL 1 658       6.212   8.936  12.049  1.00  0.48
ATOM  1094  CA  VAL 1 658       5.390   9.515  11.028  1.00  0.48
ATOM  1095  C   VAL 1 658       4.052   9.814  11.615  1.00  0.48
ATOM  1096  O   VAL 1 658       3.559   9.094  12.481  1.00  0.48
ATOM  1097  CB  VAL 1 658       5.186   8.627   9.835  1.00  0.48
ATOM  1098  CG1 VAL 1 658       4.409   7.379  10.285  1.00  0.48
ATOM  1099  CG2 VAL 1 658       4.476   9.439   8.740  1.00  0.48
ATOM  1100  N   SER 1 659       3.433  10.913  11.145  1.00  0.33
ATOM  1101  CA  SER 1 659       2.174  11.328  11.685  1.00  0.33
ATOM  1102  C   SER 1 659       1.103  11.079  10.671  1.00  0.33
ATOM  1103  O   SER 1 659       1.317  11.168   9.463  1.00  0.33
ATOM  1104  CB  SER 1 659       2.133  12.823  12.043  1.00  0.33
ATOM  1105  OG  SER 1 659       3.071  13.105  13.069  1.00  0.33
ATOM  1106  N   TYR 1 660      -0.109  10.799  11.175  1.00  0.39
ATOM  1107  CA  TYR 1 660      -1.245  10.449  10.377  1.00  0.39
ATOM  1108  C   TYR 1 660      -1.494  11.533   9.376  1.00  0.39
ATOM  1109  O   TYR 1 660      -1.664  11.257   8.191  1.00  0.39
ATOM  1110  CB  TYR 1 660      -2.492  10.287  11.262  1.00  0.39
ATOM  1111  CG  TYR 1 660      -3.708  10.080  10.430  1.00  0.39
ATOM  1112  CD1 TYR 1 660      -4.415  11.165   9.970  1.00  0.39
ATOM  1113  CD2 TYR 1 660      -4.142   8.814  10.116  1.00  0.39
ATOM  1114  CE1 TYR 1 660      -5.545  10.989   9.211  1.00  0.39
ATOM  1115  CE2 TYR 1 660      -5.274   8.632   9.356  1.00  0.39
ATOM  1116  CZ  TYR 1 660      -5.975   9.723   8.904  1.00  0.39
ATOM  1117  OH  TYR 1 660      -7.137   9.553   8.127  1.00  0.39
ATOM  1118  N   GLU 1 661      -1.466  12.804   9.817  1.00  0.36
ATOM  1119  CA  GLU 1 661      -1.754  13.901   8.938  1.00  0.36
ATOM  1120  C   GLU 1 661      -0.746  13.930   7.832  1.00  0.36
ATOM  1121  O   GLU 1 661      -1.076  14.301   6.706  1.00  0.36
ATOM  1122  CB  GLU 1 661      -1.719  15.268   9.645  1.00  0.36
ATOM  1123  CG  GLU 1 661      -2.864  15.467  10.642  1.00  0.36
ATOM  1124  CD  GLU 1 661      -2.565  14.634  11.881  1.00  0.36
ATOM  1125  OE1 GLU 1 661      -1.391  14.207  12.038  1.00  0.36
ATOM  1126  OE2 GLU 1 661      -3.508  14.418  12.688  1.00  0.36
ATOM  1127  N   GLU 1 662       0.524  13.591   8.133  1.00  0.23
ATOM  1128  CA  GLU 1 662       1.551  13.575   7.125  1.00  0.23
ATOM  1129  C   GLU 1 662       1.317  12.434   6.184  1.00  0.23
ATOM  1130  O   GLU 1 662       1.569  12.533   4.984  1.00  0.23
ATOM  1131  CB  GLU 1 662       2.968  13.378   7.687  1.00  0.23
ATOM  1132  CG  GLU 1 662       3.493  14.567   8.489  1.00  0.23
ATOM  1133  CD  GLU 1 662       4.891  14.209   8.965  1.00  0.23
ATOM  1134  OE1 GLU 1 662       5.669  13.651   8.145  1.00  0.23
ATOM  1135  OE2 GLU 1 662       5.204  14.494  10.151  1.00  0.23
ATOM  1136  N   TYR 1 663       0.819  11.313   6.731  1.00  0.31
ATOM  1137  CA  TYR 1 663       0.667  10.083   6.013  1.00  0.31
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ATOM  1138  C   TYR 1 663    -0.231  10.312   4.845  1.00  0.31
ATOM  1139  O   TYR 1 663     0.076   9.940   3.710  1.00  0.31
ATOM  1140  CB  TYR 1 663    -0.070   9.047   6.866  1.00  0.31
ATOM  1141  CG  TYR 1 663     0.473   7.805   6.318  1.00  0.31
ATOM  1142  CD1 TYR 1 663     1.757   7.581   6.691  1.00  0.31
ATOM  1143  CD2 TYR 1 663    -0.175   6.941   5.463  1.00  0.31
ATOM  1144  CE1 TYR 1 663     2.411   6.485   6.248  1.00  0.31
ATOM  1145  CE2 TYR 1 663     0.491   5.822   5.012  1.00  0.31
ATOM  1146  CZ  TYR 1 663     1.789   5.609   5.421  1.00  0.31
ATOM  1147  OH  TYR 1 663     2.569   4.512   5.023  1.00  0.31
ATOM  1148  N   LEU 1 664    -1.376  10.951   5.113  1.00  0.36
ATOM  1149  CA  LEU 1 664    -2.358  11.202   4.104  1.00  0.36
ATOM  1150  C   LEU 1 664    -1.794  12.138   3.088  1.00  0.36
ATOM  1151  O   LEU 1 664    -2.156  12.078   1.914  1.00  0.36
ATOM  1152  CB  LEU 1 664    -3.654  11.824   4.650  1.00  0.36
ATOM  1153  CG  LEU 1 664    -4.516  10.837   5.459  1.00  0.36
ATOM  1154  CD1 LEU 1 664    -3.780  10.338   6.710  1.00  0.36
ATOM  1155  CD2 LEU 1 664    -5.896  11.435   5.776  1.00  0.36
ATOM  1156  N   CYS 1 665    -0.926  13.065   3.522  1.00  0.37
ATOM  1157  CA  CYS 1 665    -0.336  13.982   2.594  1.00  0.37
ATOM  1158  C   CYS 1 665     0.482  13.184   1.632  1.00  0.37
ATOM  1159  O   CYS 1 665     0.372  13.358   0.421  1.00  0.37
ATOM  1160  CB  CYS 1 665     0.625  14.981   3.259  1.00  0.37
ATOM  1161  SG  CYS 1 665    -0.212  16.121   4.393  1.00  0.37
ATOM  1162  N   MET 1 666     1.293  12.246   2.154  1.00  0.45
ATOM  1163  CA  MET 1 666     2.172  11.464   1.336  1.00  0.45
ATOM  1164  C   MET 1 666     1.375  10.673   0.347  1.00  0.45
ATOM  1165  O   MET 1 666     1.759  10.575  -0.814  1.00  0.45
ATOM  1166  CB  MET 1 666     3.018  10.467   2.147  1.00  0.45
ATOM  1167  CG  MET 1 666     3.956   9.633   1.274  1.00  0.45
ATOM  1168  SD  MET 1 666     5.010   8.470   2.189  1.00  0.45
ATOM  1169  CE  MET 1 666     6.373   9.637   2.459  1.00  0.45
ATOM  1170  N   LYS 1 667     0.237  10.088   0.757  1.00  0.30
ATOM  1171  CA  LYS 1 667    -0.507   9.286  -0.175  1.00  0.30
ATOM  1172  C   LYS 1 667    -0.958  10.133  -1.326  1.00  0.30
ATOM  1173  O   LYS 1 667    -0.840   9.744  -2.487  1.00  0.30
ATOM  1174  CB  LYS 1 667    -1.785   8.696   0.426  1.00  0.30
ATOM  1175  CG  LYS 1 667    -1.550   7.656   1.515  1.00  0.30
ATOM  1176  CD  LYS 1 667    -2.849   7.288   2.226  1.00  0.30
ATOM  1177  CE  LYS 1 667    -2.758   6.022   3.068  1.00  0.30
ATOM  1178  NZ  LYS 1 667    -4.121   5.496   3.299  1.00  0.30
ATOM  1179  N   THR 1 668    -1.476  11.336  -1.031  1.00  0.20
ATOM  1180  CA  THR 1 668    -1.979  12.209  -2.052  1.00  0.20
ATOM  1181  C   THR 1 668    -0.879  12.491  -3.017  1.00  0.20
ATOM  1182  O   THR 1 668    -1.107  12.489  -4.228  1.00  0.20
ATOM  1183  CB  THR 1 668    -2.402  13.536  -1.484  1.00  0.20
ATOM  1184  OG1 THR 1 668    -3.495  13.371  -0.595  1.00  0.20
ATOM  1185  CG2 THR 1 668    -2.732  14.526  -2.617  1.00  0.20
ATOM  1186  N   LEU 1 669     0.343  12.742  -2.503  1.00  0.37
ATOM  1187  CA  LEU 1 669     1.433  13.036  -3.388  1.00  0.37
ATOM  1188  C   LEU 1 669     1.656  11.861  -4.283  1.00  0.37
ATOM  1189  O   LEU 1 669     1.853  12.038  -5.484  1.00  0.37
ATOM  1190  CB  LEU 1 669     2.822  13.276  -2.742  1.00  0.37
ATOM  1191  CG  LEU 1 669     3.081  14.631  -2.046  1.00  0.37
ATOM  1192  CD1 LEU 1 669     2.497  14.704  -0.634  1.00  0.37
ATOM  1193  CD2 LEU 1 669     4.577  14.979  -2.072  1.00  0.37
ATOM  1194  N   LEU 1 670     1.629  10.629  -3.732  1.00  0.59
ATOM  1195  CA  LEU 1 670     1.882   9.492  -4.572  1.00  0.59
ATOM  1196  C   LEU 1 670     0.874   9.452  -5.663  1.00  0.59
ATOM  1197  O   LEU 1 670     1.230   9.194  -6.811  1.00  0.59
ATOM  1198  CB  LEU 1 670     1.785   8.122  -3.883  1.00  0.59
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ATOM 1199 CG LEU 1 670 3.047 7.742 -3.111 1.00 0.59
ATOM 1200 CD1 LEU 1 670 4.214 7.424 -4.058 1.00 0.59
ATOM 1201 CD2 LEU 1 670 3.402 8.843 -2.123 1.00 0.59
ATOM 1202 N LEU 1 671 -0.409 9.705 -5.340 1.00 0.65
ATOM 1203 CA LEU 1 671 -1.397 9.629 -6.375 1.00 0.65
ATOM 1204 C LEU 1 671 -1.038 10.568 -7.470 1.00 0.65
ATOM 1205 O LEU 1 671 -0.835 10.166 -8.610 1.00 0.65
ATOM 1206 CB LEU 1 671 -2.799 10.126 -5.970 1.00 0.65
ATOM 1207 CG LEU 1 671 -3.703 9.172 -5.185 1.00 0.65
ATOM 1208 CD1 LEU 1 671 -5.038 9.852 -4.883 1.00 0.65
ATOM 1209 CD2 LEU 1 671 -3.954 7.872 -5.951 1.00 0.65
ATOM 1210 N LEU 1 672 -0.900 11.852 -7.135 1.00 0.38
ATOM 1211 CA LEU 1 672 -0.726 12.829 -8.161 1.00 0.38
ATOM 1212 C LEU 1 672 0.607 12.768 -8.850 1.00 0.38
ATOM 1213 O LEU 1 672 0.650 13.085 -10.033 1.00 0.38
ATOM 1214 CB LEU 1 672 -1.020 14.240 -7.643 1.00 0.38
ATOM 1215 CG LEU 1 672 -2.500 14.386 -7.248 1.00 0.38
ATOM 1216 CD1 LEU 1 672 -2.818 15.790 -6.727 1.00 0.38
ATOM 1217 CD2 LEU 1 672 -3.419 13.962 -8.403 1.00 0.38
ATOM 1218 N SER 1 673 1.705 12.430 -8.134 1.00 0.29
ATOM 1219 CA SER 1 673 3.082 12.426 -8.596 1.00 0.29
ATOM 1220 C SER 1 673 3.549 11.254 -9.428 1.00 0.29
ATOM 1221 O SER 1 673 4.437 11.413 -10.265 1.00 0.29
ATOM 1222 CB SER 1 673 4.077 12.541 -7.428 1.00 0.29
ATOM 1223 OG SER 1 673 5.410 12.535 -7.921 1.00 0.29
ATOM 1224 N SER 1 674 3.027 10.038 -9.221 1.00 0.48
ATOM 1225 CA SER 1 674 3.583 8.903 -9.911 1.00 0.48
ATOM 1226 C SER 1 674 3.374 8.971 -11.400 1.00 0.48
ATOM 1227 O SER 1 674 4.267 8.606 -12.161 1.00 0.48
ATOM 1228 CB SER 1 674 2.982 7.579 -9.435 1.00 0.48
ATOM 1229 OG SER 1 674 1.642 7.481 -9.888 1.00 0.48
ATOM 1230 N VAL 1 675 2.190 9.408 -11.869 1.00 0.57
ATOM 1231 CA VAL 1 675 1.945 9.412 -13.290 1.00 0.57
ATOM 1232 C VAL 1 675 1.945 10.799 -13.936 1.00 0.57
ATOM 1233 O VAL 1 675 1.416 10.900 -15.043 1.00 0.57
ATOM 1234 CB VAL 1 675 0.635 8.762 -13.627 1.00 0.57
ATOM 1235 CG1 VAL 1 675 -0.491 9.748 -13.281 1.00 0.57
ATOM 1236 CG2 VAL 1 675 0.655 8.272 -15.086 1.00 0.57
ATOM 1237 N PRO 1 676 2.488 11.888 -13.439 1.00 0.65
ATOM 1238 CA PRO 1 676 2.417 13.095 -14.211 1.00 0.65
ATOM 1239 C PRO 1 676 3.203 13.051 -15.468 1.00 0.65
ATOM 1240 O PRO 1 676 2.954 13.897 -16.323 1.00 0.65
ATOM 1241 CB PRO 1 676 2.950 14.214 -13.339 1.00 0.65
ATOM 1242 CG PRO 1 676 2.582 13.762 -11.938 1.00 0.65
ATOM 1243 CD PRO 1 676 2.432 12.239 -12.039 1.00 0.65
ATOM 1244 N LYS 1 677 4.169 12.127 -15.600 1.00 0.81
ATOM 1245 CA LYS 1 677 4.988 12.215 -16.772 1.00 0.81
ATOM 1246 C LYS 1 677 4.357 11.485 -17.906 1.00 0.81
ATOM 1247 O LYS 1 677 5.035 10.801 -18.672 1.00 0.81
ATOM 1248 CB LYS 1 677 6.414 11.670 -16.591 1.00 0.81
ATOM 1249 CG LYS 1 677 6.511 10.152 -16.450 1.00 0.81
ATOM 1250 CD LYS 1 677 7.937 9.637 -16.666 1.00 0.81
ATOM 1251 CE LYS 1 677 8.078 8.121 -16.535 1.00 0.81
ATOM 1252 NZ LYS 1 677 9.482 7.727 -16.788 1.00 0.81
ATOM 1253 N ASP 1 678 3.030 11.611 -18.057 1.00 0.80
ATOM 1254 CA ASP 1 678 2.404 11.004 -19.187 1.00 0.80
ATOM 1255 C ASP 1 678 1.320 11.940 -19.604 1.00 0.80
ATOM 1256 O ASP 1 678 0.978 12.874 -18.882 1.00 0.80
ATOM 1257 CB ASP 1 678 1.746 9.646 -18.885 1.00 0.80
ATOM 1258 CG ASP 1 678 2.859 8.628 -18.686 1.00 0.80
ATOM 1259 OD1 ASP 1 678 3.855 8.684 -19.456 1.00 0.80

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ATOM  1260 OD2 ASP 1 678     2.726  7.775 -17.767 1.00 0.80
ATOM  1261 N  GLY 1 679      0.778 11.730 -20.816 1.00 0.77
ATOM  1262 CA GLY 1 679     -0.315 12.523 -21.302 1.00 0.77
ATOM  1263 C  GLY 1 679      0.169 13.900 -21.640 1.00 0.77
ATOM  1264 O  GLY 1 679      0.890 14.513 -20.858 1.00 0.77
ATOM  1265 N  LEU 1 680     -0.158 14.402 -22.851 1.00 1.01
ATOM  1266 CA LEU 1 680      0.175 15.758 -23.203 1.00 1.01
ATOM  1267 C  LEU 1 680     -0.728 16.705 -22.482 1.00 1.01
ATOM  1268 O  LEU 1 680     -0.252 17.616 -21.805 1.00 1.01
ATOM  1269 CB LEU 1 680      0.021 16.043 -24.713 1.00 1.01
ATOM  1270 CG LEU 1 680      0.318 17.497 -25.160 1.00 1.01
ATOM  1271 CD1 LEU 1 680    -0.825 18.473 -24.825 1.00 1.01
ATOM  1272 CD2 LEU 1 680     1.670 17.981 -24.612 1.00 1.01
ATOM  1273 N  LYS 1 681     -2.053 16.438 -22.600 1.00 1.15
ATOM  1274 CA LYS 1 681     -3.194 17.213 -22.173 1.00 1.15
ATOM  1275 C  LYS 1 681     -2.806 18.505 -21.555 1.00 1.15
ATOM  1276 O  LYS 1 681     -3.104 18.782 -20.396 1.00 1.15
ATOM  1277 CB LYS 1 681     -4.149 16.469 -21.217 1.00 1.15
ATOM  1278 CG LYS 1 681     -5.363 17.294 -20.764 1.00 1.15
ATOM  1279 CD LYS 1 681     -6.308 17.721 -21.892 1.00 1.15
ATOM  1280 CE LYS 1 681     -5.970 19.085 -22.502 1.00 1.15
ATOM  1281 NZ LYS 1 681     -6.934 19.413 -23.578 1.00 1.15
ATOM  1282 N  SER 1 682     -2.145 19.337 -22.371 1.00 1.05
ATOM  1283 CA SER 1 682     -1.702 20.644 -22.022 1.00 1.05
ATOM  1284 C  SER 1 682     -0.818 20.681 -20.819 1.00 1.05
ATOM  1285 O  SER 1 682     -0.938 19.922 -19.859 1.00 1.05
ATOM  1286 CB SER 1 682     -2.842 21.658 -21.831 1.00 1.05
ATOM  1287 OG SER 1 682     -2.302 22.944 -21.572 1.00 1.05
ATOM  1288 N  GLN 1 683      0.158 21.601 -20.869 1.00 0.99
ATOM  1289 CA GLN 1 683      0.986 21.803 -19.729 1.00 0.99
ATOM  1290 C  GLN 1 683      0.069 22.382 -18.708 1.00 0.99
ATOM  1291 O  GLN 1 683      0.325 22.312 -17.509 1.00 0.99
ATOM  1292 CB GLN 1 683      2.164 22.774 -19.941 1.00 0.99
ATOM  1293 CG GLN 1 683      1.767 24.207 -20.292 1.00 0.99
ATOM  1294 CD GLN 1 683      1.612 24.282 -21.802 1.00 0.99
ATOM  1295 OE1 GLN 1 683     1.650 23.263 -22.491 1.00 0.99
ATOM  1296 NE2 GLN 1 683     1.440 25.520 -22.335 1.00 0.99
ATOM  1297 N  GLU 1 684     -1.033 22.982 -19.192 1.00 0.75
ATOM  1298 CA GLU 1 684     -2.011 23.633 -18.374 1.00 0.75
ATOM  1299 C  GLU 1 684     -2.541 22.635 -17.391 1.00 0.75
ATOM  1300 O  GLU 1 684     -2.633 22.918 -16.198 1.00 0.75
ATOM  1301 CB GLU 1 684     -3.209 24.109 -19.213 1.00 0.75
ATOM  1302 CG GLU 1 684     -3.940 25.323 -18.649 1.00 0.75
ATOM  1303 CD GLU 1 684     -3.232 26.542 -19.221 1.00 0.75
ATOM  1304 OE1 GLU 1 684    -2.717 26.434 -20.366 1.00 0.75
ATOM  1305 OE2 GLU 1 684    -3.192 27.592 -18.527 1.00 0.75
ATOM  1306 N  LEU 1 685     -2.901 21.428 -17.867 1.00 0.40
ATOM  1307 CA LEU 1 685     -3.422 20.422 -16.986 1.00 0.40
ATOM  1308 C  LEU 1 685     -2.344 20.017 -16.029 1.00 0.40
ATOM  1309 O  LEU 1 685     -2.601 19.817 -14.844 1.00 0.40
ATOM  1310 CB LEU 1 685     -3.924 19.177 -17.735 1.00 0.40
ATOM  1311 CG LEU 1 685     -5.213 19.443 -18.538 1.00 0.40
ATOM  1312 CD1 LEU 1 685    -6.401 19.716 -17.603 1.00 0.40
ATOM  1313 CD2 LEU 1 685    -5.014 20.567 -19.569 1.00 0.40
ATOM  1314 N  PHE 1 686     -1.094 19.908 -16.519 1.00 0.20
ATOM  1315 CA PHE 1 686     -0.004 19.513 -15.673 1.00 0.20
ATOM  1316 C  PHE 1 686      0.119 20.522 -14.590 1.00 0.20
ATOM  1317 O  PHE 1 686      0.333 20.181 -13.429 1.00 0.20
ATOM  1318 CB PHE 1 686      1.374 19.552 -16.353 1.00 0.20
ATOM  1319 CG PHE 1 686      1.516 18.437 -17.319 1.00 0.20
ATOM  1320 CD1 PHE 1 686     1.108 18.581 -18.622 1.00 0.20
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ATOM  1321 CD2 PHE 1 686     2.074  17.251 -16.908  1.00  0.20
ATOM  1322 CE1 PHE 1 686     1.252  17.545 -19.510  1.00  0.20
ATOM  1323 CE2 PHE 1 686     2.221  16.209 -17.786  1.00  0.20
ATOM  1324 CZ  PHE 1 686     1.811  16.365 -19.085  1.00  0.20
ATOM  1325 N   ASP 1 687    -0.023  21.803 -14.961  1.00  0.18
ATOM  1326 CA  ASP 1 687     0.161  22.880 -14.041  1.00  0.18
ATOM  1327 C   ASP 1 687    -0.821  22.719 -12.931  1.00  0.18
ATOM  1328 O   ASP 1 687    -0.471  22.872 -11.761  1.00  0.18
ATOM  1329 CB  ASP 1 687    -0.105  24.251 -14.688  1.00  0.18
ATOM  1330 CG  ASP 1 687     0.351  25.336 -13.726  1.00  0.18
ATOM  1331 OD1 ASP 1 687     1.266  25.055 -12.907  1.00  0.18
ATOM  1332 OD2 ASP 1 687    -0.219  26.458 -13.789  1.00  0.18
ATOM  1333 N   GLU 1 688    -2.072  22.360 -13.266  1.00  0.34
ATOM  1334 CA  GLU 1 688    -3.077  22.276 -12.249  1.00  0.34
ATOM  1335 C   GLU 1 688    -2.642  21.283 -11.225  1.00  0.34
ATOM  1336 O   GLU 1 688    -2.756  21.530 -10.026  1.00  0.34
ATOM  1337 CB  GLU 1 688    -4.446  21.820 -12.785  1.00  0.34
ATOM  1338 CG  GLU 1 688    -5.126  22.848 -13.690  1.00  0.34
ATOM  1339 CD  GLU 1 688    -6.457  22.266 -14.139  1.00  0.34
ATOM  1340 OE1 GLU 1 688    -6.749  21.099 -13.761  1.00  0.34
ATOM  1341 OE2 GLU 1 688    -7.202  22.977 -14.864  1.00  0.34
ATOM  1342 N   ILE 1 689    -2.134  20.120 -11.661  1.00  0.52
ATOM  1343 CA  ILE 1 689    -1.692  19.186 -10.674  1.00  0.52
ATOM  1344 C   ILE 1 689    -0.476  19.711  -9.981  1.00  0.52
ATOM  1345 O   ILE 1 689    -0.302  19.488  -8.787  1.00  0.52
ATOM  1346 CB  ILE 1 689    -1.580  17.763 -11.167  1.00  0.52
ATOM  1347 CG1 ILE 1 689    -0.713  17.619 -12.424  1.00  0.52
ATOM  1348 CG2 ILE 1 689    -3.007  17.219 -11.322  1.00  0.52
ATOM  1349 CD1 ILE 1 689    -0.618  16.168 -12.902  1.00  0.52
ATOM  1350 N   ARG 1 690     0.375  20.475 -10.685  1.00  0.58
ATOM  1351 CA  ARG 1 690     1.570  21.000 -10.086  1.00  0.58
ATOM  1352 C   ARG 1 690     1.205  21.876  -8.919  1.00  0.58
ATOM  1353 O   ARG 1 690     1.872  21.838  -7.887  1.00  0.58
ATOM  1354 CB  ARG 1 690     2.395  21.846 -11.073  1.00  0.58
ATOM  1355 CG  ARG 1 690     2.876  21.049 -12.289  1.00  0.58
ATOM  1356 CD  ARG 1 690     3.698  21.869 -13.287  1.00  0.58
ATOM  1357 NE  ARG 1 690     5.061  22.037 -12.708  1.00  0.58
ATOM  1358 CZ  ARG 1 690     6.127  22.282 -13.526  1.00  0.58
ATOM  1359 NH1 ARG 1 690     5.949  22.370 -14.877  1.00  0.58
ATOM  1360 NH2 ARG 1 690     7.373  22.439 -12.991  1.00  0.58
ATOM  1361 N   MET 1 691     0.148  22.704  -9.052  1.00  0.57
ATOM  1362 CA  MET 1 691    -0.257  23.562  -7.971  1.00  0.57
ATOM  1363 C   MET 1 691    -0.751  22.736  -6.830  1.00  0.57
ATOM  1364 O   MET 1 691    -0.517  23.066  -5.668  1.00  0.57
ATOM  1365 CB  MET 1 691    -1.405  24.534  -8.307  1.00  0.57
ATOM  1366 CG  MET 1 691    -1.007  25.800  -9.067  1.00  0.57
ATOM  1367 SD  MET 1 691    -0.638  25.574 -10.827  1.00  0.57
ATOM  1368 CE  MET 1 691    -0.327  27.335 -11.148  1.00  0.57
ATOM  1369 N   THR 1 692    -1.487  21.649  -7.108  1.00  0.47
ATOM  1370 CA  THR 1 692    -1.976  20.900  -5.993  1.00  0.47
ATOM  1371 C   THR 1 692    -0.798  20.310  -5.283  1.00  0.47
ATOM  1372 O   THR 1 692    -0.778  20.269  -4.052  1.00  0.47
ATOM  1373 CB  THR 1 692    -2.930  19.795  -6.349  1.00  0.47
ATOM  1374 OG1 THR 1 692    -3.587  19.327  -5.181  1.00  0.47
ATOM  1375 CG2 THR 1 692    -2.147  18.640  -6.976  1.00  0.47
ATOM  1376 N   TYR 1 693     0.229  19.855  -6.039  1.00  0.41
ATOM  1377 CA  TYR 1 693     1.366  19.242  -5.406  1.00  0.41
ATOM  1378 C   TYR 1 693     1.979  20.255  -4.506  1.00  0.41
ATOM  1379 O   TYR 1 693     2.279  19.971  -3.347  1.00  0.41
ATOM  1380 CB  TYR 1 693     2.564  18.873  -6.316  1.00  0.41
ATOM  1381 CG  TYR 1 693     2.140  18.002  -7.437  1.00  0.41
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ATOM 1382 CD1 TYR 1 693 1.664 16.735 -7.211 1.00 0.41
ATOM 1383 CD2 TYR 1 693 2.219 18.473 -8.724 1.00 0.41
ATOM 1384 CE1 TYR 1 693 1.261 15.968 -8.273 1.00 0.41
ATOM 1385 CE2 TYR 1 693 1.814 17.709 -9.788 1.00 0.41
ATOM 1386 CZ TYR 1 693 1.330 16.449 -9.554 1.00 0.41
ATOM 1387 OH TYR 1 693 0.901 15.648 -10.626 1.00 0.41
ATOM 1388 N ILE 1 694 2.176 21.482 -5.022 1.00 0.49
ATOM 1389 CA ILE 1 694 2.828 22.476 -4.228 1.00 0.49
ATOM 1390 C ILE 1 694 1.964 22.742 -3.047 1.00 0.49
ATOM 1391 O ILE 1 694 2.454 22.994 -1.949 1.00 0.49
ATOM 1392 CB ILE 1 694 3.091 23.776 -4.943 1.00 0.49
ATOM 1393 CG1 ILE 1 694 4.098 24.616 -4.141 1.00 0.49
ATOM 1394 CG2 ILE 1 694 1.758 24.501 -5.174 1.00 0.49
ATOM 1395 CD1 ILE 1 694 5.495 24.000 -4.085 1.00 0.49
ATOM 1396 N LYS 1 695 0.636 22.677 -3.244 1.00 0.48
ATOM 1397 CA LYS 1 695 -0.261 22.939 -2.163 1.00 0.48
ATOM 1398 C LYS 1 695 -0.026 21.937 -1.074 1.00 0.48
ATOM 1399 O LYS 1 695 0.007 22.294 0.103 1.00 0.48
ATOM 1400 CB LYS 1 695 -1.731 22.841 -2.580 1.00 0.48
ATOM 1401 CG LYS 1 695 -2.652 23.125 -1.404 1.00 0.48
ATOM 1402 CD LYS 1 695 -4.097 23.419 -1.775 1.00 0.48
ATOM 1403 CE LYS 1 695 -4.909 23.685 -0.516 1.00 0.48
ATOM 1404 NZ LYS 1 695 -4.012 24.318 0.480 1.00 0.48
ATOM 1405 N GLU 1 696 0.150 20.653 -1.435 1.00 0.53
ATOM 1406 CA GLU 1 696 0.333 19.620 -0.456 1.00 0.53
ATOM 1407 C GLU 1 696 1.620 19.825 0.281 1.00 0.53
ATOM 1408 O GLU 1 696 1.708 19.539 1.474 1.00 0.53
ATOM 1409 CB GLU 1 696 0.324 18.217 -1.073 1.00 0.53
ATOM 1410 CG GLU 1 696 0.482 17.109 -0.039 1.00 0.53
ATOM 1411 CD GLU 1 696 -0.216 15.890 -0.609 1.00 0.53
ATOM 1412 OE1 GLU 1 696 0.118 15.476 -1.754 1.00 0.53
ATOM 1413 OE2 GLU 1 696 -1.124 15.376 0.094 1.00 0.53
ATOM 1414 N LEU 1 697 2.664 20.309 -0.413 1.00 0.53
ATOM 1415 CA LEU 1 697 3.923 20.528 0.235 1.00 0.53
ATOM 1416 C LEU 1 697 3.675 21.553 1.294 1.00 0.53
ATOM 1417 O LEU 1 697 4.124 21.409 2.431 1.00 0.53
ATOM 1418 CB LEU 1 697 4.979 21.072 -0.754 1.00 0.53
ATOM 1419 CG LEU 1 697 6.432 21.204 -0.237 1.00 0.53
ATOM 1420 CD1 LEU 1 697 7.343 21.760 -1.342 1.00 0.53
ATOM 1421 CD2 LEU 1 697 6.556 22.030 1.052 1.00 0.53
ATOM 1422 N GLY 1 698 2.918 22.610 0.947 1.00 0.46
ATOM 1423 CA GLY 1 698 2.678 23.669 1.882 1.00 0.46
ATOM 1424 C GLY 1 698 2.004 23.090 3.082 1.00 0.46
ATOM 1425 O GLY 1 698 2.368 23.403 4.215 1.00 0.46
ATOM 1426 N LYS 1 699 1.007 22.213 2.863 1.00 0.51
ATOM 1427 CA LYS 1 699 0.292 21.641 3.965 1.00 0.51
ATOM 1428 C LYS 1 699 1.257 20.845 4.780 1.00 0.51
ATOM 1429 O LYS 1 699 1.223 20.891 6.008 1.00 0.51
ATOM 1430 CB LYS 1 699 -0.839 20.695 3.531 1.00 0.51
ATOM 1431 CG LYS 1 699 -1.677 20.116 4.678 1.00 0.51
ATOM 1432 CD LYS 1 699 -0.960 19.104 5.576 1.00 0.51
ATOM 1433 CE LYS 1 699 -1.900 18.336 6.503 1.00 0.51
ATOM 1434 NZ LYS 1 699 -2.649 17.334 5.716 1.00 0.51
ATOM 1435 N ALA 1 700 2.147 20.088 4.116 1.00 0.30
ATOM 1436 CA ALA 1 700 3.064 19.273 4.856 1.00 0.30
ATOM 1437 C ALA 1 700 3.878 20.181 5.719 1.00 0.30
ATOM 1438 O ALA 1 700 4.070 19.912 6.901 1.00 0.30
ATOM 1439 CB ALA 1 700 4.032 18.493 3.951 1.00 0.30
ATOM 1440 N ILE 1 701 4.363 21.300 5.154 1.00 0.10
ATOM 1441 CA ILE 1 701 5.161 22.196 5.940 1.00 0.10
ATOM 1442 C ILE 1 701 4.318 22.798 7.019 1.00 0.10

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ATOM  1443  O   ILE 1 701     4.811  23.027   8.119  1.00  0.10
ATOM  1444  CB  ILE 1 701     5.779  23.316   5.157  1.00  0.10
ATOM  1445  CG1 ILE 1 701     6.800  22.756   4.156  1.00  0.10
ATOM  1446  CG2 ILE 1 701     6.380  24.319   6.154  1.00  0.10
ATOM  1447  CD1 ILE 1 701     7.389  23.822   3.239  1.00  0.10
ATOM  1448  N   VAL 1 702     3.027  23.067   6.751  1.00  0.25
ATOM  1449  CA  VAL 1 702     2.179  23.698   7.728  1.00  0.25
ATOM  1450  C   VAL 1 702     2.105  22.838   8.953  1.00  0.25
ATOM  1451  O   VAL 1 702     2.160  23.345  10.074  1.00  0.25
ATOM  1452  CB  VAL 1 702     0.773  23.893   7.237  1.00  0.25
ATOM  1453  CG1 VAL 1 702    -0.072  24.462   8.390  1.00  0.25
ATOM  1454  CG2 VAL 1 702     0.804  24.793   5.992  1.00  0.25
ATOM  1455  N   LYS 1 703     1.976  21.510   8.782  1.00  0.54
ATOM  1456  CA  LYS 1 703     1.907  20.638   9.921  1.00  0.54
ATOM  1457  C   LYS 1 703     3.202  20.763  10.655  1.00  0.54
ATOM  1458  O   LYS 1 703     3.252  20.709  11.882  1.00  0.54
ATOM  1459  CB  LYS 1 703     1.736  19.156   9.544  1.00  0.54
ATOM  1460  CG  LYS 1 703     0.302  18.767   9.175  1.00  0.54
ATOM  1461  CD  LYS 1 703    -0.678  18.913  10.343  1.00  0.54
ATOM  1462  CE  LYS 1 703    -2.115  18.520   9.997  1.00  0.54
ATOM  1463  NZ  LYS 1 703    -2.697  19.497   9.051  1.00  0.54
ATOM  1464  N   ARG 1 704     4.285  20.916   9.876  1.00  0.56
ATOM  1465  CA  ARG 1 704     5.649  21.052  10.296  1.00  0.56
ATOM  1466  C   ARG 1 704     5.826  22.375  10.975  1.00  0.56
ATOM  1467  O   ARG 1 704     6.790  22.569  11.706  1.00  0.56
ATOM  1468  CB  ARG 1 704     6.621  21.060   9.110  1.00  0.56
ATOM  1469  CG  ARG 1 704     6.476  19.841   8.203  1.00  0.56
ATOM  1470  CD  ARG 1 704     7.538  18.769   8.399  1.00  0.56
ATOM  1471  NE  ARG 1 704     7.227  17.677   7.435  1.00  0.56
ATOM  1472  CZ  ARG 1 704     7.577  17.824   6.126  1.00  0.56
ATOM  1473  NH1 ARG 1 704     8.094  19.016   5.707  1.00  0.56
ATOM  1474  NH2 ARG 1 704     7.393  16.800   5.241  1.00  0.56
ATOM  1475  N   GLU 1 705     4.943  23.351  10.703  1.00  0.33
ATOM  1476  CA  GLU 1 705     5.067  24.660  11.273  1.00  0.33
ATOM  1477  C   GLU 1 705     5.018  24.487  12.745  1.00  0.33
ATOM  1478  O   GLU 1 705     5.553  25.308  13.487  1.00  0.33
ATOM  1479  CB  GLU 1 705     3.927  25.610  10.865  1.00  0.33
ATOM  1480  CG  GLU 1 705     3.971  26.009   9.388  1.00  0.33
ATOM  1481  CD  GLU 1 705     2.801  26.945   9.116  1.00  0.33
ATOM  1482  OE1 GLU 1 705     1.661  26.599   9.526  1.00  0.33
ATOM  1483  OE2 GLU 1 705     3.033  28.020   8.502  1.00  0.33
ATOM  1484  N   GLY 1 706     4.349  23.411  13.199  1.00  0.32
ATOM  1485  CA  GLY 1 706     4.308  23.157  14.606  1.00  0.32
ATOM  1486  C   GLY 1 706     5.740  23.077  15.057  1.00  0.32
ATOM  1487  O   GLY 1 706     6.110  23.626  16.093  1.00  0.32
ATOM  1488  N   ASN 1 707     6.583  22.380  14.269  1.00  0.57
ATOM  1489  CA  ASN 1 707     8.003  22.293  14.495  1.00  0.57
ATOM  1490  C   ASN 1 707     8.678  23.518  13.914  1.00  0.57
ATOM  1491  O   ASN 1 707     8.123  24.615  13.978  1.00  0.57
ATOM  1492  CB  ASN 1 707     8.675  21.053  13.883  1.00  0.57
ATOM  1493  CG  ASN 1 707     8.450  19.896  14.845  1.00  0.57
ATOM  1494  OD1 ASN 1 707     8.562  20.061  16.059  1.00  0.57
ATOM  1495  ND2 ASN 1 707     8.128  18.695  14.295  1.00  0.57
ATOM  1496  N   SER 1 708     9.913  23.381  13.351  1.00  0.75
ATOM  1497  CA  SER 1 708    10.585  24.562  12.856  1.00  0.75
ATOM  1498  C   SER 1 708    11.409  24.261  11.624  1.00  0.75
ATOM  1499  O   SER 1 708    10.923  23.649  10.675  1.00  0.75
ATOM  1500  CB  SER 1 708    11.518  25.203  13.903  1.00  0.75
ATOM  1501  OG  SER 1 708    11.979  26.472  13.456  1.00  0.75
ATOM  1502  N   SER 1 709    12.701  24.680  11.637  1.00  0.78
ATOM  1503  CA  SER 1 709    13.639  24.623  10.539  1.00  0.78
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ATOM  1504  C   SER 1 709    13.812  23.206  10.131  1.00  0.78
ATOM  1505  O   SER 1 709    14.038  22.890   8.963  1.00  0.78
ATOM  1506  CB  SER 1 709    15.027  25.173  10.906  1.00  0.78
ATOM  1507  OG  SER 1 709    15.895  25.089   9.785  1.00  0.78
ATOM  1508  N   GLN 1 710    13.662  22.297  11.097  1.00  0.75
ATOM  1509  CA  GLN 1 710    13.776  20.896  10.850  1.00  0.75
ATOM  1510  C   GLN 1 710    12.756  20.537   9.812  1.00  0.75
ATOM  1511  O   GLN 1 710    12.848  19.490   9.176  1.00  0.75
ATOM  1512  CB  GLN 1 710    13.556  20.062  12.126  1.00  0.75
ATOM  1513  CG  GLN 1 710    12.186  20.243  12.786  1.00  0.75
ATOM  1514  CD  GLN 1 710    11.210  19.233  12.201  1.00  0.75
ATOM  1515  OE1 GLN 1 710    10.623  19.439  11.140  1.00  0.75
ATOM  1516  NE2 GLN 1 710    11.024  18.097  12.925  1.00  0.75
ATOM  1517  N   ASN 1 711    11.739  21.396   9.614  1.00  0.76
ATOM  1518  CA  ASN 1 711    10.693  21.096   8.687  1.00  0.76
ATOM  1519  C   ASN 1 711    11.273  20.783   7.340  1.00  0.76
ATOM  1520  O   ASN 1 711    10.878  19.797   6.721  1.00  0.76
ATOM  1521  CB  ASN 1 711     9.669  22.243   8.500  1.00  0.76
ATOM  1522  CG  ASN 1 711    10.266  23.392   7.691  1.00  0.76
ATOM  1523  OD1 ASN 1 711     9.671  23.816   6.701  1.00  0.76
ATOM  1524  ND2 ASN 1 711    11.464  23.898   8.088  1.00  0.76
ATOM  1525  N   TRP 1 712    12.239  21.579   6.841  1.00  0.75
ATOM  1526  CA  TRP 1 712    12.723  21.288   5.526  1.00  0.75
ATOM  1527  C   TRP 1 712    13.425  19.976   5.555  1.00  0.75
ATOM  1528  O   TRP 1 712    13.300  19.181   4.626  1.00  0.75
ATOM  1529  CB  TRP 1 712    13.655  22.361   4.925  1.00  0.75
ATOM  1530  CG  TRP 1 712    14.940  22.648   5.661  1.00  0.75
ATOM  1531  CD1 TRP 1 712    15.209  23.608   6.592  1.00  0.75
ATOM  1532  CD2 TRP 1 712    16.165  21.927   5.457  1.00  0.75
ATOM  1533  NE1 TRP 1 712    16.525  23.530   6.981  1.00  0.75
ATOM  1534  CE2 TRP 1 712    17.126  22.501   6.289  1.00  0.75
ATOM  1535  CE3 TRP 1 712    16.465  20.877   4.637  1.00  0.75
ATOM  1536  CZ2 TRP 1 712    18.406  22.030   6.315  1.00  0.75
ATOM  1537  CZ3 TRP 1 712    17.757  20.402   4.669  1.00  0.75
ATOM  1538  CH2 TRP 1 712    18.710  20.967   5.492  1.00  0.75
ATOM  1539  N   GLN 1 713    14.177  19.695   6.634  1.00  0.74
ATOM  1540  CA  GLN 1 713    14.891  18.457   6.634  1.00  0.74
ATOM  1541  C   GLN 1 713    13.930  17.308   6.637  1.00  0.74
ATOM  1542  O   GLN 1 713    14.136  16.347   5.898  1.00  0.74
ATOM  1543  CB  GLN 1 713    15.880  18.271   7.805  1.00  0.74
ATOM  1544  CG  GLN 1 713    15.253  18.190   9.195  1.00  0.74
ATOM  1545  CD  GLN 1 713    16.378  18.001  10.202  1.00  0.74
ATOM  1546  OE1 GLN 1 713    17.241  17.142  10.026  1.00  0.74
ATOM  1547  NE2 GLN 1 713    16.375  18.824  11.285  1.00  0.74
ATOM  1548  N   ARG 1 714    12.852  17.354   7.452  1.00  0.79
ATOM  1549  CA  ARG 1 714    12.025  16.180   7.441  1.00  0.79
ATOM  1550  C   ARG 1 714    11.270  16.111   6.153  1.00  0.79
ATOM  1551  O   ARG 1 714    10.972  15.018   5.677  1.00  0.79
ATOM  1552  CB  ARG 1 714    11.013  15.980   8.582  1.00  0.79
ATOM  1553  CG  ARG 1 714     9.787  16.880   8.603  1.00  0.79
ATOM  1554  CD  ARG 1 714     8.678  16.232   9.436  1.00  0.79
ATOM  1555  NE  ARG 1 714     8.479  14.866   8.866  1.00  0.79
ATOM  1556  CZ  ARG 1 714     8.281  13.792   9.687  1.00  0.79
ATOM  1557  NH1 ARG 1 714     8.141  13.974  11.032  1.00  0.79
ATOM  1558  NH2 ARG 1 714     8.236  12.531   9.163  1.00  0.79
ATOM  1559  N   PHE 1 715    10.938  17.275   5.557  1.00  0.65
ATOM  1560  CA  PHE 1 715    10.213  17.296   4.317  1.00  0.65
ATOM  1561  C   PHE 1 715    10.983  16.458   3.352  1.00  0.65
ATOM  1562  O   PHE 1 715    10.428  15.591   2.677  1.00  0.65
ATOM  1563  CB  PHE 1 715    10.144  18.722   3.732  1.00  0.65
ATOM  1564  CG  PHE 1 715     9.605  18.677   2.343  1.00  0.65
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ATOM  1565 CD1 PHE 1 715    10.456 18.485  1.279 1.00 0.65
ATOM  1566 CD2 PHE 1 715     8.261 18.839  2.098 1.00 0.65
ATOM  1567 CE1 PHE 1 715     9.980 18.442 -0.009 1.00 0.65
ATOM  1568 CE2 PHE 1 715     7.778 18.796  0.810 1.00 0.65
ATOM  1569 CZ  PHE 1 715     8.636 18.600 -0.245 1.00 0.65
ATOM  1570 N   TYR 1 716    12.304 16.684  3.293 1.00 0.39
ATOM  1571 CA  TYR 1 716    13.139 15.973  2.374 1.00 0.39
ATOM  1572 C   TYR 1 716    13.190 14.523  2.758 1.00 0.39
ATOM  1573 O   TYR 1 716    13.166 13.645  1.898 1.00 0.39
ATOM  1574 CB  TYR 1 716    14.574 16.527  2.358 1.00 0.39
ATOM  1575 CG  TYR 1 716    15.270 15.962  1.170 1.00 0.39
ATOM  1576 CD1 TYR 1 716    14.998 16.459 -0.084 1.00 0.39
ATOM  1577 CD2 TYR 1 716    16.199 14.958  1.303 1.00 0.39
ATOM  1578 CE1 TYR 1 716    15.632 15.958 -1.196 1.00 0.39
ATOM  1579 CE2 TYR 1 716    16.835 14.453  0.193 1.00 0.39
ATOM  1580 CZ  TYR 1 716    16.553 14.949 -1.057 1.00 0.39
ATOM  1581 OH  TYR 1 716    17.210 14.426 -2.192 1.00 0.39
ATOM  1582 N   GLN 1 717    13.246 14.226  4.069 1.00 0.36
ATOM  1583 CA  GLN 1 717    13.376 12.867  4.515 1.00 0.36
ATOM  1584 C   GLN 1 717    12.169 12.094  4.088 1.00 0.36
ATOM  1585 O   GLN 1 717    12.266 10.940  3.674 1.00 0.36
ATOM  1586 CB  GLN 1 717    13.486 12.774  6.047 1.00 0.36
ATOM  1587 CG  GLN 1 717    14.732 13.473  6.595 1.00 0.36
ATOM  1588 CD  GLN 1 717    14.729 13.344  8.112 1.00 0.36
ATOM  1589 OE1 GLN 1 717    13.812 12.773  8.699 1.00 0.36
ATOM  1590 NE2 GLN 1 717    15.784 13.899  8.767 1.00 0.36
ATOM  1591 N   LEU 1 718    10.995 12.730  4.195 1.00 0.57
ATOM  1592 CA  LEU 1 718     9.732 12.125  3.904 1.00 0.57
ATOM  1593 C   LEU 1 718     9.666 11.818  2.429 1.00 0.57
ATOM  1594 O   LEU 1 718     9.368 10.690  2.038 1.00 0.57
ATOM  1595 CB  LEU 1 718     8.641 13.110  4.380 1.00 0.57
ATOM  1596 CG  LEU 1 718     7.234 12.552  4.638 1.00 0.57
ATOM  1597 CD1 LEU 1 718     6.404 12.443  3.364 1.00 0.57
ATOM  1598 CD2 LEU 1 718     7.308 11.232  5.423 1.00 0.57
ATOM  1599 N   THR 1 719    10.036 12.791  1.569 1.00 0.57
ATOM  1600 CA  THR 1 719     9.946 12.619  0.142 1.00 0.57
ATOM  1601 C   THR 1 719    10.827 11.486 -0.296 1.00 0.57
ATOM  1602 O   THR 1 719    10.443 10.696 -1.157 1.00 0.57
ATOM  1603 CB  THR 1 719    10.346 13.839 -0.634 1.00 0.57
ATOM  1604 OG1 THR 1 719    10.019 13.674 -2.006 1.00 0.57
ATOM  1605 CG2 THR 1 719    11.858 14.065 -0.477 1.00 0.57
ATOM  1606 N   LYS 1 720    12.023 11.354  0.307 1.00 0.38
ATOM  1607 CA  LYS 1 720    12.934 10.319 -0.099 1.00 0.38
ATOM  1608 C   LYS 1 720    12.274  8.996  0.098 1.00 0.38
ATOM  1609 O   LYS 1 720    12.531  8.055 -0.652 1.00 0.38
ATOM  1610 CB  LYS 1 720    14.252 10.265  0.693 1.00 0.38
ATOM  1611 CG  LYS 1 720    15.349 11.205  0.189 1.00 0.38
ATOM  1612 CD  LYS 1 720    16.603 11.178  1.068 1.00 0.38
ATOM  1613 CE  LYS 1 720    17.860 11.700  0.369 1.00 0.38
ATOM  1614 NZ  LYS 1 720    19.019 11.637  1.288 1.00 0.38
ATOM  1615 N   LEU 1 721    11.410  8.889  1.118 1.00 0.41
ATOM  1616 CA  LEU 1 721    10.767  7.646  1.426 1.00 0.41
ATOM  1617 C   LEU 1 721     9.983  7.235  0.221 1.00 0.41
ATOM  1618 O   LEU 1 721     9.905  6.051 -0.104 1.00 0.41
ATOM  1619 CB  LEU 1 721     9.819  7.794  2.641 1.00 0.41
ATOM  1620 CG  LEU 1 721     9.144  6.513  3.195 1.00 0.41
ATOM  1621 CD1 LEU 1 721     8.249  6.867  4.393 1.00 0.41
ATOM  1622 CD2 LEU 1 721     8.357  5.719  2.139 1.00 0.41
ATOM  1623 N   LEU 1 722    9.394  8.208 -0.496 1.00 0.46
ATOM  1624 CA  LEU 1 722    8.576  7.876 -1.624 1.00 0.46
ATOM  1625 C   LEU 1 722    9.408  7.127 -2.616 1.00 0.46
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ATOM  1626  O   LEU 1 722     8.915   6.230  -3.299  1.00  0.46
ATOM  1627  CB  LEU 1 722     7.969   9.106  -2.310  1.00  0.46
ATOM  1628  CG  LEU 1 722     7.062   9.891  -1.348  1.00  0.46
ATOM  1629  CD1 LEU 1 722     5.991   8.978  -0.757  1.00  0.46
ATOM  1630  CD2 LEU 1 722     7.853  10.594  -0.247  1.00  0.46
ATOM  1631  N   ASP 1 723    10.702   7.472  -2.713  1.00  0.32
ATOM  1632  CA  ASP 1 723    11.577   6.833  -3.653  1.00  0.32
ATOM  1633  C   ASP 1 723    11.612   5.365  -3.353  1.00  0.32
ATOM  1634  O   ASP 1 723    11.535   4.538  -4.260  1.00  0.32
ATOM  1635  CB  ASP 1 723    13.016   7.366  -3.553  1.00  0.32
ATOM  1636  CG  ASP 1 723    13.820   6.816  -4.720  1.00  0.32
ATOM  1637  OD1 ASP 1 723    13.280   5.949  -5.460  1.00  0.32
ATOM  1638  OD2 ASP 1 723    14.986   7.261  -4.891  1.00  0.32
ATOM  1639  N   SER 1 724    11.725   4.993  -2.064  1.00  0.37
ATOM  1640  CA  SER 1 724    11.768   3.605  -1.698  1.00  0.37
ATOM  1641  C   SER 1 724    10.451   2.992  -2.035  1.00  0.37
ATOM  1642  O   SER 1 724    10.378   1.874  -2.545  1.00  0.37
ATOM  1643  CB  SER 1 724    11.996   3.386  -0.193  1.00  0.37
ATOM  1644  OG  SER 1 724    13.290   3.839   0.179  1.00  0.37
ATOM  1645  N   MET 1 725     9.361   3.729  -1.762  1.00  0.66
ATOM  1646  CA  MET 1 725     8.072   3.193  -2.052  1.00  0.66
ATOM  1647  C   MET 1 725     7.970   2.854  -3.501  1.00  0.66
ATOM  1648  O   MET 1 725     7.555   1.752  -3.852  1.00  0.66
ATOM  1649  CB  MET 1 725     6.932   4.153  -1.772  1.00  0.66
ATOM  1650  CG  MET 1 725     5.871   3.883  -2.820  1.00  0.66
ATOM  1651  SD  MET 1 725     4.224   3.695  -2.158  1.00  0.66
ATOM  1652  CE  MET 1 725     4.459   1.902  -2.141  1.00  0.66
ATOM  1653  N   HIS 1 726     8.371   3.782  -4.387  1.00  0.61
ATOM  1654  CA  HIS 1 726     8.237   3.502  -5.783  1.00  0.61
ATOM  1655  C   HIS 1 726     9.095   2.305  -6.065  1.00  0.61
ATOM  1656  O   HIS 1 726     8.780   1.475  -6.915  1.00  0.61
ATOM  1657  CB  HIS 1 726     8.711   4.639  -6.711  1.00  0.61
ATOM  1658  CG  HIS 1 726    10.055   4.399  -7.336  1.00  0.61
ATOM  1659  ND1 HIS 1 726    11.249   4.906  -6.875  1.00  0.61
ATOM  1660  CD2 HIS 1 726    10.368   3.665  -8.439  1.00  0.61
ATOM  1661  CE1 HIS 1 726    12.217   4.456  -7.713  1.00  0.61
ATOM  1662  NE2 HIS 1 726    11.731   3.696  -8.679  1.00  0.61
ATOM  1663  N   GLU 1 727    10.225   2.180  -5.350  1.00  0.31
ATOM  1664  CA  GLU 1 727    11.096   1.064  -5.583  1.00  0.31
ATOM  1665  C   GLU 1 727    10.346  -0.202  -5.309  1.00  0.31
ATOM  1666  O   GLU 1 727    10.375  -1.135  -6.109  1.00  0.31
ATOM  1667  CB  GLU 1 727    12.319   1.061  -4.647  1.00  0.31
ATOM  1668  CG  GLU 1 727    13.277  -0.115  -4.861  1.00  0.31
ATOM  1669  CD  GLU 1 727    14.217   0.223  -6.009  1.00  0.31
ATOM  1670  OE1 GLU 1 727    14.052   1.322  -6.600  1.00  0.31
ATOM  1671  OE2 GLU 1 727    15.116  -0.610  -6.307  1.00  0.31
ATOM  1672  N   VAL 1 728     9.625  -0.260  -4.173  1.00  0.24
ATOM  1673  CA  VAL 1 728     8.946  -1.466  -3.797  1.00  0.24
ATOM  1674  C   VAL 1 728     7.895  -1.812  -4.811  1.00  0.24
ATOM  1675  O   VAL 1 728     7.779  -2.966  -5.215  1.00  0.24
ATOM  1676  CB  VAL 1 728     8.270  -1.359  -2.460  1.00  0.24
ATOM  1677  CG1 VAL 1 728     7.544  -2.684  -2.179  1.00  0.24
ATOM  1678  CG2 VAL 1 728     9.328  -0.993  -1.403  1.00  0.24
ATOM  1679  N   VAL 1 729     7.106  -0.824  -5.277  1.00  0.27
ATOM  1680  CA  VAL 1 729     6.049  -1.153  -6.196  1.00  0.27
ATOM  1681  C   VAL 1 729     6.627  -1.732  -7.446  1.00  0.27
ATOM  1682  O   VAL 1 729     6.080  -2.685  -7.999  1.00  0.27
ATOM  1683  CB  VAL 1 729     5.187   0.011  -6.578  1.00  0.27
ATOM  1684  CG1 VAL 1 729     6.083   1.141  -7.070  1.00  0.27
ATOM  1685  CG2 VAL 1 729     4.225  -0.450  -7.682  1.00  0.27
ATOM  1686  N   GLU 1 730     7.755  -1.181  -7.930  1.00  0.20
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ATOM  1687  CA  GLU 1 730     8.331  -1.697  -9.137  1.00  0.20
ATOM  1688  C   GLU 1 730     8.701  -3.128  -8.906  1.00  0.20
ATOM  1689  O   GLU 1 730     8.432  -3.992  -9.739  1.00  0.20
ATOM  1690  CB  GLU 1 730     9.622  -0.967  -9.548  1.00  0.20
ATOM  1691  CG  GLU 1 730     9.411   0.480  -9.995  1.00  0.20
ATOM  1692  CD  GLU 1 730    10.775   1.052 -10.361  1.00  0.20
ATOM  1693  OE1 GLU 1 730    11.795   0.364 -10.089  1.00  0.20
ATOM  1694  OE2 GLU 1 730    10.815   2.182 -10.918  1.00  0.20
ATOM  1695  N   ASN 1 731     9.320  -3.425  -7.747  1.00  0.32
ATOM  1696  CA  ASN 1 731     9.750  -4.770  -7.476  1.00  0.32
ATOM  1697  C   ASN 1 731     8.540  -5.653  -7.428  1.00  0.32
ATOM  1698  O   ASN 1 731     8.524  -6.750  -7.984  1.00  0.32
ATOM  1699  CB  ASN 1 731    10.439  -4.911  -6.106  1.00  0.32
ATOM  1700  CG  ASN 1 731    11.757  -4.150  -6.131  1.00  0.32
ATOM  1701  OD1 ASN 1 731    11.966  -3.220  -5.353  1.00  0.32
ATOM  1702  ND2 ASN 1 731    12.677  -4.561  -7.043  1.00  0.32
ATOM  1703  N   LEU 1 732     7.485  -5.154  -6.767  1.00  0.58
ATOM  1704  CA  LEU 1 732     6.243  -5.819  -6.490  1.00  0.58
ATOM  1705  C   LEU 1 732     5.591  -6.183  -7.788  1.00  0.58
ATOM  1706  O   LEU 1 732     5.074  -7.284  -7.968  1.00  0.58
ATOM  1707  CB  LEU 1 732     5.328  -4.808  -5.758  1.00  0.58
ATOM  1708  CG  LEU 1 732     3.972  -5.281  -5.199  1.00  0.58
ATOM  1709  CD1 LEU 1 732     3.073  -5.879  -6.288  1.00  0.58
ATOM  1710  CD2 LEU 1 732     4.136  -6.139  -3.935  1.00  0.58
ATOM  1711  N   LEU 1 733     5.610  -5.243  -8.741  1.00  0.50
ATOM  1712  CA  LEU 1 733     4.987  -5.442 -10.012  1.00  0.50
ATOM  1713  C   LEU 1 733     5.675  -6.592 -10.665  1.00  0.50
ATOM  1714  O   LEU 1 733     5.035  -7.455 -11.264  1.00  0.50
ATOM  1715  CB  LEU 1 733     5.120  -4.169 -10.881  1.00  0.50
ATOM  1716  CG  LEU 1 733     4.505  -4.206 -12.297  1.00  0.50
ATOM  1717  CD1 LEU 1 733     4.515  -2.802 -12.923  1.00  0.50
ATOM  1718  CD2 LEU 1 733     5.231  -5.199 -13.215  1.00  0.50
ATOM  1719  N   ASN 1 734     7.011  -6.640 -10.542  1.00  0.49
ATOM  1720  CA  ASN 1 734     7.777  -7.666 -11.173  1.00  0.49
ATOM  1721  C   ASN 1 734     7.385  -8.993 -10.610  1.00  0.49
ATOM  1722  O   ASN 1 734     7.142  -9.935 -11.364  1.00  0.49
ATOM  1723  CB  ASN 1 734     9.285  -7.497 -10.929  1.00  0.49
ATOM  1724  CG  ASN 1 734     9.726  -6.207 -11.606  1.00  0.49
ATOM  1725  OD1 ASN 1 734    10.835  -5.724 -11.385  1.00  0.49
ATOM  1726  ND2 ASN 1 734     8.829  -5.626 -12.446  1.00  0.49
ATOM  1727  N   TYR 1 735     7.291  -9.120  -9.270  1.00  0.60
ATOM  1728  CA  TYR 1 735     7.005 -10.439  -8.801  1.00  0.60
ATOM  1729  C   TYR 1 735     5.599 -10.789  -9.177  1.00  0.60
ATOM  1730  O   TYR 1 735     5.313 -11.930  -9.530  1.00  0.60
ATOM  1731  CB  TYR 1 735     7.184 -10.691  -7.286  1.00  0.60
ATOM  1732  CG  TYR 1 735     6.309 -11.797  -6.820  1.00  0.60
ATOM  1733  CD1 TYR 1 735     6.817 -13.073  -6.700  1.00  0.60
ATOM  1734  CD2 TYR 1 735     5.000 -11.570  -6.487  1.00  0.60
ATOM  1735  CE1 TYR 1 735     6.032 -14.115  -6.271  1.00  0.60
ATOM  1736  CE2 TYR 1 735     4.213 -12.610  -6.058  1.00  0.60
ATOM  1737  CZ  TYR 1 735     4.720 -13.880  -5.945  1.00  0.60
ATOM  1738  OH  TYR 1 735     3.896 -14.937  -5.502  1.00  0.60
ATOM  1739  N   CYS 1 736     4.679  -9.807  -9.118  1.00  0.35
ATOM  1740  CA  CYS 1 736     3.307 -10.089  -9.430  1.00  0.35
ATOM  1741  C   CYS 1 736     3.190 -10.561 -10.845  1.00  0.35
ATOM  1742  O   CYS 1 736     2.445 -11.495 -11.129  1.00  0.35
ATOM  1743  CB  CYS 1 736     2.372  -8.880  -9.264  1.00  0.35
ATOM  1744  SG  CYS 1 736     0.657  -9.282  -9.704  1.00  0.35
ATOM  1745  N   PHE 1 737     3.916  -9.929 -11.781  1.00  0.23
ATOM  1746  CA  PHE 1 737     3.843 -10.330 -13.159  1.00  0.23
ATOM  1747  C   PHE 1 737     4.403 -11.702 -13.327  1.00  0.23
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ATOM 1748 O PHE 1 737 3.948 -12.460 -14.182 1.00 0.23
ATOM 1749 CB PHE 1 737 4.580 -9.375 -14.112 1.00 0.23
ATOM 1750 CG PHE 1 737 3.649 -8.243 -14.374 1.00 0.23
ATOM 1751 CD1 PHE 1 737 3.272 -7.390 -13.365 1.00 0.23
ATOM 1752 CD2 PHE 1 737 3.162 -8.024 -15.642 1.00 0.23
ATOM 1753 CE1 PHE 1 737 2.417 -6.343 -13.610 1.00 0.23
ATOM 1754 CE2 PHE 1 737 2.307 -6.979 -15.897 1.00 0.23
ATOM 1755 CZ PHE 1 737 1.932 -6.135 -14.879 1.00 0.23
ATOM 1756 N GLN 1 738 5.406 -12.066 -12.510 1.00 0.51
ATOM 1757 CA GLN 1 738 6.023 -13.349 -12.668 1.00 0.51
ATOM 1758 C GLN 1 738 4.972 -14.401 -12.517 1.00 0.51
ATOM 1759 O GLN 1 738 4.969 -15.382 -13.259 1.00 0.51
ATOM 1760 CB GLN 1 738 7.117 -13.623 -11.624 1.00 0.51
ATOM 1761 CG GLN 1 738 7.780 -14.992 -11.789 1.00 0.51
ATOM 1762 CD GLN 1 738 8.835 -15.134 -10.704 1.00 0.51
ATOM 1763 OE1 GLN 1 738 9.512 -16.157 -10.608 1.00 0.51
ATOM 1764 NE2 GLN 1 738 8.986 -14.076 -9.863 1.00 0.51
ATOM 1765 N THR 1 739 4.048 -14.244 -11.550 1.00 0.90
ATOM 1766 CA THR 1 739 3.029 -15.247 -11.419 1.00 0.90
ATOM 1767 C THR 1 739 2.174 -15.225 -12.654 1.00 0.90
ATOM 1768 O THR 1 739 1.803 -16.279 -13.166 1.00 0.90
ATOM 1769 CB THR 1 739 2.142 -15.068 -10.217 1.00 0.90
ATOM 1770 OG1 THR 1 739 1.347 -16.230 -10.027 1.00 0.90
ATOM 1771 CG2 THR 1 739 1.232 -13.847 -10.419 1.00 0.90
ATOM 1772 N PHE 1 740 1.885 -14.006 -13.162 1.00 1.13
ATOM 1773 CA PHE 1 740 1.060 -13.667 -14.296 1.00 1.13
ATOM 1774 C PHE 1 740 -0.092 -14.595 -14.496 1.00 1.13
ATOM 1775 O PHE 1 740 0.046 -15.748 -14.904 1.00 1.13
ATOM 1776 CB PHE 1 740 1.801 -13.428 -15.632 1.00 1.13
ATOM 1777 CG PHE 1 740 2.485 -14.665 -16.094 1.00 1.13
ATOM 1778 CD1 PHE 1 740 3.764 -14.948 -15.680 1.00 1.13
ATOM 1779 CD2 PHE 1 740 1.856 -15.534 -16.954 1.00 1.13
ATOM 1780 CE1 PHE 1 740 4.405 -16.086 -16.105 1.00 1.13
ATOM 1781 CE2 PHE 1 740 2.491 -16.675 -17.384 1.00 1.13
ATOM 1782 CZ PHE 1 740 3.768 -16.953 -16.960 1.00 1.13
ATOM 1783 N LEU 1 741 -1.299 -14.062 -14.231 1.00 0.91
ATOM 1784 CA LEU 1 741 -2.516 -14.800 -14.363 1.00 0.91
ATOM 1785 C LEU 1 741 -2.585 -15.245 -15.795 1.00 0.91
ATOM 1786 O LEU 1 741 -1.798 -14.796 -16.627 1.00 0.91
ATOM 1787 CB LEU 1 741 -3.734 -13.946 -13.914 1.00 0.91
ATOM 1788 CG LEU 1 741 -5.116 -14.632 -13.813 1.00 0.91
ATOM 1789 CD1 LEU 1 741 -6.063 -13.813 -12.921 1.00 0.91
ATOM 1790 CD2 LEU 1 741 -5.774 -14.842 -15.181 1.00 0.91
ATOM 1791 N ASP 1 742 -3.497 -16.191 -16.097 1.00 0.71
ATOM 1792 CA ASP 1 742 -3.666 -16.809 -17.383 1.00 0.71
ATOM 1793 C ASP 1 742 -3.861 -15.793 -18.466 1.00 0.71
ATOM 1794 O ASP 1 742 -3.692 -14.590 -18.274 1.00 0.71
ATOM 1795 CB ASP 1 742 -4.868 -17.767 -17.437 1.00 0.71
ATOM 1796 CG ASP 1 742 -4.569 -18.945 -16.523 1.00 0.71
ATOM 1797 OD1 ASP 1 742 -3.413 -19.028 -16.026 1.00 0.71
ATOM 1798 OD2 ASP 1 742 -5.488 -19.779 -16.312 1.00 0.71
ATOM 1799 N LYS 1 743 -4.243 -16.293 -19.661 1.00 0.84
ATOM 1800 CA LYS 1 743 -4.406 -15.475 -20.827 1.00 0.84
ATOM 1801 C LYS 1 743 -5.329 -14.369 -20.453 1.00 0.84
ATOM 1802 O LYS 1 743 -5.007 -13.196 -20.640 1.00 0.84
ATOM 1803 CB LYS 1 743 -5.006 -16.263 -22.010 1.00 0.84
ATOM 1804 CG LYS 1 743 -5.190 -15.460 -23.300 1.00 0.84
ATOM 1805 CD LYS 1 743 -6.291 -14.398 -23.237 1.00 0.84
ATOM 1806 CE LYS 1 743 -7.656 -14.917 -23.697 1.00 0.84
ATOM 1807 NZ LYS 1 743 -8.094 -16.034 -22.830 1.00 0.84
ATOM 1808 N THR 1 744 -6.500 -14.709 -19.892 1.00 0.84

ATOM 1809 CA THR 1 744 -7.332 -13.651 -19.420 1.00 0.84
ATOM 1810 C THR 1 744 -6.812 -13.353 -18.055 1.00 0.84
ATOM 1811 O THR 1 744 -7.419 -13.704 -17.045 1.00 0.84
ATOM 1812 CB THR 1 744 -8.785 -14.025 -19.345 1.00 0.84
ATOM 1813 OG1 THR 1 744 -8.976 -15.151 -18.500 1.00 0.84
ATOM 1814 CG2 THR 1 744 -9.272 -14.343 -20.769 1.00 0.84
ATOM 1815 N MET 1 745 -5.662 -12.654 -18.017 1.00 0.84
ATOM 1816 CA MET 1 745 -4.952 -12.372 -16.808 1.00 0.84
ATOM 1817 C MET 1 745 -5.849 -11.640 -15.886 1.00 0.84
ATOM 1818 O MET 1 745 -5.684 -11.743 -14.673 1.00 0.84
ATOM 1819 CB MET 1 745 -3.711 -11.490 -17.017 1.00 0.84
ATOM 1820 CG MET 1 745 -2.968 -11.199 -15.713 1.00 0.84
ATOM 1821 SD MET 1 745 -1.485 -10.163 -15.900 1.00 0.84
ATOM 1822 CE MET 1 745 -1.092 -10.137 -14.128 1.00 0.84
ATOM 1823 N SER 1 746 -6.793 -10.877 -16.467 1.00 1.05
ATOM 1824 CA SER 1 746 -7.760 -10.055 -15.802 1.00 1.05
ATOM 1825 C SER 1 746 -7.333 -8.683 -16.106 1.00 1.05
ATOM 1826 O SER 1 746 -6.261 -8.265 -15.673 1.00 1.05
ATOM 1827 CB SER 1 746 -7.886 -10.209 -14.269 1.00 1.05
ATOM 1828 OG SER 1 746 -8.876 -9.333 -13.750 1.00 1.05
ATOM 1829 N ILE 1 747 -8.164 -8.021 -16.932 1.00 1.19
ATOM 1830 CA ILE 1 747 -8.108 -6.670 -17.393 1.00 1.19
ATOM 1831 C ILE 1 747 -8.073 -5.783 -16.187 1.00 1.19
ATOM 1832 O ILE 1 747 -9.044 -5.151 -15.774 1.00 1.19
ATOM 1833 CB ILE 1 747 -9.231 -6.532 -18.420 1.00 1.19
ATOM 1834 CG1 ILE 1 747 -8.658 -6.825 -19.821 1.00 1.19
ATOM 1835 CG2 ILE 1 747 -10.165 -5.327 -18.267 1.00 1.19
ATOM 1836 CD1 ILE 1 747 -8.097 -8.235 -19.995 1.00 1.19
ATOM 1837 N GLU 1 748 -6.863 -5.764 -15.594 1.00 1.16
ATOM 1838 CA GLU 1 748 -6.527 -5.086 -14.392 1.00 1.16
ATOM 1839 C GLU 1 748 -6.244 -3.643 -14.601 1.00 1.16
ATOM 1840 O GLU 1 748 -6.780 -2.817 -13.867 1.00 1.16
ATOM 1841 CB GLU 1 748 -5.313 -5.690 -13.672 1.00 1.16
ATOM 1842 CG GLU 1 748 -4.996 -4.930 -12.388 1.00 1.16
ATOM 1843 CD GLU 1 748 -6.286 -4.866 -11.578 1.00 1.16
ATOM 1844 OE1 GLU 1 748 -7.179 -5.725 -11.808 1.00 1.16
ATOM 1845 OE2 GLU 1 748 -6.399 -3.946 -10.724 1.00 1.16
ATOM 1846 N PHE 1 749 -5.380 -3.260 -15.565 1.00 1.07
ATOM 1847 CA PHE 1 749 -5.167 -1.844 -15.542 1.00 1.07
ATOM 1848 C PHE 1 749 -6.057 -0.830 -16.231 1.00 1.07
ATOM 1849 O PHE 1 749 -6.666 -0.153 -15.426 1.00 1.07
ATOM 1850 CB PHE 1 749 -3.708 -1.384 -15.525 1.00 1.07
ATOM 1851 CG PHE 1 749 -3.490 -1.527 -14.058 1.00 1.07
ATOM 1852 CD1 PHE 1 749 -4.079 -0.621 -13.203 1.00 1.07
ATOM 1853 CD2 PHE 1 749 -2.740 -2.551 -13.532 1.00 1.07
ATOM 1854 CE1 PHE 1 749 -3.924 -0.728 -11.843 1.00 1.07
ATOM 1855 CE2 PHE 1 749 -2.580 -2.664 -12.172 1.00 1.07
ATOM 1856 CZ PHE 1 749 -3.175 -1.757 -11.330 1.00 1.07
ATOM 1857 N PRO 1 750 -6.247 -0.589 -17.529 1.00 0.90
ATOM 1858 CA PRO 1 750 -7.221 0.431 -17.979 1.00 0.90
ATOM 1859 C PRO 1 750 -8.771 0.442 -18.016 1.00 0.90
ATOM 1860 O PRO 1 750 -9.291 1.473 -17.605 1.00 0.90
ATOM 1861 CB PRO 1 750 -6.687 0.963 -19.305 1.00 0.90
ATOM 1862 CG PRO 1 750 -5.169 0.827 -19.170 1.00 0.90
ATOM 1863 CD PRO 1 750 -4.983 -0.372 -18.237 1.00 0.90
ATOM 1864 N GLU 1 751 -9.539 -0.588 -18.489 1.00 0.84
ATOM 1865 CA GLU 1 751 -11.014 -0.740 -18.539 1.00 0.84
ATOM 1866 C GLU 1 751 -11.479 -0.956 -17.136 1.00 0.84
ATOM 1867 O GLU 1 751 -12.611 -0.771 -16.702 1.00 0.84
ATOM 1868 CB GLU 1 751 -11.508 -2.071 -19.129 1.00 0.84
ATOM 1869 CG GLU 1 751 -11.246 -2.389 -20.592 1.00 0.84

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ATOM  1870 CD  GLU 1 751   -11.804 -3.799 -20.762 1.00 0.84
ATOM  1871 OE1 GLU 1 751   -12.632 -4.206 -19.902 1.00 0.84
ATOM  1872 OE2 GLU 1 751   -11.407 -4.491 -21.736 1.00 0.84
ATOM  1873 N   MET 1 752   -10.435 -1.330 -16.468 1.00 1.00
ATOM  1874 CA  MET 1 752    -9.749 -1.826 -15.370 1.00 1.00
ATOM  1875 C   MET 1 752    -9.587 -0.479 -14.739 1.00 1.00
ATOM  1876 O   MET 1 752    -9.038  0.421 -15.327 1.00 1.00
ATOM  1877 CB  MET 1 752    -8.464 -2.412 -15.976 1.00 1.00
ATOM  1878 CG  MET 1 752    -8.681 -2.977 -17.397 1.00 1.00
ATOM  1879 SD  MET 1 752    -7.488 -3.879 -18.478 1.00 1.00
ATOM  1880 CE  MET 1 752    -5.812 -3.234 -18.336 1.00 1.00
ATOM  1881 N   LEU 1 753   -10.177 -0.119 -13.608 1.00 0.82
ATOM  1882 CA  LEU 1 753   -10.723  1.132 -13.156 1.00 0.82
ATOM  1883 C   LEU 1 753   -11.151  2.199 -14.132 1.00 0.82
ATOM  1884 O   LEU 1 753   -11.750  3.146 -13.637 1.00 0.82
ATOM  1885 CB  LEU 1 753    -9.733  1.821 -12.206 1.00 0.82
ATOM  1886 CG  LEU 1 753    -9.134  0.865 -11.154 1.00 0.82
ATOM  1887 CD1 LEU 1 753    -8.168  1.601 -10.215 1.00 0.82
ATOM  1888 CD2 LEU 1 753   -10.213  0.066 -10.416 1.00 0.82
ATOM  1889 N   ALA 1 754   -10.833  2.252 -15.434 1.00 0.46
ATOM  1890 CA  ALA 1 754   -11.599  3.228 -16.176 1.00 0.46
ATOM  1891 C   ALA 1 754   -13.059  2.905 -15.999 1.00 0.46
ATOM  1892 O   ALA 1 754   -13.882  3.799 -15.806 1.00 0.46
ATOM  1893 CB  ALA 1 754   -11.365  3.231 -17.693 1.00 0.46
ATOM  1894 N   GLU 1 755   -13.440  1.617 -16.045 1.00 0.40
ATOM  1895 CA  GLU 1 755   -14.834  1.335 -15.868 1.00 0.40
ATOM  1896 C   GLU 1 755   -15.213  1.617 -14.439 1.00 0.40
ATOM  1897 O   GLU 1 755   -16.289  2.147 -14.167 1.00 0.40
ATOM  1898 CB  GLU 1 755   -15.219 -0.113 -16.213 1.00 0.40
ATOM  1899 CG  GLU 1 755   -16.662 -0.249 -16.703 1.00 0.40
ATOM  1900 CD  GLU 1 755   -16.704  0.257 -18.144 1.00 0.40
ATOM  1901 OE1 GLU 1 755   -15.627  0.649 -18.670 1.00 0.40
ATOM  1902 OE2 GLU 1 755   -17.815  0.259 -18.738 1.00 0.40
ATOM  1903 N   ILE 1 756   -14.344  1.276 -13.465 1.00 0.54
ATOM  1904 CA  ILE 1 756   -14.767  1.507 -12.107 1.00 0.54
ATOM  1905 C   ILE 1 756   -14.871  2.980 -11.844 1.00 0.54
ATOM  1906 O   ILE 1 756   -15.787  3.444 -11.166 1.00 0.54
ATOM  1907 CB  ILE 1 756   -13.882  0.897 -11.056 1.00 0.54
ATOM  1908 CG1 ILE 1 756   -14.628  0.842  -9.715 1.00 0.54
ATOM  1909 CG2 ILE 1 756   -12.589  1.712 -10.964 1.00 0.54
ATOM  1910 CD1 ILE 1 756   -13.948 -0.046  -8.675 1.00 0.54
ATOM  1911 N   ILE 1 757   -13.918  3.756 -12.381 1.00 0.68
ATOM  1912 CA  ILE 1 757   -13.860  5.171 -12.178 1.00 0.68
ATOM  1913 C   ILE 1 757   -15.065  5.770 -12.829 1.00 0.68
ATOM  1914 O   ILE 1 757   -15.686  6.676 -12.277 1.00 0.68
ATOM  1915 CB  ILE 1 757   -12.586  5.766 -12.730 1.00 0.68
ATOM  1916 CG1 ILE 1 757   -12.330  7.179 -12.179 1.00 0.68
ATOM  1917 CG2 ILE 1 757   -12.629  5.683 -14.261 1.00 0.68
ATOM  1918 CD1 ILE 1 757   -13.415  8.191 -12.530 1.00 0.68
ATOM  1919 N   THR 1 758   -15.440  5.275 -14.024 1.00 0.66
ATOM  1920 CA  THR 1 758   -16.587  5.825 -14.688 1.00 0.66
ATOM  1921 C   THR 1 758   -17.817  5.482 -13.909 1.00 0.66
ATOM  1922 O   THR 1 758   -18.720  6.305 -13.764 1.00 0.66
ATOM  1923 CB  THR 1 758   -16.759  5.334 -16.101 1.00 0.66
ATOM  1924 OG1 THR 1 758   -17.730  6.122 -16.773 1.00 0.66
ATOM  1925 CG2 THR 1 758   -17.208  3.866 -16.084 1.00 0.66
ATOM  1926 N   ASN 1 759   -17.878  4.251 -13.365 1.00 0.59
ATOM  1927 CA  ASN 1 759   -19.051  3.827 -12.658 1.00 0.59
ATOM  1928 C   ASN 1 759   -19.270  4.756 -11.512 1.00 0.59
ATOM  1929 O   ASN 1 759   -20.380  5.246 -11.304 1.00 0.59
ATOM  1930 CB  ASN 1 759   -18.912  2.404 -12.085 1.00 0.59
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ATOM   1933  ND2 ASN 1 759     -20.885   0.959 -11.921  1.00  0.59
ATOM   1934  N   GLN 1 760     -18.207   5.047 -10.745  1.00  0.63
ATOM   1935  CA  GLN 1 760     -18.377   5.911  -9.617  1.00  0.63
ATOM   1936  C   GLN 1 760     -18.731   7.261 -10.147  1.00  0.63
ATOM   1937  O   GLN 1 760     -18.410   7.597 -11.286  1.00  0.63
ATOM   1938  CB  GLN 1 760     -17.108   6.042  -8.759  1.00  0.63
ATOM   1939  CG  GLN 1 760     -17.262   6.958  -7.545  1.00  0.63
ATOM   1940  CD  GLN 1 760     -15.928   6.970  -6.815  1.00  0.63
ATOM   1941  OE1 GLN 1 760     -15.008   6.239  -7.179  1.00  0.63
ATOM   1942  NE2 GLN 1 760     -15.814   7.819  -5.758  1.00  0.63
ATOM   1943  N   ILE 1 761     -19.443   8.061  -9.333  1.00  0.75
ATOM   1944  CA  ILE 1 761     -19.806   9.378  -9.765  1.00  0.75
ATOM   1945  C   ILE 1 761     -18.957  10.329  -8.920  1.00  0.75
ATOM   1946  O   ILE 1 761     -18.295   9.822  -7.976  1.00  0.75
ATOM   1947  CB  ILE 1 761     -21.261   9.689  -9.526  1.00  0.75
ATOM   1948  CG1 ILE 1 761     -22.144   8.673 -10.271  1.00  0.75
ATOM   1949  CG2 ILE 1 761     -21.544  11.138  -9.954  1.00  0.75
ATOM   1950  CD1 ILE 1 761     -23.618   8.746  -9.878  1.00  0.75
ATOM   1951  OXT ILE 1 761     -18.946  11.557  -9.202  1.00 99.99
TER    1952      ILE 1 761
HETATM 1953  C01 UNK   1      -2.020  -7.470  -3.975  1.00 -0.03
HETATM 1954  C08 UNK   1      -2.604  -8.499  -4.716  1.00  0.00
HETATM 1955  C07 UNK   1      -3.588  -8.239  -5.676  1.00  0.00
HETATM 1956  C04 UNK   1      -4.044  -6.938  -5.927  1.00  0.15
HETATM 1957  C03 UNK   1      -3.449  -5.887  -5.194  1.00  0.00
HETATM 1958  C02 UNK   1      -2.450  -6.150  -4.229  1.00  0.00
HETATM 1959  N05 UNK   1      -5.088  -6.741  -6.891  1.00 -0.69
HETATM 1960  C06 UNK   1      -5.500  -7.809  -7.786  1.00  0.27
HETATM 1961  C09 UNK   1      -5.841  -5.513  -7.030  1.00  0.27
HETATM 1962  C19 C     2       2.863  -9.728  -3.299  1.00  0.02
HETATM 1963  C22 C     2       3.237 -10.282  -2.296  1.00 -0.39
HETATM 1964  C22 C     2       3.714 -10.953  -1.093  1.00  0.30
HETATM 1965  H100C     2       2.874 -11.106  -0.400  1.00  0.00
HETATM 1966  H101C     2       4.482 -10.332  -0.607  1.00  0.00
HETATM 1967  H102C     2       4.148 -11.927  -1.363  1.00  0.00
HETATM 1968  C01 UNK   3      -2.100  -6.783  -0.557  1.00  0.03
HETATM 1969  C02 UNK   3      -0.922  -6.070  -1.201  1.00 -0.03
HETATM 1970  C17 UNK   3      -0.435  -4.794  -0.622  1.00 -0.03
HETATM 1971  C16 UNK   3       0.740  -4.085  -1.251  1.00  0.03
HETATM 1972  C15 UNK   3       1.664  -5.067  -1.960  1.00  0.00
HETATM 1973  C14 UNK   3       0.923  -5.996  -2.938  1.00  0.14
HETATM 1974  C03 UNK   3      -0.344  -6.602  -2.292  1.00 -0.27
HETATM 1975  C04 UNK   3      -0.997  -7.843  -2.908  1.00  0.17
HETATM 1976  C05 UNK   3       0.077  -8.825  -3.425  1.00  0.00
HETATM 1977  C06 UNK   3       1.195  -8.166  -4.241  1.00  0.00
HETATM 1978  C07 UNK   3       0.631  -7.623  -5.568  1.00  0.00
HETATM 1979  C08 UNK   3       2.441  -9.040  -4.505  1.00  0.31
HETATM 1980  O09 UNK   3       2.272  -9.992  -5.534  1.00 -0.55
HETATM 1981  H10 UNK   3       1.590 -10.610  -5.262  1.00  0.31
HETATM 1982  C11 UNK   3       3.536  -8.012  -4.833  1.00  0.00
HETATM 1983  C12 UNK   3       3.149  -6.736  -4.082  1.00  0.00
HETATM 1984  C13 UNK   3       1.875  -7.132  -3.336  1.00  0.00
HETATM 1985  C18 UNK   3      -1.069  -4.259   0.508  1.00  0.00
HETATM 1986  C19 UNK   3      -2.258  -4.896   1.089  1.00  0.40
HETATM 1987  C21 UNK   3      -3.030  -5.873   0.233  1.00  0.05
HETATM 1988  O20 UNK   3      -2.621  -4.644   2.227  1.00 -0.45
CONECT 1953 1954 1958 1975
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CONECT 1955 1954 1956
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COMPND  GR_TR_V1
AUTHOR  GENERATED BY SYBYL, A PRODUCT OF TRIPOS, INC.
SEQRES  1 1  240  PRO ALA THR LEU PRO GLN LEU THR PRO THR LEU VAL SER
SEQRES  2 1  240  LEU LEU GLU VAL ILE GLU PRO GLU VAL LEU TYR ALA GLY
SEQRES  3 1  240  TYR ASP SER SER VAL PRO ASP SER THR TRP ARG ILE MET
SEQRES  4 1  240  THR THR LEU ASN MET LEU GLY GLY ARG GLN VAL ILE ALA
SEQRES  5 1  240  ALA VAL LYS TRP ALA LYS ALA ILE PRO GLY PHE ARG ASN
SEQRES  6 1  240  LEU HIS LEU ASP ASP GLN MET THR LEU LEU GLN TYR SER
SEQRES  7 1  240  TRP MET PHE LEU MET ALA PHE ALA LEU GLY TRP ARG SER
SEQRES  8 1  240  TYR ARG GLN SER SER ALA ASN LEU LEU CYS PHE ALA PRO
SEQRES  9 1  240  ASP LEU ILE ILE ASN GLU GLN ARG MET THR LEU PRO CYS
SEQRES 10 1  240  MET TYR ASP GLN CYS LYS HIS MET LEU TYR VAL SER SER
SEQRES 11 1  240  GLU LEU HIS ARG LEU GLN VAL SER TYR GLU GLU TYR LEU
SEQRES 12 1  240  CYS MET LYS THR LEU LEU LEU LEU SER SER VAL PRO LYS
SEQRES 13 1  240  ASP GLY LEU LYS SER GLN GLU LEU PHE ASP GLU ILE ARG
SEQRES 14 1  240  MET THR TYR ILE LYS GLU LEU GLY LYS ALA ILE VAL LYS
SEQRES 15 1  240  ARG GLU GLY ASN SER SER GLN ASN TRP GLN ARG PHE TYR
SEQRES 16 1  240  GLN LEU THR LYS LEU LEU ASP SER MET HIS GLU VAL VAL
SEQRES 17 1  240  GLU ASN LEU LEU ASN TYR CYS PHE GLN THR PHE LEU ASP
SEQRES 18 1  240  LYS THR MET SER ILE GLU PHE PRO GLU MET LEU ALA GLU
SEQRES 19 1  240  ILE ILE THR ASN GLN ILE
ATOM    1  N   PRO 1 522    -0.627  29.241   5.806  1.00  5.52
ATOM    2  CA  PRO 1 522    -1.732  29.968   5.121  1.00  5.52
ATOM    3  C   PRO 1 522    -3.005  29.229   5.366  1.00  5.52
ATOM    4  O   PRO 1 522    -2.966  28.016   5.546  1.00  5.52
ATOM    5  CB  PRO 1 522    -1.324  30.082   3.655  1.00  5.52
ATOM    6  CG  PRO 1 522     0.209  30.020   3.670  1.00  5.52
ATOM    7  CD  PRO 1 522     0.557  29.143   4.882  1.00  5.52
ATOM    8  N   ALA 1 523    -4.144  29.942   5.367  1.00  0.96
ATOM    9  CA  ALA 1 523    -5.430  29.392   5.693  1.00  0.96
ATOM   10  C   ALA 1 523    -5.899  28.334   4.745  1.00  0.96
ATOM   11  O   ALA 1 523    -6.411  27.298   5.168  1.00  0.96
ATOM   12  CB  ALA 1 523    -6.527  30.469   5.724  1.00  0.96
ATOM   13  N   THR 1 524    -5.708  28.546   3.432  1.00  5.12
ATOM   14  CA  THR 1 524    -6.270  27.645   2.469  1.00  5.12
ATOM   15  C   THR 1 524    -5.769  26.255   2.661  1.00  5.12
ATOM   16  O   THR 1 524    -6.508  25.289   2.476  1.00  5.12
ATOM   17  CB  THR 1 524    -5.970  28.028   1.048  1.00  5.12
ATOM   18  OG1 THR 1 524    -6.738  27.228   0.161  1.00  5.12
ATOM   19  CG2 THR 1 524    -4.469  27.825   0.775  1.00  5.12
ATOM   20  N   LEU 1 525    -4.495  26.116   3.050  1.00  4.05
ATOM   21  CA  LEU 1 525    -3.904  24.817   3.148  1.00  4.05
ATOM   22  C   LEU 1 525    -4.619  23.998   4.180  1.00  4.05
ATOM   23  O   LEU 1 525    -4.846  22.807   3.975  1.00  4.05
ATOM   24  CB  LEU 1 525    -2.406  24.884   3.473  1.00  4.05
ATOM   25  CG  LEU 1 525    -1.624  25.796   2.496  1.00  4.05
ATOM   26  CD1 LEU 1 525    -1.808  25.375   1.030  1.00  4.05
ATOM   27  CD2 LEU 1 525    -1.952  27.279   2.714  1.00  4.05
ATOM   28  N   PRO 1 526    -4.986  24.583   5.282  1.00  2.45
ATOM   29  CA  PRO 1 526    -5.729  23.833   6.245  1.00  2.45
ATOM   30  C   PRO 1 526    -7.071  23.501   5.695  1.00  2.45
ATOM   31  O   PRO 1 526    -7.745  22.642   6.253  1.00  2.45
ATOM   32  CB  PRO 1 526    -5.728  24.660   7.535  1.00  2.45
ATOM   33  CG  PRO 1 526    -4.888  25.909   7.201  1.00  2.45
ATOM   34  CD  PRO 1 526    -4.087  25.487   5.960  1.00  2.45
ATOM   35  N   GLN 1 527    -7.532  24.178   4.638  1.00  6.73
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ATOM   37  C   GLN 1 527    -8.494  22.376   3.553  1.00  6.73
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ATOM   39  CB  GLN 1 527    -9.294  24.611   2.957  1.00  6.73
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ATOM 41 CD GLN 1 527 -11.731 24.634 3.365 1.00 6.73
ATOM 42 OE1 GLN 1 527 -12.924 24.477 3.113 1.00 6.73
ATOM 43 NE2 GLN 1 527 -11.299 25.225 4.511 1.00 6.73
ATOM 44 N LEU 1 528 -7.375 22.285 2.811 1.00 1.25
ATOM 45 CA LEU 1 528 -6.989 21.077 2.149 1.00 1.25
ATOM 46 C LEU 1 528 -6.605 19.985 3.099 1.00 1.25
ATOM 47 O LEU 1 528 -6.949 18.826 2.873 1.00 1.25
ATOM 48 CB LEU 1 528 -5.827 21.278 1.167 1.00 1.25
ATOM 49 CG LEU 1 528 -5.404 19.980 0.459 1.00 1.25
ATOM 50 CD1 LEU 1 528 -6.589 19.354 -0.296 1.00 1.25
ATOM 51 CD2 LEU 1 528 -4.197 20.216 -0.460 1.00 1.25
ATOM 52 N THR 1 529 -5.883 20.309 4.187 1.00 5.96
ATOM 53 CA THR 1 529 -5.449 19.243 5.042 1.00 5.96
ATOM 54 C THR 1 529 -6.567 18.468 5.692 1.00 5.96
ATOM 55 O THR 1 529 -6.499 17.241 5.674 1.00 5.96
ATOM 56 CB THR 1 529 -4.353 19.648 6.007 1.00 5.96
ATOM 57 OG1 THR 1 529 -4.145 18.629 6.974 1.00 5.96
ATOM 58 CG2 THR 1 529 -4.595 21.030 6.638 1.00 5.96
ATOM 59 N PRO 1 530 -7.594 19.043 6.263 1.00 5.19
ATOM 60 CA PRO 1 530 -8.631 18.171 6.732 1.00 5.19
ATOM 61 C PRO 1 530 -9.396 17.473 5.656 1.00 5.19
ATOM 62 O PRO 1 530 -9.961 16.419 5.940 1.00 5.19
ATOM 63 CB PRO 1 530 -9.480 18.989 7.697 1.00 5.19
ATOM 64 CG PRO 1 530 -8.446 19.924 8.336 1.00 5.19
ATOM 65 CD PRO 1 530 -7.367 20.075 7.254 1.00 5.19
ATOM 66 N THR 1 531 -9.457 18.027 4.431 1.00 0.64
ATOM 67 CA THR 1 531 -10.190 17.352 3.401 1.00 0.64
ATOM 68 C THR 1 531 -9.495 16.061 3.114 1.00 0.64
ATOM 69 O THR 1 531 -10.110 14.995 3.091 1.00 0.64
ATOM 70 CB THR 1 531 -10.231 18.143 2.127 1.00 0.64
ATOM 71 OG1 THR 1 531 -10.823 19.412 2.362 1.00 0.64
ATOM 72 CG2 THR 1 531 -11.054 17.364 1.088 1.00 0.64
ATOM 73 N LEU 1 532 -8.165 16.133 2.924 1.00 6.54
ATOM 74 CA LEU 1 532 -7.401 14.967 2.608 1.00 6.54
ATOM 75 C LEU 1 532 -7.451 14.010 3.750 1.00 6.54
ATOM 76 O LEU 1 532 -7.628 12.816 3.537 1.00 6.54
ATOM 77 CB LEU 1 532 -5.939 15.288 2.227 1.00 6.54
ATOM 78 CG LEU 1 532 -5.114 16.074 3.268 1.00 6.54
ATOM 79 CD1 LEU 1 532 -4.690 15.205 4.462 1.00 6.54
ATOM 80 CD2 LEU 1 532 -3.922 16.777 2.601 1.00 6.54
ATOM 81 N VAL 1 533 -7.357 14.496 4.997 1.00 0.78
ATOM 82 CA VAL 1 533 -7.312 13.615 6.132 1.00 0.78
ATOM 83 C VAL 1 533 -8.569 12.811 6.247 1.00 0.78
ATOM 84 O VAL 1 533 -8.524 11.602 6.475 1.00 0.78
ATOM 85 CB VAL 1 533 -7.153 14.365 7.416 1.00 0.78
ATOM 86 CG1 VAL 1 533 -7.253 13.368 8.578 1.00 0.78
ATOM 87 CG2 VAL 1 533 -5.825 15.139 7.368 1.00 0.78
ATOM 88 N SER 1 534 -9.730 13.465 6.071 1.00 2.96
ATOM 89 CA SER 1 534 -10.989 12.790 6.208 1.00 2.96
ATOM 90 C SER 1 534 -11.018 11.730 5.164 1.00 2.96
ATOM 91 O SER 1 534 -11.546 10.637 5.366 1.00 2.96
ATOM 92 CB SER 1 534 -12.192 13.718 5.971 1.00 2.96
ATOM 93 OG SER 1 534 -13.404 12.993 6.116 1.00 2.96
ATOM 94 N LEU 1 535 -10.418 12.049 4.013 1.00 7.50
ATOM 95 CA LEU 1 535 -10.349 11.153 2.910 1.00 7.50
ATOM 96 C LEU 1 535 -9.730 9.848 3.293 1.00 7.50
ATOM 97 O LEU 1 535 -10.320 8.802 3.027 1.00 7.50
ATOM 98 CB LEU 1 535 -9.471 11.746 1.819 1.00 7.50
ATOM 99 CG LEU 1 535 -9.060 10.667 0.844 1.00 7.50
ATOM 100 CD1 LEU 1 535 -10.323 9.945 0.376 1.00 7.50

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ATOM   101  CD2 LEU 1 535     -8.144  11.236  -0.247  1.00  7.50
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ATOM   103  CA  LEU 1 536     -7.959   8.579   4.258  1.00  5.15
ATOM   104  C   LEU 1 536     -8.747   7.902   5.310  1.00  5.15
ATOM   105  O   LEU 1 536     -8.938   6.691   5.244  1.00  5.15
ATOM   106  CB  LEU 1 536     -6.518   8.550   4.791  1.00  5.15
ATOM   107  CG  LEU 1 536     -5.926   7.169   5.143  1.00  5.15
ATOM   108  CD1 LEU 1 536     -6.389   6.648   6.514  1.00  5.15
ATOM   109  CD2 LEU 1 536     -6.182   6.173   4.004  1.00  5.15
ATOM   110  N   GLU 1 537     -9.215   8.674   6.306  1.00  3.32
ATOM   111  CA  GLU 1 537     -9.876   8.087   7.433  1.00  3.32
ATOM   112  C   GLU 1 537    -11.004   7.253   6.936  1.00  3.32
ATOM   113  O   GLU 1 537    -11.180   6.113   7.366  1.00  3.32
ATOM   114  CB  GLU 1 537    -10.491   9.139   8.375  1.00  3.32
ATOM   115  CG  GLU 1 537     -9.466   9.988   9.130  1.00  3.32
ATOM   116  CD  GLU 1 537     -8.937   9.165  10.295  1.00  3.32
ATOM   117  OE1 GLU 1 537     -8.074   9.692  11.047  1.00  3.32
ATOM   118  OE2 GLU 1 537     -9.391   8.000  10.453  1.00  3.32
ATOM   119  N   VAL 1 538    -11.787   7.791   5.989  1.00  4.21
ATOM   120  CA  VAL 1 538    -12.906   7.043   5.514  1.00  4.21
ATOM   121  C   VAL 1 538    -12.485   5.790   4.802  1.00  4.21
ATOM   122  O   VAL 1 538    -13.042   4.726   5.058  1.00  4.21
ATOM   123  CB  VAL 1 538    -13.781   7.832   4.581  1.00  4.21
ATOM   124  CG1 VAL 1 538    -14.337   9.043   5.348  1.00  4.21
ATOM   125  CG2 VAL 1 538    -12.978   8.204   3.325  1.00  4.21
ATOM   126  N   ILE 1 539    -11.500   5.860   3.880  1.00  8.15
ATOM   127  CA  ILE 1 539    -11.192   4.652   3.161  1.00  8.15
ATOM   128  C   ILE 1 539    -10.371   3.670   3.930  1.00  8.15
ATOM   129  O   ILE 1 539    -10.401   2.484   3.614  1.00  8.15
ATOM   130  CB  ILE 1 539    -10.538   4.768   1.805  1.00  8.15
ATOM   131  CG1 ILE 1 539     -9.065   5.184   1.864  1.00  8.15
ATOM   132  CG2 ILE 1 539    -11.410   5.716   0.966  1.00  8.15
ATOM   133  CD1 ILE 1 539     -8.851   6.612   2.298  1.00  8.15
ATOM   134  N   GLU 1 540     -9.571   4.137   4.909  1.00  4.12
ATOM   135  CA  GLU 1 540     -8.724   3.247   5.654  1.00  4.12
ATOM   136  C   GLU 1 540     -9.574   2.205   6.301  1.00  4.12
ATOM   137  O   GLU 1 540    -10.537   2.507   7.004  1.00  4.12
ATOM   138  CB  GLU 1 540     -7.933   3.953   6.769  1.00  4.12
ATOM   139  CG  GLU 1 540     -7.018   3.017   7.560  1.00  4.12
ATOM   140  CD  GLU 1 540     -6.307   3.845   8.622  1.00  4.12
ATOM   141  OE1 GLU 1 540     -5.440   3.273   9.335  1.00  4.12
ATOM   142  OE2 GLU 1 540     -6.626   5.058   8.737  1.00  4.12
ATOM   143  N   PRO 1 541     -9.231   0.969   6.072  1.00  5.53
ATOM   144  CA  PRO 1 541    -10.006  -0.080   6.661  1.00  5.53
ATOM   145  C   PRO 1 541     -9.704  -0.127   8.111  1.00  5.53
ATOM   146  O   PRO 1 541     -8.615   0.310   8.476  1.00  5.53
ATOM   147  CB  PRO 1 541     -9.637  -1.354   5.904  1.00  5.53
ATOM   148  CG  PRO 1 541     -9.217  -0.837   4.517  1.00  5.53
ATOM   149  CD  PRO 1 541     -8.676   0.577   4.786  1.00  5.53
ATOM   150  N   GLU 1 542    -10.669  -0.632   8.912  1.00  6.38
ATOM   151  CA  GLU 1 542    -10.594  -0.794  10.337  1.00  6.38
ATOM   152  C   GLU 1 542     -9.653   0.163  10.975  1.00  6.38
ATOM   153  O   GLU 1 542     -8.445  -0.062  10.977  1.00  6.38
ATOM   154  CB  GLU 1 542    -10.213  -2.215  10.784  1.00  6.38
ATOM   155  CG  GLU 1 542    -11.367  -3.220  10.712  1.00  6.38
ATOM   156  CD  GLU 1 542    -11.704  -3.495   9.254  1.00  6.38
ATOM   157  OE1 GLU 1 542    -12.351  -2.620   8.618  1.00  6.38
ATOM   158  OE2 GLU 1 542    -11.328  -4.590   8.758  1.00  6.38
ATOM   159  N   VAL 1 543    -10.188   1.285  11.490  1.00  2.42
ATOM   160  CA  VAL 1 543     -9.342   2.211  12.175  1.00  2.42
ATOM   161  C   VAL 1 543     -8.738   1.383  13.264  1.00  2.42
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ATOM   162 O   VAL 1 543   -7.553  1.510 13.567 1.00 2.42
ATOM   163 CB  VAL 1 543  -10.100  3.338 12.810 1.00 2.42
ATOM   164 CG1 VAL 1 543   -9.104  4.218 13.584 1.00 2.42
ATOM   165 CG2 VAL 1 543  -10.870  4.089 11.711 1.00 2.42
ATOM   166 N   LEU 1 544   -9.546  0.467 13.843 1.00 7.00
ATOM   167 CA  LEU 1 544   -9.040 -0.416 14.851 1.00 7.00
ATOM   168 C   LEU 1 544   -7.965 -1.188 14.158 1.00 7.00
ATOM   169 O   LEU 1 544   -8.090 -1.557 12.992 1.00 7.00
ATOM   170 CB  LEU 1 544  -10.117 -1.354 15.443 1.00 7.00
ATOM   171 CG  LEU 1 544   -9.644 -2.308 16.564 1.00 7.00
ATOM   172 CD1 LEU 1 544  -10.842 -3.017 17.209 1.00 7.00
ATOM   173 CD2 LEU 1 544   -8.606 -3.330 16.075 1.00 7.00
ATOM   174 N   TYR 1 545   -6.872 -1.457 14.883 1.00 9.50
ATOM   175 CA  TYR 1 545   -5.668 -1.991 14.326 1.00 9.50
ATOM   176 C   TYR 1 545   -5.530 -3.441 14.662 1.00 9.50
ATOM   177 O   TYR 1 545   -6.141 -4.317 14.047 1.00 9.50
ATOM   178 CB  TYR 1 545   -4.490 -1.241 14.972 1.00 9.50
ATOM   179 CG  TYR 1 545   -3.181 -1.414 14.291 1.00 9.50
ATOM   180 CD1 TYR 1 545   -2.875 -0.615 13.212 1.00 9.50
ATOM   181 CD2 TYR 1 545   -2.157 -2.048 14.954 1.00 9.50
ATOM   182 CE1 TYR 1 545   -1.574 -0.459 12.796 1.00 9.50
ATOM   183 CE2 TYR 1 545   -0.854 -1.898 14.545 1.00 9.50
ATOM   184 CZ  TYR 1 545   -0.560 -1.084 13.481 1.00 9.50
ATOM   185 OH  TYR 1 545    0.787 -0.832 13.147 1.00 9.50
ATOM   186 N   ALA 1 546   -4.692 -3.708 15.676 1.00 1.35
ATOM   187 CA  ALA 1 546   -4.340 -5.025 16.109 1.00 1.35
ATOM   188 C   ALA 1 546   -5.523 -5.783 16.607 1.00 1.35
ATOM   189 O   ALA 1 546   -5.545 -7.007 16.515 1.00 1.35
ATOM   190 CB  ALA 1 546   -3.300 -5.025 17.242 1.00 1.35
ATOM   191 N   GLY 1 547   -6.535 -5.086 17.151 1.00 1.27
ATOM   192 CA  GLY 1 547   -7.639 -5.775 17.755 1.00 1.27
ATOM   193 C   GLY 1 547   -8.252 -6.802 16.851 1.00 1.27
ATOM   194 O   GLY 1 547   -8.407 -7.954 17.251 1.00 1.27
ATOM   195 N   TYR 1 548   -8.598 -6.437 15.601 1.00 2.17
ATOM   196 CA  TYR 1 548   -9.253 -7.419 14.782 1.00 2.17
ATOM   197 C   TYR 1 548   -8.395 -7.952 13.677 1.00 2.17
ATOM   198 O   TYR 1 548   -8.822 -7.969 12.525 1.00 2.17
ATOM   199 CB  TYR 1 548  -10.529 -6.897 14.101 1.00 2.17
ATOM   200 CG  TYR 1 548  -11.566 -6.699 15.150 1.00 2.17
ATOM   201 CD1 TYR 1 548  -11.629 -5.525 15.864 1.00 2.17
ATOM   202 CD2 TYR 1 548  -12.485 -7.689 15.406 1.00 2.17
ATOM   203 CE1 TYR 1 548  -12.607 -5.344 16.814 1.00 2.17
ATOM   204 CE2 TYR 1 548  -13.461 -7.513 16.357 1.00 2.17
ATOM   205 CZ  TYR 1 548  -13.525 -6.335 17.060 1.00 2.17
ATOM   206 OH  TYR 1 548  -14.517 -6.151 18.046 1.00 2.17
ATOM   207 N   ASP 1 549   -7.177 -8.436 13.981 1.00 5.55
ATOM   208 CA  ASP 1 549   -6.380 -8.969 12.912 1.00 5.55
ATOM   209 C   ASP 1 549   -6.134 -10.427 13.168 1.00 5.55
ATOM   210 O   ASP 1 549   -6.262 -10.894 14.297 1.00 5.55
ATOM   211 CB  ASP 1 549   -5.014 -8.281 12.761 1.00 5.55
ATOM   212 CG  ASP 1 549   -4.212 -8.527 14.029 1.00 5.55
ATOM   213 OD1 ASP 1 549   -2.972 -8.307 13.984 1.00 5.55
ATOM   214 OD2 ASP 1 549   -4.816 -8.944 15.053 1.00 5.55
ATOM   215 N   SER 1 550   -5.790 -11.196 12.113 1.00 0.80
ATOM   216 CA  SER 1 550   -5.537 -12.600 12.289 1.00 0.80
ATOM   217 C   SER 1 550   -4.246 -12.948 11.606 1.00 0.80
ATOM   218 O   SER 1 550   -3.812 -12.245 10.695 1.00 0.80
ATOM   219 CB  SER 1 550   -6.620 -13.499 11.672 1.00 0.80
ATOM   220 OG  SER 1 550   -6.619 -13.359 10.259 1.00 0.80
ATOM   221 N   SER 1 551   -3.594 -14.046 12.051 1.00 3.97
ATOM   222 CA  SER 1 551   -2.348 -14.482 11.474 1.00 3.97
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ATOM 223 C SER 1 551 -2.628 -15.435 10.351 1.00 3.97
ATOM 224 O SER 1 551 -3.668 -16.089 10.330 1.00 3.97
ATOM 225 CB SER 1 551 -1.416 -15.187 12.477 1.00 3.97
ATOM 226 OG SER 1 551 -2.010 -16.390 12.944 1.00 3.97
ATOM 227 N VAL 1 552 -1.703 -15.526 9.363 1.00 2.63
ATOM 228 CA VAL 1 552 -1.933 -16.318 8.175 1.00 2.63
ATOM 229 C VAL 1 552 -0.573 -16.748 7.601 1.00 2.63
ATOM 230 O VAL 1 552 0.265 -15.862 7.505 1.00 2.63
ATOM 231 CB VAL 1 552 -2.676 -15.415 7.202 1.00 2.63
ATOM 232 CG1 VAL 1 552 -2.855 -16.023 5.823 1.00 2.63
ATOM 233 CG2 VAL 1 552 -4.042 -15.059 7.811 1.00 2.63
ATOM 234 N PRO 1 553 -0.231 -18.027 7.329 1.00 9.93
ATOM 235 CA PRO 1 553 1.065 -18.358 6.679 1.00 9.93
ATOM 236 C PRO 1 553 1.126 -18.968 5.236 1.00 9.93
ATOM 237 O PRO 1 553 0.475 -19.998 5.072 1.00 9.93
ATOM 238 CB PRO 1 553 1.784 -19.288 7.649 1.00 9.93
ATOM 239 CG PRO 1 553 0.631 -20.005 8.368 1.00 9.93
ATOM 240 CD PRO 1 553 -0.490 -18.956 8.420 1.00 9.93
ATOM 241 N ASP 1 554 1.928 -18.474 4.211 1.00 7.69
ATOM 242 CA ASP 1 554 2.026 -19.177 2.915 1.00 7.69
ATOM 243 C ASP 1 554 2.850 -18.555 1.745 1.00 7.69
ATOM 244 O ASP 1 554 3.467 -17.502 1.910 1.00 7.69
ATOM 245 CB ASP 1 554 0.671 -19.618 2.359 1.00 7.69
ATOM 246 CG ASP 1 554 0.992 -20.935 1.676 1.00 7.69
ATOM 247 OD1 ASP 1 554 2.167 -21.375 1.764 1.00 7.69
ATOM 248 OD2 ASP 1 554 0.069 -21.531 1.072 1.00 7.69
ATOM 249 N SER 1 555 2.873 -19.195 0.516 1.00 5.28
ATOM 250 CA SER 1 555 3.725 -18.879 -0.634 1.00 5.28
ATOM 251 C SER 1 555 2.970 -18.889 -1.948 1.00 5.28
ATOM 252 O SER 1 555 1.762 -19.104 -1.955 1.00 5.28
ATOM 253 CB SER 1 555 4.897 -19.883 -0.739 1.00 5.28
ATOM 254 OG SER 1 555 5.767 -19.577 -1.819 1.00 5.28
ATOM 255 N THR 1 556 3.665 -18.594 -3.079 1.00 9.81
ATOM 256 CA THR 1 556 3.098 -18.498 -4.399 1.00 9.81
ATOM 257 C THR 1 556 2.078 -19.549 -4.606 1.00 9.81
ATOM 258 O THR 1 556 2.322 -20.712 -4.296 1.00 9.81
ATOM 259 CB THR 1 556 4.110 -18.631 -5.498 1.00 9.81
ATOM 260 OG1 THR 1 556 4.727 -19.910 -5.444 1.00 9.81
ATOM 261 CG2 THR 1 556 5.165 -17.525 -5.339 1.00 9.81
ATOM 262 N TRP 1 557 0.895 -19.108 -5.085 1.00 5.43
ATOM 263 CA TRP 1 557 -0.253 -19.917 -5.357 1.00 5.43
ATOM 264 C TRP 1 557 -1.190 -19.773 -4.203 1.00 5.43
ATOM 265 O TRP 1 557 -2.096 -18.941 -4.231 1.00 5.43
ATOM 266 CB TRP 1 557 0.057 -21.409 -5.621 1.00 5.43
ATOM 267 CG TRP 1 557 0.908 -21.586 -6.860 1.00 5.43
ATOM 268 CD1 TRP 1 557 1.247 -20.638 -7.782 1.00 5.43
ATOM 269 CD2 TRP 1 557 1.570 -22.798 -7.266 1.00 5.43
ATOM 270 NE1 TRP 1 557 2.062 -21.184 -8.742 1.00 5.43
ATOM 271 CE2 TRP 1 557 2.273 -22.511 -8.437 1.00 5.43
ATOM 272 CE3 TRP 1 557 1.595 -24.046 -6.710 1.00 5.43
ATOM 273 CZ2 TRP 1 557 3.012 -23.468 -9.072 1.00 5.43
ATOM 274 CZ3 TRP 1 557 2.341 -25.008 -7.354 1.00 5.43
ATOM 275 CH2 TRP 1 557 3.037 -24.726 -8.512 1.00 5.43
ATOM 276 N ARG 1 558 -0.986 -20.580 -3.147 1.00 4.12
ATOM 277 CA ARG 1 558 -1.870 -20.583 -2.018 1.00 4.12
ATOM 278 C ARG 1 558 -1.869 -19.291 -1.243 1.00 4.12
ATOM 279 O ARG 1 558 -2.939 -18.741 -0.987 1.00 4.12
ATOM 280 CB ARG 1 558 -1.570 -21.770 -1.089 1.00 4.12
ATOM 281 CG ARG 1 558 -2.483 -21.915 0.132 1.00 4.12
ATOM 282 CD ARG 1 558 -2.129 -23.147 0.976 1.00 4.12
ATOM 283 NE ARG 1 558 -2.927 -23.111 2.231 1.00 4.12

ATOM 284 CZ ARG 1 558 -4.086 -23.824 2.321 1.00 4.12
ATOM 285 NH1 ARG 1 558 -4.518 -24.562 1.258 1.00 4.12
ATOM 286 NH2 ARG 1 558 -4.799 -23.816 3.484 1.00 4.12
ATOM 287 N ILE 1 559 -0.695 -18.747 -0.843 1.00 7.58
ATOM 288 CA ILE 1 559 -0.761 -17.491 -0.136 1.00 7.58
ATOM 289 C ILE 1 559 -1.163 -16.455 -1.122 1.00 7.58
ATOM 290 O ILE 1 559 -1.922 -15.554 -0.783 1.00 7.58
ATOM 291 CB ILE 1 559 0.492 -17.071 0.590 1.00 7.58
ATOM 292 CG1 ILE 1 559 0.360 -15.803 1.440 1.00 7.58
ATOM 293 CG2 ILE 1 559 1.567 -16.870 -0.411 1.00 7.58
ATOM 294 CD1 ILE 1 559 -0.030 -14.472 0.828 1.00 7.58
ATOM 295 N MET 1 560 -0.726 -16.591 -2.389 1.00 1.02
ATOM 296 CA MET 1 560 -1.077 -15.624 -3.390 1.00 1.02
ATOM 297 C MET 1 560 -2.568 -15.530 -3.413 1.00 1.02
ATOM 298 O MET 1 560 -3.133 -14.446 -3.546 1.00 1.02
ATOM 299 CB MET 1 560 -0.619 -16.020 -4.805 1.00 1.02
ATOM 300 CG MET 1 560 -0.959 -14.967 -5.865 1.00 1.02
ATOM 301 SD MET 1 560 -0.338 -15.332 -7.535 1.00 1.02
ATOM 302 CE MET 1 560 -1.515 -16.668 -7.887 1.00 1.02
ATOM 303 N THR 1 561 -3.245 -16.676 -3.233 1.00 0.75
ATOM 304 CA THR 1 561 -4.675 -16.664 -3.213 1.00 0.75
ATOM 305 C THR 1 561 -5.142 -15.836 -2.058 1.00 0.75
ATOM 306 O THR 1 561 -6.070 -15.039 -2.189 1.00 0.75
ATOM 307 CB THR 1 561 -5.280 -18.020 -3.010 1.00 0.75
ATOM 308 OG1 THR 1 561 -4.864 -18.913 -4.033 1.00 0.75
ATOM 309 CG2 THR 1 561 -6.811 -17.868 -3.035 1.00 0.75
ATOM 310 N THR 1 562 -4.503 -15.997 -0.883 1.00 4.60
ATOM 311 CA THR 1 562 -4.985 -15.299 0.272 1.00 4.60
ATOM 312 C THR 1 562 -4.840 -13.814 0.133 1.00 4.60
ATOM 313 O THR 1 562 -5.749 -13.078 0.514 1.00 4.60
ATOM 314 CB THR 1 562 -4.347 -15.723 1.571 1.00 4.60
ATOM 315 OG1 THR 1 562 -5.143 -15.272 2.658 1.00 4.60
ATOM 316 CG2 THR 1 562 -2.945 -15.112 1.703 1.00 4.60
ATOM 317 N LEU 1 563 -3.710 -13.318 -0.419 1.00 3.84
ATOM 318 CA LEU 1 563 -3.589 -11.887 -0.483 1.00 3.84
ATOM 319 C LEU 1 563 -4.655 -11.438 -1.412 1.00 3.84
ATOM 320 O LEU 1 563 -5.340 -10.444 -1.182 1.00 3.84
ATOM 321 CB LEU 1 563 -2.329 -11.312 -1.161 1.00 3.84
ATOM 322 CG LEU 1 563 -0.992 -11.979 -0.831 1.00 3.84
ATOM 323 CD1 LEU 1 563 -0.839 -13.222 -1.707 1.00 3.84
ATOM 324 CD2 LEU 1 563 0.197 -11.014 -0.964 1.00 3.84
ATOM 325 N ASN 1 564 -4.818 -12.207 -2.499 1.00 3.56
ATOM 326 CA ASN 1 564 -5.696 -11.869 -3.572 1.00 3.56
ATOM 327 C ASN 1 564 -7.113 -11.760 -3.109 1.00 3.56
ATOM 328 O ASN 1 564 -7.853 -10.902 -3.586 1.00 3.56
ATOM 329 CB ASN 1 564 -5.638 -12.914 -4.692 1.00 3.56
ATOM 330 CG ASN 1 564 -6.061 -12.202 -5.953 1.00 3.56
ATOM 331 OD1 ASN 1 564 -7.106 -12.483 -6.539 1.00 3.56
ATOM 332 ND2 ASN 1 564 -5.205 -11.231 -6.370 1.00 3.56
ATOM 333 N MET 1 565 -7.531 -12.613 -2.155 1.00 5.34
ATOM 334 CA MET 1 565 -8.898 -12.577 -1.713 1.00 5.34
ATOM 335 C MET 1 565 -9.213 -11.199 -1.222 1.00 5.34
ATOM 336 O MET 1 565 -10.265 -10.646 -1.540 1.00 5.34
ATOM 337 CB MET 1 565 -9.165 -13.522 -0.524 1.00 5.34
ATOM 338 CG MET 1 565 -9.227 -15.013 -0.868 1.00 5.34
ATOM 339 SD MET 1 565 -10.846 -15.587 -1.472 1.00 5.34
ATOM 340 CE MET 1 565 -11.623 -15.702 0.166 1.00 5.34
ATOM 341 N LEU 1 566 -8.304 -10.627 -0.412 1.00 1.68
ATOM 342 CA LEU 1 566 -8.430 -9.317 0.170 1.00 1.68
ATOM 343 C LEU 1 566 -8.206 -8.166 -0.760 1.00 1.68
ATOM 344 O LEU 1 566 -8.694 -7.069 -0.497 1.00 1.68

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ATOM   345 CB  LEU 1 566    -7.494 -9.071  1.368 1.00 1.68
ATOM   346 CG  LEU 1 566    -7.870 -9.869  2.628 1.00 1.68
ATOM   347 CD1 LEU 1 566    -6.977 -9.475  3.815 1.00 1.68
ATOM   348 CD2 LEU 1 566    -9.368 -9.737  2.945 1.00 1.68
ATOM   349 N   GLY 1 567    -7.446 -8.371 -1.852 1.00 1.08
ATOM   350 CA  GLY 1 567    -7.005 -7.298 -2.704 1.00 1.08
ATOM   351 C   GLY 1 567    -8.083 -6.411 -3.249 1.00 1.08
ATOM   352 O   GLY 1 567    -7.882 -5.202 -3.354 1.00 1.08
ATOM   353 N   GLY 1 568    -9.245 -6.968 -3.633 1.00 0.69
ATOM   354 CA  GLY 1 568   -10.276 -6.151 -4.209 1.00 0.69
ATOM   355 C   GLY 1 568   -10.734 -5.095 -3.250 1.00 0.69
ATOM   356 O   GLY 1 568   -10.984 -3.958 -3.637 1.00 0.69
ATOM   357 N   ARG 1 569   -10.894 -5.421 -1.963 1.00 8.50
ATOM   358 CA  ARG 1 569   -11.347 -4.412 -1.049 1.00 8.50
ATOM   359 C   ARG 1 569   -10.311 -3.332 -0.953 1.00 8.50
ATOM   360 O   ARG 1 569   -10.625 -2.143 -0.913 1.00 8.50
ATOM   361 CB  ARG 1 569   -11.586 -4.953  0.372 1.00 8.50
ATOM   362 CG  ARG 1 569   -12.843 -5.819  0.536 1.00 8.50
ATOM   363 CD  ARG 1 569   -12.824 -7.141 -0.237 1.00 8.50
ATOM   364 NE  ARG 1 569   -13.206 -6.855 -1.650 1.00 8.50
ATOM   365 CZ  ARG 1 569   -12.718 -7.634 -2.660 1.00 8.50
ATOM   366 NH1 ARG 1 569   -11.861 -8.659 -2.377 1.00 8.50
ATOM   367 NH2 ARG 1 569   -13.087 -7.391 -3.951 1.00 8.50
ATOM   368 N   GLN 1 570    -9.030 -3.730 -0.922 1.00 0.65
ATOM   369 CA  GLN 1 570    -7.957 -2.791 -0.774 1.00 0.65
ATOM   370 C   GLN 1 570    -7.918 -1.860 -1.944 1.00 0.65
ATOM   371 O   GLN 1 570    -7.699 -0.660 -1.780 1.00 0.65
ATOM   372 CB  GLN 1 570    -6.584 -3.476 -0.703 1.00 0.65
ATOM   373 CG  GLN 1 570    -6.407 -4.379  0.518 1.00 0.65
ATOM   374 CD  GLN 1 570    -5.012 -4.978  0.446 1.00 0.65
ATOM   375 OE1 GLN 1 570    -4.262 -4.718 -0.494 1.00 0.65
ATOM   376 NE2 GLN 1 570    -4.651 -5.807  1.462 1.00 0.65
ATOM   377 N   VAL 1 571    -8.116 -2.396 -3.162 1.00 4.09
ATOM   378 CA  VAL 1 571    -8.061 -1.597 -4.350 1.00 4.09
ATOM   379 C   VAL 1 571    -9.161 -0.576 -4.319 1.00 4.09
ATOM   380 O   VAL 1 571    -8.904  0.612 -4.488 1.00 4.09
ATOM   381 CB  VAL 1 571    -8.180 -2.448 -5.611 1.00 4.09
ATOM   382 CG1 VAL 1 571    -9.582 -3.028 -5.750 1.00 4.09
ATOM   383 CG2 VAL 1 571    -7.855 -1.633 -6.856 1.00 4.09
ATOM   384 N   ILE 1 572   -10.419 -0.955 -4.025 1.00 7.34
ATOM   385 CA  ILE 1 572   -11.411  0.081 -4.132 1.00 7.34
ATOM   386 C   ILE 1 572   -11.182  1.164 -3.124 1.00 7.34
ATOM   387 O   ILE 1 572   -11.483  2.326 -3.386 1.00 7.34
ATOM   388 CB  ILE 1 572   -12.868 -0.317 -4.065 1.00 7.34
ATOM   389 CG1 ILE 1 572   -13.301 -0.901 -2.715 1.00 7.34
ATOM   390 CG2 ILE 1 572   -13.127 -1.259 -5.252 1.00 7.34
ATOM   391 CD1 ILE 1 572   -12.853 -2.332 -2.490 1.00 7.34
ATOM   392 N   ALA 1 573   -10.612  0.818 -1.957 1.00 0.75
ATOM   393 CA  ALA 1 573   -10.379  1.810 -0.949 1.00 0.75
ATOM   394 C   ALA 1 573    -9.475  2.880 -1.482 1.00 0.75
ATOM   395 O   ALA 1 573    -9.693  4.063 -1.229 1.00 0.75
ATOM   396 CB  ALA 1 573    -9.718  1.230  0.313 1.00 0.75
ATOM   397 N   ALA 1 574    -8.428  2.496 -2.236 1.00 0.63
ATOM   398 CA  ALA 1 574    -7.516  3.468 -2.772 1.00 0.63
ATOM   399 C   ALA 1 574    -8.244  4.342 -3.747 1.00 0.63
ATOM   400 O   ALA 1 574    -8.018  5.549 -3.802 1.00 0.63
ATOM   401 CB  ALA 1 574    -6.310  2.829 -3.482 1.00 0.63
ATOM   402 N   VAL 1 575    -9.147  3.744 -4.550 1.00 0.59
ATOM   403 CA  VAL 1 575    -9.902  4.488 -5.519 1.00 0.59
ATOM   404 C   VAL 1 575   -10.779  5.467 -4.804 1.00 0.59
ATOM   405 O   VAL 1 575   -10.914  6.615 -5.221 1.00 0.59
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ATOM  406  CB  VAL 1 575    -10.806   3.616  -6.340  1.00  0.59
ATOM  407  CG1 VAL 1 575    -11.582   4.505  -7.326  1.00  0.59
ATOM  408  CG2 VAL 1 575     -9.960   2.527  -7.019  1.00  0.59
ATOM  409  N   LYS 1 576    -11.392   5.025  -3.688  1.00  5.66
ATOM  410  CA  LYS 1 576    -12.292   5.853  -2.937  1.00  5.66
ATOM  411  C   LYS 1 576    -11.533   7.030  -2.426  1.00  5.66
ATOM  412  O   LYS 1 576    -12.029   8.155  -2.424  1.00  5.66
ATOM  413  CB  LYS 1 576    -12.875   5.132  -1.709  1.00  5.66
ATOM  414  CG  LYS 1 576    -13.748   3.926  -2.060  1.00  5.66
ATOM  415  CD  LYS 1 576    -14.972   4.279  -2.907  1.00  5.66
ATOM  416  CE  LYS 1 576    -15.839   3.066  -3.254  1.00  5.66
ATOM  417  NZ  LYS 1 576    -15.076   2.130  -4.109  1.00  5.66
ATOM  418  N   TRP 1 577    -10.288   6.789  -1.982  1.00  0.85
ATOM  419  CA  TRP 1 577     -9.473   7.831  -1.446  1.00  0.85
ATOM  420  C   TRP 1 577     -9.309   8.899  -2.481  1.00  0.85
ATOM  421  O   TRP 1 577     -9.578  10.076  -2.248  1.00  0.85
ATOM  422  CB  TRP 1 577     -8.070   7.313  -1.085  1.00  0.85
ATOM  423  CG  TRP 1 577     -7.130   8.338  -0.507  1.00  0.85
ATOM  424  CD1 TRP 1 577     -6.897   8.652   0.799  1.00  0.85
ATOM  425  CD2 TRP 1 577     -6.244   9.157  -1.286  1.00  0.85
ATOM  426  NE1 TRP 1 577     -5.917   9.608   0.878  1.00  0.85
ATOM  427  CE2 TRP 1 577     -5.505   9.931  -0.393  1.00  0.85
ATOM  428  CE3 TRP 1 577     -6.055   9.251  -2.634  1.00  0.85
ATOM  429  CZ2 TRP 1 577     -4.570  10.822  -0.833  1.00  0.85
ATOM  430  CZ3 TRP 1 577     -5.108  10.150  -3.074  1.00  0.85
ATOM  431  CH2 TRP 1 577     -4.381  10.922  -2.193  1.00  0.85
ATOM  432  N   ALA 1 578     -8.926   8.508  -3.699  1.00  1.04
ATOM  433  CA  ALA 1 578     -8.660   9.480  -4.717  1.00  1.04
ATOM  434  C   ALA 1 578     -9.883  10.278  -5.039  1.00  1.04
ATOM  435  O   ALA 1 578     -9.799  11.479  -5.289  1.00  1.04
ATOM  436  CB  ALA 1 578     -8.169   8.837  -6.026  1.00  1.04
ATOM  437  N   LYS 1 579    -11.062   9.636  -5.045  1.00  4.62
ATOM  438  CA  LYS 1 579    -12.259  10.335  -5.412  1.00  4.62
ATOM  439  C   LYS 1 579    -12.592  11.437  -4.454  1.00  4.62
ATOM  440  O   LYS 1 579    -13.125  12.471  -4.855  1.00  4.62
ATOM  441  CB  LYS 1 579    -13.477   9.411  -5.561  1.00  4.62
ATOM  442  CG  LYS 1 579    -13.391   8.576  -6.839  1.00  4.62
ATOM  443  CD  LYS 1 579    -14.419   7.452  -6.939  1.00  4.62
ATOM  444  CE  LYS 1 579    -14.310   6.661  -8.245  1.00  4.62
ATOM  445  NZ  LYS 1 579    -14.577   7.549  -9.399  1.00  4.62
ATOM  446  N   ALA 1 580    -12.288  11.248  -3.159  1.00  1.29
ATOM  447  CA  ALA 1 580    -12.598  12.223  -2.151  1.00  1.29
ATOM  448  C   ALA 1 580    -11.822  13.493  -2.321  1.00  1.29
ATOM  449  O   ALA 1 580    -12.196  14.518  -1.753  1.00  1.29
ATOM  450  CB  ALA 1 580    -12.371  11.733  -0.717  1.00  1.29
ATOM  451  N   ILE 1 581    -10.682  13.451  -3.042  1.00  3.84
ATOM  452  CA  ILE 1 581     -9.885  14.636  -3.206  1.00  3.84
ATOM  453  C   ILE 1 581    -10.346  15.411  -4.410  1.00  3.84
ATOM  454  O   ILE 1 581    -10.388  14.917  -5.536  1.00  3.84
ATOM  455  CB  ILE 1 581     -8.415  14.317  -3.325  1.00  3.84
ATOM  456  CG1 ILE 1 581     -7.541  15.562  -3.135  1.00  3.84
ATOM  457  CG2 ILE 1 581     -8.166  13.584  -4.651  1.00  3.84
ATOM  458  CD1 ILE 1 581     -6.071  15.199  -2.925  1.00  3.84
ATOM  459  N   PRO 1 582    -10.712  16.640  -4.160  1.00  3.26
ATOM  460  CA  PRO 1 582    -11.266  17.522  -5.155  1.00  3.26
ATOM  461  C   PRO 1 582    -10.417  17.677  -6.381  1.00  3.26
ATOM  462  O   PRO 1 582    -10.967  17.695  -7.481  1.00  3.26
ATOM  463  CB  PRO 1 582    -11.447  18.862  -4.446  1.00  3.26
ATOM  464  CG  PRO 1 582    -10.333  18.851  -3.381  1.00  3.26
ATOM  465  CD  PRO 1 582    -10.191  17.365  -3.012  1.00  3.26
ATOM  466  N   GLY 1 583     -9.088  17.794  -6.227  1.00  0.75
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ATOM   467  CA  GLY 1 583     -8.238  18.027  -7.358  1.00  0.75
ATOM   468  C   GLY 1 583     -8.296  16.878  -8.311  1.00  0.75
ATOM   469  O   GLY 1 583     -8.201  17.067  -9.521  1.00  0.75
ATOM   470  N   PHE 1 584     -8.420  15.655  -7.768  1.00  1.03
ATOM   471  CA  PHE 1 584     -8.409  14.430  -8.520  1.00  1.03
ATOM   472  C   PHE 1 584     -9.581  14.306  -9.446  1.00  1.03
ATOM   473  O   PHE 1 584     -9.430  13.931 -10.608  1.00  1.03
ATOM   474  CB  PHE 1 584     -8.422  13.217  -7.568  1.00  1.03
ATOM   475  CG  PHE 1 584     -8.361  11.929  -8.319  1.00  1.03
ATOM   476  CD1 PHE 1 584     -7.161  11.470  -8.810  1.00  1.03
ATOM   477  CD2 PHE 1 584     -9.444  11.078  -8.324  1.00  1.03
ATOM   478  CE1 PHE 1 584     -7.049  10.201  -9.329  1.00  1.03
ATOM   479  CE2 PHE 1 584     -9.337   9.805  -8.837  1.00  1.03
ATOM   480  CZ  PHE 1 584     -8.134   9.359  -9.328  1.00  1.03
ATOM   481  N   ARG 1 585    -10.782  14.653  -8.951  1.00  5.26
ATOM   482  CA  ARG 1 585    -11.990  14.486  -9.706  1.00  5.26
ATOM   483  C   ARG 1 585    -11.955  15.324 -10.940  1.00  5.26
ATOM   484  O   ARG 1 585    -12.483  14.934 -11.980  1.00  5.26
ATOM   485  CB  ARG 1 585    -13.247  14.881  -8.912  1.00  5.26
ATOM   486  CG  ARG 1 585    -14.548  14.666  -9.688  1.00  5.26
ATOM   487  CD  ARG 1 585    -15.802  15.056  -8.904  1.00  5.26
ATOM   488  NE  ARG 1 585    -16.977  14.796  -9.784  1.00  5.26
ATOM   489  CZ  ARG 1 585    -18.231  14.750  -9.249  1.00  5.26
ATOM   490  NH1 ARG 1 585    -19.307  14.502 -10.052  1.00  5.26
ATOM   491  NH2 ARG 1 585    -18.411  14.954  -7.910  1.00  5.26
ATOM   492  N   ASN 1 586    -11.322  16.506 -10.856  1.00  0.91
ATOM   493  CA  ASN 1 586    -11.280  17.411 -11.966  1.00  0.91
ATOM   494  C   ASN 1 586    -10.596  16.779 -13.138  1.00  0.91
ATOM   495  O   ASN 1 586    -10.973  17.026 -14.282  1.00  0.91
ATOM   496  CB  ASN 1 586    -10.529  18.714 -11.645  1.00  0.91
ATOM   497  CG  ASN 1 586    -11.381  19.523 -10.676  1.00  0.91
ATOM   498  OD1 ASN 1 586    -12.586  19.670 -10.867  1.00  0.91
ATOM   499  ND2 ASN 1 586    -10.739  20.060  -9.604  1.00  0.91
ATOM   500  N   LEU 1 587     -9.569  15.947 -12.892  1.00  4.04
ATOM   501  CA  LEU 1 587     -8.834  15.380 -13.988  1.00  4.04
ATOM   502  C   LEU 1 587     -9.724  14.592 -14.891  1.00  4.04
ATOM   503  O   LEU 1 587    -10.793  14.129 -14.499  1.00  4.04
ATOM   504  CB  LEU 1 587     -7.698  14.425 -13.571  1.00  4.04
ATOM   505  CG  LEU 1 587     -6.611  15.067 -12.690  1.00  4.04
ATOM   506  CD1 LEU 1 587     -7.107  15.257 -11.255  1.00  4.04
ATOM   507  CD2 LEU 1 587     -5.287  14.295 -12.751  1.00  4.04
ATOM   508  N   HIS 1 588     -9.290  14.422 -16.155  1.00  3.17
ATOM   509  CA  HIS 1 588    -10.079  13.664 -17.076  1.00  3.17
ATOM   510  C   HIS 1 588    -10.007  12.242 -16.633  1.00  3.17
ATOM   511  O   HIS 1 588     -9.091  11.842 -15.917  1.00  3.17
ATOM   512  CB  HIS 1 588     -9.598  13.754 -18.533  1.00  3.17
ATOM   513  CG  HIS 1 588     -9.688  15.146 -19.088  1.00  3.17
ATOM   514  ND1 HIS 1 588     -8.713  16.103 -18.921  1.00  3.17
ATOM   515  CD2 HIS 1 588    -10.655  15.730 -19.848  1.00  3.17
ATOM   516  CE1 HIS 1 588     -9.134  17.211 -19.581  1.00  3.17
ATOM   517  NE2 HIS 1 588    -10.309  17.033 -20.159  1.00  3.17
ATOM   518  N   LEU 1 589    -10.986  11.432 -17.066  1.00  6.31
ATOM   519  CA  LEU 1 589    -11.066  10.071 -16.633  1.00  6.31
ATOM   520  C   LEU 1 589     -9.832   9.331 -17.025  1.00  6.31
ATOM   521  O   LEU 1 589     -9.335   8.501 -16.267  1.00  6.31
ATOM   522  CB  LEU 1 589    -12.264   9.322 -17.240  1.00  6.31
ATOM   523  CG  LEU 1 589    -12.366   7.856 -16.779  1.00  6.31
ATOM   524  CD1 LEU 1 589    -12.605   7.759 -15.265  1.00  6.31
ATOM   525  CD2 LEU 1 589    -13.414   7.086 -17.599  1.00  6.31
ATOM   526  N   ASP 1 590     -9.298   9.614 -18.224  1.00  4.07
ATOM   527  CA  ASP 1 590     -8.153   8.874 -18.669  1.00  4.07
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ATOM 528 C ASP 1 590 -6.992 9.057 -17.744 1.00 4.07
ATOM 529 O ASP 1 590 -6.344 8.084 -17.365 1.00 4.07
ATOM 530 CB ASP 1 590 -7.704 9.236 -20.099 1.00 4.07
ATOM 531 CG ASP 1 590 -7.307 10.703 -20.151 1.00 4.07
ATOM 532 OD1 ASP 1 590 -7.873 11.496 -19.353 1.00 4.07
ATOM 533 OD2 ASP 1 590 -6.436 11.053 -20.992 1.00 4.07
ATOM 534 N ASP 1 591 -6.691 10.304 -17.343 1.00 5.67
ATOM 535 CA ASP 1 591 -5.581 10.496 -16.462 1.00 5.67
ATOM 536 C ASP 1 591 -5.860 9.994 -15.078 1.00 5.67
ATOM 537 O ASP 1 591 -4.955 9.560 -14.366 1.00 5.67
ATOM 538 CB ASP 1 591 -4.982 11.914 -16.507 1.00 5.67
ATOM 539 CG ASP 1 591 -6.017 12.981 -16.269 1.00 5.67
ATOM 540 OD1 ASP 1 591 -5.748 13.867 -15.419 1.00 5.67
ATOM 541 OD2 ASP 1 591 -7.067 12.957 -16.959 1.00 5.67
ATOM 542 N GLN 1 592 -7.139 10.019 -14.668 1.00 3.91
ATOM 543 CA GLN 1 592 -7.529 9.540 -13.376 1.00 3.91
ATOM 544 C GLN 1 592 -7.134 8.098 -13.282 1.00 3.91
ATOM 545 O GLN 1 592 -6.576 7.658 -12.277 1.00 3.91
ATOM 546 CB GLN 1 592 -9.055 9.639 -13.213 1.00 3.91
ATOM 547 CG GLN 1 592 -9.601 9.161 -11.873 1.00 3.91
ATOM 548 CD GLN 1 592 -11.113 9.338 -11.900 1.00 3.91
ATOM 549 OE1 GLN 1 592 -11.867 8.413 -11.598 1.00 3.91
ATOM 550 NE2 GLN 1 592 -11.574 10.564 -12.269 1.00 3.91
ATOM 551 N MET 1 593 -7.404 7.323 -14.351 1.00 7.01
ATOM 552 CA MET 1 593 -7.112 5.919 -14.356 1.00 7.01
ATOM 553 C MET 1 593 -5.636 5.669 -14.286 1.00 7.01
ATOM 554 O MET 1 593 -5.177 4.839 -13.503 1.00 7.01
ATOM 555 CB MET 1 593 -7.648 5.216 -15.618 1.00 7.01
ATOM 556 CG MET 1 593 -7.623 3.686 -15.552 1.00 7.01
ATOM 557 SD MET 1 593 -5.971 2.929 -15.626 1.00 7.01
ATOM 558 CE MET 1 593 -6.578 1.220 -15.511 1.00 7.01
ATOM 559 N THR 1 594 -4.845 6.403 -15.092 1.00 0.78
ATOM 560 CA THR 1 594 -3.429 6.170 -15.146 1.00 0.78
ATOM 561 C THR 1 594 -2.828 6.465 -13.814 1.00 0.78
ATOM 562 O THR 1 594 -1.933 5.772 -13.335 1.00 0.78
ATOM 563 CB THR 1 594 -2.739 7.045 -16.151 1.00 0.78
ATOM 564 OG1 THR 1 594 -3.268 6.813 -17.448 1.00 0.78
ATOM 565 CG2 THR 1 594 -1.234 6.727 -16.129 1.00 0.78
ATOM 566 N LEU 1 595 -3.332 7.530 -13.187 1.00 6.73
ATOM 567 CA LEU 1 595 -2.861 8.039 -11.943 1.00 6.73
ATOM 568 C LEU 1 595 -3.069 7.019 -10.875 1.00 6.73
ATOM 569 O LEU 1 595 -2.176 6.702 -10.090 1.00 6.73
ATOM 570 CB LEU 1 595 -3.723 9.246 -11.624 1.00 6.73
ATOM 571 CG LEU 1 595 -3.056 10.184 -10.664 1.00 6.73
ATOM 572 CD1 LEU 1 595 -1.680 10.521 -11.250 1.00 6.73
ATOM 573 CD2 LEU 1 595 -3.970 11.395 -10.435 1.00 6.73
ATOM 574 N LEU 1 596 -4.286 6.462 -10.859 1.00 6.22
ATOM 575 CA LEU 1 596 -4.726 5.531 -9.876 1.00 6.22
ATOM 576 C LEU 1 596 -3.874 4.315 -10.036 1.00 6.22
ATOM 577 O LEU 1 596 -3.404 3.721 -9.067 1.00 6.22
ATOM 578 CB LEU 1 596 -6.201 5.209 -10.157 1.00 6.22
ATOM 579 CG LEU 1 596 -6.995 4.659 -8.972 1.00 6.22
ATOM 580 CD1 LEU 1 596 -7.054 5.683 -7.827 1.00 6.22
ATOM 581 CD2 LEU 1 596 -8.393 4.211 -9.414 1.00 6.22
ATOM 582 N GLN 1 597 -3.624 3.936 -11.296 1.00 3.34
ATOM 583 CA GLN 1 597 -2.857 2.764 -11.591 1.00 3.34
ATOM 584 C GLN 1 597 -1.445 2.904 -11.116 1.00 3.34
ATOM 585 O GLN 1 597 -0.871 1.959 -10.580 1.00 3.34
ATOM 586 CB GLN 1 597 -2.806 2.471 -13.097 1.00 3.34
ATOM 587 CG GLN 1 597 -1.995 1.225 -13.456 1.00 3.34
ATOM 588 CD GLN 1 597 -2.036 1.069 -14.968 1.00 3.34

ATOM 589 OE1 GLN 1 597 -3.114 1.065 -15.570 1.00 3.34
ATOM 590 NE2 GLN 1 597 -0.844 0.946 -15.606 1.00 3.34
ATOM 591 N TYR 1 598 -0.840 4.086 -11.323 1.00 7.16
ATOM 592 CA TYR 1 598 0.539 4.275 -10.976 1.00 7.16
ATOM 593 C TYR 1 598 0.810 4.257 -9.501 1.00 7.16
ATOM 594 O TYR 1 598 1.769 3.635 -9.051 1.00 7.16
ATOM 595 CB TYR 1 598 1.093 5.591 -11.532 1.00 7.16
ATOM 596 CG TYR 1 598 2.525 5.717 -11.138 1.00 7.16
ATOM 597 CD1 TYR 1 598 3.517 5.120 -11.883 1.00 7.16
ATOM 598 CD2 TYR 1 598 2.881 6.510 -10.073 1.00 7.16
ATOM 599 CE1 TYR 1 598 4.842 5.306 -11.566 1.00 7.16
ATOM 600 CE2 TYR 1 598 4.205 6.712 -9.763 1.00 7.16
ATOM 601 CZ TYR 1 598 5.188 6.108 -10.506 1.00 7.16
ATOM 602 OH TYR 1 598 6.547 6.317 -10.185 1.00 7.16
ATOM 603 N SER 1 599 -0.013 4.975 -8.716 1.00 4.48
ATOM 604 CA SER 1 599 0.146 5.134 -7.293 1.00 4.48
ATOM 605 C SER 1 599 -0.364 3.986 -6.474 1.00 4.48
ATOM 606 O SER 1 599 -0.056 3.853 -5.291 1.00 4.48
ATOM 607 CB SER 1 599 -0.501 6.433 -6.784 1.00 4.48
ATOM 608 OG SER 1 599 0.029 6.770 -5.511 1.00 4.48
ATOM 609 N TRP 1 600 -1.166 3.123 -7.103 1.00 2.83
ATOM 610 CA TRP 1 600 -1.945 2.101 -6.479 1.00 2.83
ATOM 611 C TRP 1 600 -1.188 1.302 -5.467 1.00 2.83
ATOM 612 O TRP 1 600 -1.561 1.258 -4.294 1.00 2.83
ATOM 613 CB TRP 1 600 -2.341 1.109 -7.565 1.00 2.83
ATOM 614 CG TRP 1 600 -3.591 0.441 -7.181 1.00 2.83
ATOM 615 CD1 TRP 1 600 -3.942 -0.815 -6.793 1.00 2.83
ATOM 616 CD2 TRP 1 600 -4.693 1.293 -6.907 1.00 2.83
ATOM 617 NE1 TRP 1 600 -5.257 -0.809 -6.409 1.00 2.83
ATOM 618 CE2 TRP 1 600 -5.718 0.492 -6.479 1.00 2.83
ATOM 619 CE3 TRP 1 600 -4.818 2.647 -6.992 1.00 2.83
ATOM 620 CZ2 TRP 1 600 -6.916 1.047 -6.205 1.00 2.83
ATOM 621 CZ3 TRP 1 600 -6.018 3.201 -6.627 1.00 2.83
ATOM 622 CH2 TRP 1 600 -7.081 2.405 -6.290 1.00 2.83
ATOM 623 N MET 1 601 -0.100 0.641 -5.888 1.00 4.56
ATOM 624 CA MET 1 601 0.614 -0.167 -4.950 1.00 4.56
ATOM 625 C MET 1 601 1.324 0.717 -3.974 1.00 4.56
ATOM 626 O MET 1 601 1.564 0.322 -2.836 1.00 4.56
ATOM 627 CB MET 1 601 1.602 -1.163 -5.582 1.00 4.56
ATOM 628 CG MET 1 601 3.025 -0.654 -5.783 1.00 4.56
ATOM 629 SD MET 1 601 4.060 -0.617 -4.285 1.00 4.56
ATOM 630 CE MET 1 601 4.167 -2.419 -4.091 1.00 4.56
ATOM 631 N PHE 1 602 1.706 1.937 -4.408 1.00 6.98
ATOM 632 CA PHE 1 602 2.410 2.844 -3.542 1.00 6.98
ATOM 633 C PHE 1 602 1.582 3.074 -2.317 1.00 6.98
ATOM 634 O PHE 1 602 2.086 2.981 -1.200 1.00 6.98
ATOM 635 CB PHE 1 602 2.534 4.278 -4.096 1.00 6.98
ATOM 636 CG PHE 1 602 3.498 4.431 -5.217 1.00 6.98
ATOM 637 CD1 PHE 1 602 3.158 4.051 -6.495 1.00 6.98
ATOM 638 CD2 PHE 1 602 4.567 5.281 -5.046 1.00 6.98
ATOM 639 CE1 PHE 1 602 3.924 4.447 -7.564 1.00 6.98
ATOM 640 CE2 PHE 1 602 5.340 5.673 -6.109 1.00 6.98
ATOM 641 CZ PHE 1 602 5.042 5.221 -7.369 1.00 6.98
ATOM 642 N LEU 1 603 0.286 3.407 -2.501 1.00 3.79
ATOM 643 CA LEU 1 603 -0.551 3.686 -1.365 1.00 3.79
ATOM 644 C LEU 1 603 -0.740 2.459 -0.541 1.00 3.79
ATOM 645 O LEU 1 603 -0.676 2.509 0.685 1.00 3.79
ATOM 646 CB LEU 1 603 -1.995 4.128 -1.677 1.00 3.79
ATOM 647 CG LEU 1 603 -2.165 5.496 -2.352 1.00 3.79
ATOM 648 CD1 LEU 1 603 -1.536 6.626 -1.521 1.00 3.79
ATOM 649 CD2 LEU 1 603 -1.720 5.453 -3.813 1.00 3.79

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ATOM    650  N   MET 1 604     -0.978   1.317  -1.209  1.00  5.17
ATOM    651  CA  MET 1 604     -1.284   0.101  -0.519  1.00  5.17
ATOM    652  C   MET 1 604     -0.137  -0.248   0.370  1.00  5.17
ATOM    653  O   MET 1 604     -0.322  -0.589   1.537  1.00  5.17
ATOM    654  CB  MET 1 604     -1.430  -1.091  -1.479  1.00  5.17
ATOM    655  CG  MET 1 604     -2.428  -0.856  -2.612  1.00  5.17
ATOM    656  SD  MET 1 604     -4.150  -0.604  -2.106  1.00  5.17
ATOM    657  CE  MET 1 604     -4.639  -0.119  -3.784  1.00  5.17
ATOM    658  N   ALA 1 605      1.090  -0.153  -0.170  1.00  0.70
ATOM    659  CA  ALA 1 605      2.263  -0.519   0.565  1.00  0.70
ATOM    660  C   ALA 1 605      2.414   0.368   1.754  1.00  0.70
ATOM    661  O   ALA 1 605      2.793  -0.090   2.830  1.00  0.70
ATOM    662  CB  ALA 1 605      3.551  -0.397  -0.268  1.00  0.70
ATOM    663  N   PHE 1 606      2.133   1.673   1.590  1.00  4.22
ATOM    664  CA  PHE 1 606      2.309   2.548   2.707  1.00  4.22
ATOM    665  C   PHE 1 606      1.317   2.211   3.776  1.00  4.22
ATOM    666  O   PHE 1 606      1.648   2.206   4.960  1.00  4.22
ATOM    667  CB  PHE 1 606      2.157   4.042   2.396  1.00  4.22
ATOM    668  CG  PHE 1 606      2.785   4.728   3.563  1.00  4.22
ATOM    669  CD1 PHE 1 606      2.099   4.905   4.743  1.00  4.22
ATOM    670  CD2 PHE 1 606      4.109   5.095   3.513  1.00  4.22
ATOM    671  CE1 PHE 1 606      2.706   5.477   5.835  1.00  4.22
ATOM    672  CE2 PHE 1 606      4.725   5.668   4.600  1.00  4.22
ATOM    673  CZ  PHE 1 606      4.022   5.863   5.765  1.00  4.22
ATOM    674  N   ALA 1 607      0.069   1.893   3.381  1.00  0.92
ATOM    675  CA  ALA 1 607     -0.960   1.605   4.338  1.00  0.92
ATOM    676  C   ALA 1 607     -0.537   0.427   5.153  1.00  0.92
ATOM    677  O   ALA 1 607     -0.765   0.376   6.361  1.00  0.92
ATOM    678  CB  ALA 1 607     -2.302   1.253   3.676  1.00  0.92
ATOM    679  N   LEU 1 608      0.067  -0.568   4.487  1.00  4.26
ATOM    680  CA  LEU 1 608      0.559  -1.747   5.129  1.00  4.26
ATOM    681  C   LEU 1 608      1.704  -1.393   6.034  1.00  4.26
ATOM    682  O   LEU 1 608      1.779  -1.876   7.161  1.00  4.26
ATOM    683  CB  LEU 1 608      1.010  -2.780   4.068  1.00  4.26
ATOM    684  CG  LEU 1 608      1.578  -4.119   4.573  1.00  4.26
ATOM    685  CD1 LEU 1 608      1.752  -5.104   3.410  1.00  4.26
ATOM    686  CD2 LEU 1 608      2.921  -3.927   5.286  1.00  4.26
ATOM    687  N   GLY 1 609      2.631  -0.542   5.551  1.00  0.62
ATOM    688  CA  GLY 1 609      3.824  -0.209   6.281  1.00  0.62
ATOM    689  C   GLY 1 609      3.521   0.478   7.577  1.00  0.62
ATOM    690  O   GLY 1 609      4.164   0.210   8.589  1.00  0.62
ATOM    691  N   TRP 1 610      2.542   1.395   7.598  1.00  3.39
ATOM    692  CA  TRP 1 610      2.246   2.087   8.821  1.00  3.39
ATOM    693  C   TRP 1 610      1.768   1.108   9.843  1.00  3.39
ATOM    694  O   TRP 1 610      1.936   1.305  11.045  1.00  3.39
ATOM    695  CB  TRP 1 610      1.172   3.178   8.672  1.00  3.39
ATOM    696  CG  TRP 1 610      0.730   3.769   9.990  1.00  3.39
ATOM    697  CD1 TRP 1 610     -0.435   3.565  10.671  1.00  3.39
ATOM    698  CD2 TRP 1 610      1.575   4.541  10.858  1.00  3.39
ATOM    699  NE1 TRP 1 610     -0.391   4.210  11.884  1.00  3.39
ATOM    700  CE2 TRP 1 610      0.846   4.805  12.018  1.00  3.39
ATOM    701  CE3 TRP 1 610      2.860   4.981  10.709  1.00  3.39
ATOM    702  CZ2 TRP 1 610      1.388   5.525  13.044  1.00  3.39
ATOM    703  CZ3 TRP 1 610      3.408   5.692  11.754  1.00  3.39
ATOM    704  CH2 TRP 1 610      2.684   5.966  12.895  1.00  3.39
ATOM    705  N   ARG 1 611      1.110   0.045   9.366  1.00  4.02
ATOM    706  CA  ARG 1 611      0.550  -1.005  10.161  1.00  4.02
ATOM    707  C   ARG 1 611      1.493  -2.017  10.738  1.00  4.02
ATOM    708  O   ARG 1 611      1.046  -2.871  11.500  1.00  4.02
ATOM    709  CB  ARG 1 611     -0.632  -1.729   9.497  1.00  4.02
ATOM    710  CG  ARG 1 611     -1.429  -0.764   8.613  1.00  4.02
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ATOM   711  CD  ARG 1 611     -2.571  -1.408   7.827  1.00  4.02
ATOM   712  NE  ARG 1 611     -1.971  -2.364   6.856  1.00  4.02
ATOM   713  CZ  ARG 1 611     -2.100  -2.115   5.520  1.00  4.02
ATOM   714  NH1 ARG 1 611     -2.768  -1.002   5.099  1.00  4.02
ATOM   715  NH2 ARG 1 611     -1.570  -2.977   4.605  1.00  4.02
ATOM   716  N   SER 1 612      2.787  -2.048  10.363  1.00  4.05
ATOM   717  CA  SER 1 612      3.539  -3.105  10.979  1.00  4.05
ATOM   718  C   SER 1 612      3.668  -2.931  12.454  1.00  4.05
ATOM   719  O   SER 1 612      3.685  -1.817  12.976  1.00  4.05
ATOM   720  CB  SER 1 612      4.919  -3.410  10.387  1.00  4.05
ATOM   721  OG  SER 1 612      5.539  -4.473  11.094  1.00  4.05
ATOM   722  N   TYR 1 613      3.743  -4.074  13.163  1.00  4.51
ATOM   723  CA  TYR 1 613      3.792  -4.072  14.594  1.00  4.51
ATOM   724  C   TYR 1 613      5.133  -4.616  14.963  1.00  4.51
ATOM   725  O   TYR 1 613      5.519  -5.697  14.522  1.00  4.51
ATOM   726  CB  TYR 1 613      2.716  -4.995  15.193  1.00  4.51
ATOM   727  CG  TYR 1 613      2.510  -4.676  16.633  1.00  4.51
ATOM   728  CD1 TYR 1 613      3.337  -5.181  17.606  1.00  4.51
ATOM   729  CD2 TYR 1 613      1.402  -3.951  17.009  1.00  4.51
ATOM   730  CE1 TYR 1 613      3.064  -4.947  18.934  1.00  4.51
ATOM   731  CE2 TYR 1 613      1.125  -3.716  18.335  1.00  4.51
ATOM   732  CZ  TYR 1 613      1.959  -4.221  19.302  1.00  4.51
ATOM   733  OH  TYR 1 613      1.675  -4.003  20.667  1.00  4.51
ATOM   734  N   ARG 1 614      5.891  -3.866  15.783  1.00  6.30
ATOM   735  CA  ARG 1 614      7.211  -4.286  16.147  1.00  6.30
ATOM   736  C   ARG 1 614      7.154  -5.564  16.919  1.00  6.30
ATOM   737  O   ARG 1 614      7.863  -6.520  16.608  1.00  6.30
ATOM   738  CB  ARG 1 614      7.917  -3.260  17.047  1.00  6.30
ATOM   739  CG  ARG 1 614      8.166  -1.916  16.361  1.00  6.30
ATOM   740  CD  ARG 1 614      6.880  -1.217  15.918  1.00  6.30
ATOM   741  NE  ARG 1 614      6.009  -1.054  17.116  1.00  6.30
ATOM   742  CZ  ARG 1 614      4.734  -0.591  16.966  1.00  6.30
ATOM   743  NH1 ARG 1 614      4.264  -0.277  15.724  1.00  6.30
ATOM   744  NH2 ARG 1 614      3.928  -0.444  18.057  1.00  6.30
ATOM   745  N   GLN 1 615      6.284  -5.619  17.943  1.00  3.13
ATOM   746  CA  GLN 1 615      6.219  -6.789  18.769  1.00  3.13
ATOM   747  C   GLN 1 615      5.740  -7.940  17.956  1.00  3.13
ATOM   748  O   GLN 1 615      6.283  -9.042  18.030  1.00  3.13
ATOM   749  CB  GLN 1 615      5.251  -6.635  19.952  1.00  3.13
ATOM   750  CG  GLN 1 615      5.665  -5.548  20.943  1.00  3.13
ATOM   751  CD  GLN 1 615      6.925  -6.023  21.650  1.00  3.13
ATOM   752  OE1 GLN 1 615      7.457  -7.089  21.342  1.00  3.13
ATOM   753  NE2 GLN 1 615      7.419  -5.214  22.625  1.00  3.13
ATOM   754  N   SER 1 616      4.708  -7.696  17.134  1.00  4.46
ATOM   755  CA  SER 1 616      4.133  -8.738  16.345  1.00  4.46
ATOM   756  C   SER 1 616      5.206  -9.213  15.424  1.00  4.46
ATOM   757  O   SER 1 616      5.342 -10.416  15.200  1.00  4.46
ATOM   758  CB  SER 1 616      2.943  -8.225  15.520  1.00  4.46
ATOM   759  OG  SER 1 616      2.192  -9.316  15.016  1.00  4.46
ATOM   760  N   SER 1 617      5.978  -8.253  14.871  1.00  6.06
ATOM   761  CA  SER 1 617      7.119  -8.454  14.019  1.00  6.06
ATOM   762  C   SER 1 617      7.082  -7.438  12.943  1.00  6.06
ATOM   763  O   SER 1 617      6.016  -7.070  12.454  1.00  6.06
ATOM   764  CB  SER 1 617      7.235  -9.826  13.321  1.00  6.06
ATOM   765  OG  SER 1 617      7.691 -10.813  14.235  1.00  6.06
ATOM   766  N   ALA 1 618      8.272  -6.952  12.548  1.00  1.34
ATOM   767  CA  ALA 1 618      8.328  -6.034  11.458  1.00  1.34
ATOM   768  C   ALA 1 618      7.780  -6.872  10.363  1.00  1.34
ATOM   769  O   ALA 1 618      7.040  -6.399   9.503  1.00  1.34
ATOM   770  CB  ALA 1 618      9.763  -5.633  11.080  1.00  1.34
ATOM   771  N   ASN 1 619      8.117  -8.172  10.420  1.00  2.27
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ATOM   772  CA  ASN 1 619      7.655  -9.121   9.458  1.00  2.27
ATOM   773  C   ASN 1 619      6.170  -9.004   9.485  1.00  2.27
ATOM   774  O   ASN 1 619      5.521  -8.973   8.442  1.00  2.27
ATOM   775  CB  ASN 1 619      7.978 -10.575   9.852  1.00  2.27
ATOM   776  CG  ASN 1 619      9.489 -10.762   9.929  1.00  2.27
ATOM   777  OD1 ASN 1 619      8.505 -11.245  10.491  1.00  2.27
ATOM   778  ND2 ASN 1 619      9.749  -9.835   8.973  1.00  2.27
ATOM   779  N   LEU 1 620      5.590  -8.915  10.698  1.00  1.42
ATOM   780  CA  LEU 1 620      4.167  -8.832  10.788  1.00  1.42
ATOM   781  C   LEU 1 620      3.676  -7.466  10.447  1.00  1.42
ATOM   782  O   LEU 1 620      3.870  -6.484  11.166  1.00  1.42
ATOM   783  CB  LEU 1 620      3.611  -9.328  12.134  1.00  1.42
ATOM   784  CG  LEU 1 620      3.876 -10.842  12.293  1.00  1.42
ATOM   785  CD1 LEU 1 620      3.339 -11.415  13.612  1.00  1.42
ATOM   786  CD2 LEU 1 620      3.363 -11.618  11.071  1.00  1.42
ATOM   787  N   LEU 1 621      3.019  -7.413   9.278  1.00  1.28
ATOM   788  CA  LEU 1 621      2.463  -6.252   8.661  1.00  1.28
ATOM   789  C   LEU 1 621      1.007  -6.575   8.629  1.00  1.28
ATOM   790  O   LEU 1 621      0.629  -7.744   8.704  1.00  1.28
ATOM   791  CB  LEU 1 621      2.927  -6.155   7.203  1.00  1.28
ATOM   792  CG  LEU 1 621      4.463  -6.148   7.063  1.00  1.28
ATOM   793  CD1 LEU 1 621      4.910  -6.052   5.593  1.00  1.28
ATOM   794  CD2 LEU 1 621      5.093  -5.062   7.948  1.00  1.28
ATOM   795  N   CYS 1 622      0.131  -5.561   8.548  1.00  1.26
ATOM   796  CA  CYS 1 622     -1.253  -5.921   8.517  1.00  1.26
ATOM   797  C   CYS 1 622     -1.831  -5.468   7.213  1.00  1.26
ATOM   798  O   CYS 1 622     -1.836  -4.277   6.907  1.00  1.26
ATOM   799  CB  CYS 1 622     -2.053  -5.269   9.652  1.00  1.26
ATOM   800  SG  CYS 1 622     -3.717  -5.966   9.791  1.00  1.26
ATOM   801  N   PHE 1 623     -2.346  -6.415   6.402  1.00  4.97
ATOM   802  CA  PHE 1 623     -2.922  -6.047   5.139  1.00  4.97
ATOM   803  C   PHE 1 623     -4.365  -5.819   5.378  1.00  4.97
ATOM   804  O   PHE 1 623     -4.995  -6.711   5.951  1.00  4.97
ATOM   805  CB  PHE 1 623     -2.879  -7.140   4.054  1.00  4.97
ATOM   806  CG  PHE 1 623     -1.505  -7.278   3.496  1.00  4.97
ATOM   807  CD1 PHE 1 623     -0.586  -8.126   4.069  1.00  4.97
ATOM   808  CD2 PHE 1 623     -1.182  -6.645   2.317  1.00  4.97
ATOM   809  CE1 PHE 1 623      0.634  -8.337   3.468  1.00  4.97
ATOM   810  CE2 PHE 1 623      0.040  -6.846   1.721  1.00  4.97
ATOM   811  CZ  PHE 1 623      0.946  -7.707   2.290  1.00  4.97
ATOM   812  N   ALA 1 624     -4.872  -4.641   4.901  1.00  5.16
ATOM   813  CA  ALA 1 624     -6.224  -4.152   5.033  1.00  5.16
ATOM   814  C   ALA 1 624     -6.657  -4.675   6.332  1.00  5.16
ATOM   815  O   ALA 1 624     -7.324  -5.698   6.295  1.00  5.16
ATOM   816  CB  ALA 1 624     -7.182  -4.694   3.959  1.00  5.16
ATOM   817  N   PRO 1 625     -6.437  -3.914   7.376  1.00  4.05
ATOM   818  CA  PRO 1 625     -6.315  -4.317   8.776  1.00  4.05
ATOM   819  C   PRO 1 625     -6.730  -5.645   9.373  1.00  4.05
ATOM   820  O   PRO 1 625     -6.476  -5.826  10.559  1.00  4.05
ATOM   821  CB  PRO 1 625     -6.868  -3.160   9.606  1.00  4.05
ATOM   822  CG  PRO 1 625     -7.701  -2.347   8.614  1.00  4.05
ATOM   823  CD  PRO 1 625     -7.007  -2.584   7.272  1.00  4.05
ATOM   824  N   ASP 1 626     -7.415  -6.545   8.659  1.00  3.31
ATOM   825  CA  ASP 1 626     -7.765  -7.863   9.076  1.00  3.31
ATOM   826  C   ASP 1 626     -6.607  -8.827   9.191  1.00  3.31
ATOM   827  O   ASP 1 626     -6.482  -9.506  10.208  1.00  3.31
ATOM   828  CB  ASP 1 626     -8.752  -8.509   8.092  1.00  3.31
ATOM   829  CG  ASP 1 626    -10.028  -7.681   8.097  1.00  3.31
ATOM   830  OD1 ASP 1 626    -10.848  -7.855   7.156  1.00  3.31
ATOM   831  OD2 ASP 1 626    -10.199  -6.858   9.037  1.00  3.31
ATOM   832  N   LEU 1 627     -5.704  -8.921   8.184  1.00  5.46
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ATOM   833  CA  LEU 1 627     -4.737  -9.984   8.288  1.00  5.46
ATOM   834  C   LEU 1 627     -3.336  -9.532   8.542  1.00  5.46
ATOM   835  O   LEU 1 627     -2.848  -8.558   7.972  1.00  5.46
ATOM   836  CB  LEU 1 627     -4.741 -10.955   7.086  1.00  5.46
ATOM   837  CG  LEU 1 627     -4.364 -10.353   5.716  1.00  5.46
ATOM   838  CD1 LEU 1 627     -2.877  -9.976   5.633  1.00  5.46
ATOM   839  CD2 LEU 1 627     -4.785 -11.295   4.576  1.00  5.46
ATOM   840  N   ILE 1 628     -2.646 -10.255   9.447  1.00  3.87
ATOM   841  CA  ILE 1 628     -1.294  -9.909   9.743  1.00  3.87
ATOM   842  C   ILE 1 628     -0.443 -10.972   9.139  1.00  3.87
ATOM   843  O   ILE 1 628     -0.757 -12.158   9.228  1.00  3.87
ATOM   844  CB  ILE 1 628     -0.993  -9.828  11.209  1.00  3.87
ATOM   845  CG1 ILE 1 628      0.352  -9.122  11.429  1.00  3.87
ATOM   846  CG2 ILE 1 628     -1.070 -11.245  11.799  1.00  3.87
ATOM   847  CD1 ILE 1 628      0.558  -8.654  12.866  1.00  3.87
ATOM   848  N   ILE 1 629      0.654 -10.561   8.479  1.00  7.73
ATOM   849  CA  ILE 1 629      1.481 -11.529   7.822  1.00  7.73
ATOM   850  C   ILE 1 629      2.901 -11.255   8.179  1.00  7.73
ATOM   851  O   ILE 1 629      3.262 -10.131   8.521  1.00  7.73
ATOM   852  CB  ILE 1 629      1.408 -11.466   6.322  1.00  7.73
ATOM   853  CG1 ILE 1 629      1.985 -10.137   5.798  1.00  7.73
ATOM   854  CG2 ILE 1 629     -0.054 -11.708   5.914  1.00  7.73
ATOM   855  CD1 ILE 1 629      1.253  -8.890   6.291  1.00  7.73
ATOM   856  N   ASN 1 630      3.742 -12.304   8.121  1.00  3.80
ATOM   857  CA  ASN 1 630      5.137 -12.184   8.419  1.00  3.80
ATOM   858  C   ASN 1 630      5.869 -11.907   7.147  1.00  3.80
ATOM   859  O   ASN 1 630      5.289 -11.908   6.062  1.00  3.80
ATOM   860  CB  ASN 1 630      5.738 -13.461   9.031  1.00  3.80
ATOM   861  CG  ASN 1 630      5.595 -14.578   8.007  1.00  3.80
ATOM   862  OD1 ASN 1 630      4.673 -14.573   7.192  1.00  3.80
ATOM   863  ND2 ASN 1 630      6.526 -15.567   8.050  1.00  3.80
ATOM   864  N   GLU 1 631      7.187 -11.662   7.263  1.00  3.57
ATOM   865  CA  GLU 1 631      7.988 -11.375   6.109  1.00  3.57
ATOM   866  C   GLU 1 631      7.926 -12.536   5.169  1.00  3.57
ATOM   867  O   GLU 1 631      7.764 -12.366   3.961  1.00  3.57
ATOM   868  CB  GLU 1 631      9.475 -11.173   6.450  1.00  3.57
ATOM   869  CG  GLU 1 631     10.345 -10.866   5.228  1.00  3.57
ATOM   870  CD  GLU 1 631     11.786 -10.712   5.696  1.00  3.57
ATOM   871  OE1 GLU 1 631     12.099  -9.663   6.319  1.00  3.57
ATOM   872  OE2 GLU 1 631     12.594 -11.644   5.436  1.00  3.57
ATOM   873  N   GLN 1 632      8.037 -13.761   5.707  1.00  5.74
ATOM   874  CA  GLN 1 632      8.056 -14.926   4.874  1.00  5.74
ATOM   875  C   GLN 1 632      6.771 -15.100   4.112  1.00  5.74
ATOM   876  O   GLN 1 632      6.799 -15.379   2.915  1.00  5.74
ATOM   877  CB  GLN 1 632      8.307 -16.215   5.684  1.00  5.74
ATOM   878  CG  GLN 1 632      8.337 -17.501   4.853  1.00  5.74
ATOM   879  CD  GLN 1 632      6.906 -17.987   4.659  1.00  5.74
ATOM   880  OE1 GLN 1 632      6.206 -18.306   5.619  1.00  5.74
ATOM   881  NE2 GLN 1 632      6.451 -18.027   3.378  1.00  5.74
ATOM   882  N   ARG 1 633      5.604 -14.942   4.770  1.00  6.29
ATOM   883  CA  ARG 1 633      4.389 -15.210   4.043  1.00  6.29
ATOM   884  C   ARG 1 633      4.211 -14.188   2.992  1.00  6.29
ATOM   885  O   ARG 1 633      3.685 -14.524   1.937  1.00  6.29
ATOM   886  CB  ARG 1 633      3.055 -15.288   4.868  1.00  6.29
ATOM   887  CG  ARG 1 633      1.781 -15.671   4.039  1.00  6.29
ATOM   888  CD  ARG 1 633      0.503 -16.120   4.825  1.00  6.29
ATOM   889  NE  ARG 1 633     -0.537 -16.684   3.894  1.00  6.29
ATOM   890  CZ  ARG 1 633     -1.381 -17.769   3.971  1.00  6.29
ATOM   891  NH1 ARG 1 633     -1.669 -18.475   5.103  1.00  6.29
ATOM   892  NH2 ARG 1 633     -2.050 -18.131   2.839  1.00  6.29
ATOM   893  N   MET 1 634      4.592 -12.927   3.267  1.00  5.30
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ATOM 894 CA MET 1 634 4.490 -11.824 2.355 1.00 5.30
ATOM 895 C MET 1 634 5.504 -11.870 1.253 1.00 5.30
ATOM 896 O MET 1 634 5.243 -11.342 0.176 1.00 5.30
ATOM 897 CB MET 1 634 4.655 -10.467 3.043 1.00 5.30
ATOM 898 CG MET 1 634 6.088 -10.242 3.497 1.00 5.30
ATOM 899 SD MET 1 634 6.423 -8.596 4.165 1.00 5.30
ATOM 900 CE MET 1 634 8.197 -8.946 4.143 1.00 5.30
ATOM 901 N THR 1 635 6.704 -12.449 1.496 1.00 5.56
ATOM 902 CA THR 1 635 7.691 -12.574 0.448 1.00 5.56
ATOM 903 C THR 1 635 7.291 -13.593 -0.573 1.00 5.56
ATOM 904 O THR 1 635 7.247 -13.321 -1.770 1.00 5.56
ATOM 905 CB THR 1 635 9.057 -12.970 0.948 1.00 5.56
ATOM 906 OG1 THR 1 635 9.976 -13.019 -0.133 1.00 5.56
ATOM 907 CG2 THR 1 635 9.006 -14.304 1.693 1.00 5.56
ATOM 908 N LEU 1 636 6.921 -14.809 -0.133 1.00 4.24
ATOM 909 CA LEU 1 636 6.544 -15.813 -1.089 1.00 4.24
ATOM 910 C LEU 1 636 5.264 -15.595 -1.893 1.00 4.24
ATOM 911 O LEU 1 636 5.255 -16.010 -3.054 1.00 4.24
ATOM 912 CB LEU 1 636 6.419 -17.222 -0.478 1.00 4.24
ATOM 913 CG LEU 1 636 7.748 -17.820 0.028 1.00 4.24
ATOM 914 CD1 LEU 1 636 8.241 -17.113 1.295 1.00 4.24
ATOM 915 CD2 LEU 1 636 7.656 -19.343 0.208 1.00 4.24
ATOM 916 N PRO 1 637 4.186 -15.012 -1.382 1.00 3.86
ATOM 917 CA PRO 1 637 2.948 -14.924 -2.088 1.00 3.86
ATOM 918 C PRO 1 637 3.115 -14.366 -3.410 1.00 3.86
ATOM 919 O PRO 1 637 2.533 -14.923 -4.330 1.00 3.86
ATOM 920 CB PRO 1 637 2.043 -14.013 -1.293 1.00 3.86
ATOM 921 CG PRO 1 637 3.014 -12.991 -0.736 1.00 3.86
ATOM 922 CD PRO 1 637 4.304 -13.807 -0.651 1.00 3.86
ATOM 923 N CYS 1 638 3.829 -13.241 -3.498 1.00 3.09
ATOM 924 CA CYS 1 638 4.111 -12.683 -4.764 1.00 3.09
ATOM 925 C CYS 1 638 5.156 -11.654 -4.537 1.00 3.09
ATOM 926 O CYS 1 638 6.022 -11.460 -5.376 1.00 3.09
ATOM 927 CB CYS 1 638 2.939 -11.903 -5.397 1.00 3.09
ATOM 928 SG CYS 1 638 1.629 -12.922 -6.146 1.00 3.09
ATOM 929 N MET 1 639 5.197 -11.038 -3.350 1.00 6.02
ATOM 930 CA MET 1 639 6.036 -9.884 -3.188 1.00 6.02
ATOM 931 C MET 1 639 7.487 -10.110 -3.503 1.00 6.02
ATOM 932 O MET 1 639 8.080 -9.347 -4.263 1.00 6.02
ATOM 933 CB MET 1 639 5.971 -9.336 -1.753 1.00 6.02
ATOM 934 CG MET 1 639 4.557 -8.953 -1.308 1.00 6.02
ATOM 935 SD MET 1 639 3.806 -7.570 -2.217 1.00 6.02
ATOM 936 CE MET 1 639 2.242 -7.588 -1.297 1.00 6.02
ATOM 937 N TYR 1 640 8.110 -11.154 -2.931 1.00 5.37
ATOM 938 CA TYR 1 640 9.491 -11.430 -3.201 1.00 5.37
ATOM 939 C TYR 1 640 10.263 -10.413 -2.419 1.00 5.37
ATOM 940 O TYR 1 640 9.991 -10.188 -1.245 1.00 5.37
ATOM 941 CB TYR 1 640 9.826 -11.396 -4.717 1.00 5.37
ATOM 942 CG TYR 1 640 11.224 -11.840 -5.002 1.00 5.37
ATOM 943 CD1 TYR 1 640 12.204 -10.952 -5.390 1.00 5.37
ATOM 944 CD2 TYR 1 640 11.555 -13.171 -4.890 1.00 5.37
ATOM 945 CE1 TYR 1 640 13.483 -11.373 -5.655 1.00 5.37
ATOM 946 CE2 TYR 1 640 12.830 -13.603 -5.162 1.00 5.37
ATOM 947 CZ TYR 1 640 13.797 -12.705 -5.546 1.00 5.37
ATOM 948 OH TYR 1 640 15.105 -13.146 -5.831 1.00 5.37
ATOM 949 N ASP 1 641 11.239 -9.752 -3.053 1.00 4.19
ATOM 950 CA ASP 1 641 12.078 -8.786 -2.414 1.00 4.19
ATOM 951 C ASP 1 641 11.284 -7.584 -2.016 1.00 4.19
ATOM 952 O ASP 1 641 11.648 -6.875 -1.080 1.00 4.19
ATOM 953 CB ASP 1 641 13.244 -8.321 -3.306 1.00 4.19
ATOM 954 CG ASP 1 641 12.688 -7.658 -4.559 1.00 4.19

ATOM 955 OD1 ASP 1 641 11.502 -7.911 -4.902 1.00 4.19
ATOM 956 OD2 ASP 1 641 13.457 -6.891 -5.196 1.00 4.19
ATOM 957 N GLN 1 642 10.173 -7.320 -2.723 1.00 3.89
ATOM 958 CA GLN 1 642 9.398 -6.150 -2.438 1.00 3.89
ATOM 959 C GLN 1 642 8.913 -6.211 -1.024 1.00 3.89
ATOM 960 O GLN 1 642 8.788 -5.182 -0.361 1.00 3.89
ATOM 961 CB GLN 1 642 8.180 -5.965 -3.361 1.00 3.89
ATOM 962 CG GLN 1 642 7.354 -4.712 -3.086 1.00 3.89
ATOM 963 CD GLN 1 642 6.027 -4.871 -3.815 1.00 3.89
ATOM 964 OE1 GLN 1 642 5.823 -4.303 -4.883 1.00 3.89
ATOM 965 NE2 GLN 1 642 5.097 -5.669 -3.220 1.00 3.89
ATOM 966 N CYS 1 643 8.626 -7.425 -0.521 1.00 3.75
ATOM 967 CA CYS 1 643 8.132 -7.555 0.820 1.00 3.75
ATOM 968 C CYS 1 643 9.163 -7.043 1.775 1.00 3.75
ATOM 969 O CYS 1 643 8.832 -6.384 2.760 1.00 3.75
ATOM 970 CB CYS 1 643 7.811 -9.006 1.219 1.00 3.75
ATOM 971 SG CYS 1 643 9.300 -10.002 1.508 1.00 3.75
ATOM 972 N LYS 1 644 10.451 -7.320 1.500 1.00 8.40
ATOM 973 CA LYS 1 644 11.497 -6.922 2.387 1.00 8.40
ATOM 974 C LYS 1 644 11.477 -5.434 2.423 1.00 8.40
ATOM 975 O LYS 1 644 11.625 -4.826 3.481 1.00 8.40
ATOM 976 CB LYS 1 644 12.884 -7.374 1.899 1.00 8.40
ATOM 977 CG LYS 1 644 13.980 -7.257 2.959 1.00 8.40
ATOM 978 CD LYS 1 644 13.803 -8.232 4.126 1.00 8.40
ATOM 979 CE LYS 1 644 13.697 -9.696 3.689 1.00 8.40
ATOM 980 NZ LYS 1 644 15.006 -10.177 3.191 1.00 8.40
ATOM 981 N HIS 1 645 11.256 -4.811 1.251 1.00 2.06
ATOM 982 CA HIS 1 645 11.262 -3.382 1.157 1.00 2.06
ATOM 983 C HIS 1 645 10.183 -2.804 2.017 1.00 2.06
ATOM 984 O HIS 1 645 10.409 -1.832 2.734 1.00 2.06
ATOM 985 CB HIS 1 645 11.040 -2.882 -0.279 1.00 2.06
ATOM 986 CG HIS 1 645 11.300 -1.414 -0.432 1.00 2.06
ATOM 987 ND1 HIS 1 645 11.608 -0.808 -1.630 1.00 2.06
ATOM 988 CD2 HIS 1 645 11.279 -0.416 0.493 1.00 2.06
ATOM 989 CE1 HIS 1 645 11.762 0.515 -1.371 1.00 2.06
ATOM 990 NE2 HIS 1 645 11.572 0.801 -0.096 1.00 2.06
ATOM 991 N MET 1 646 8.976 -3.394 1.970 1.00 2.52
ATOM 992 CA MET 1 646 7.880 -2.894 2.749 1.00 2.52
ATOM 993 C MET 1 646 8.163 -3.056 4.213 1.00 2.52
ATOM 994 O MET 1 646 7.864 -2.167 5.008 1.00 2.52
ATOM 995 CB MET 1 646 6.557 -3.626 2.455 1.00 2.52
ATOM 996 CG MET 1 646 6.032 -3.396 1.036 1.00 2.52
ATOM 997 SD MET 1 646 4.470 -4.249 0.661 1.00 2.52
ATOM 998 CE MET 1 646 4.358 -3.638 -1.046 1.00 2.52
ATOM 999 N LEU 1 647 8.741 -4.200 4.623 1.00 1.01
ATOM 1000 CA LEU 1 647 8.998 -4.389 6.025 1.00 1.01
ATOM 1001 C LEU 1 647 9.958 -3.366 6.506 1.00 1.01
ATOM 1002 O LEU 1 647 9.743 -2.749 7.548 1.00 1.01
ATOM 1003 CB LEU 1 647 9.690 -5.708 6.383 1.00 1.01
ATOM 1004 CG LEU 1 647 8.838 -6.958 6.180 1.00 1.01
ATOM 1005 CD1 LEU 1 647 9.605 -8.211 6.620 1.00 1.01
ATOM 1006 CD2 LEU 1 647 7.461 -6.831 6.834 1.00 1.01
ATOM 1007 N TYR 1 648 11.063 -3.160 5.767 1.00 6.90
ATOM 1008 CA TYR 1 648 11.990 -2.202 6.272 1.00 6.90
ATOM 1009 C TYR 1 648 11.426 -0.823 6.265 1.00 6.90
ATOM 1010 O TYR 1 648 11.736 -0.029 7.153 1.00 6.90
ATOM 1011 CB TYR 1 648 13.429 -2.259 5.705 1.00 6.90
ATOM 1012 CG TYR 1 648 13.499 -2.469 4.232 1.00 6.90
ATOM 1013 CD1 TYR 1 648 13.274 -1.450 3.336 1.00 6.90
ATOM 1014 CD2 TYR 1 648 14.075 -3.633 3.776 1.00 6.90
ATOM 1015 CE1 TYR 1 648 13.566 -1.623 2.002 1.00 6.90

ATOM 1016 CE2 TYR 1 648 14.368 -3.814 2.447 1.00 6.90
ATOM 1017 CZ TYR 1 648 14.122 -2.800 1.556 1.00 6.90
ATOM 1018 OH TYR 1 648 14.436 -2.970 0.191 1.00 6.90
ATOM 1019 N VAL 1 649 10.571 -0.484 5.282 1.00 3.24
ATOM 1020 CA VAL 1 649 10.016 0.835 5.329 1.00 3.24
ATOM 1021 C VAL 1 649 9.185 0.944 6.569 1.00 3.24
ATOM 1022 O VAL 1 649 9.226 1.955 7.268 1.00 3.24
ATOM 1023 CB VAL 1 649 9.165 1.206 4.143 1.00 3.24
ATOM 1024 CG1 VAL 1 649 7.840 0.434 4.182 1.00 3.24
ATOM 1025 CG2 VAL 1 649 8.973 2.732 4.155 1.00 3.24
ATOM 1026 N SER 1 650 8.423 -0.116 6.895 1.00 3.01
ATOM 1027 CA SER 1 650 7.588 -0.062 8.057 1.00 3.01
ATOM 1028 C SER 1 650 8.382 0.080 9.315 1.00 3.01
ATOM 1029 O SER 1 650 7.972 0.789 10.232 1.00 3.01
ATOM 1030 CB SER 1 650 6.728 -1.292 8.289 1.00 3.01
ATOM 1031 OG SER 1 650 6.141 -1.100 9.562 1.00 3.01
ATOM 1032 N SER 1 651 9.529 -0.615 9.408 1.00 3.21
ATOM 1033 CA SER 1 651 10.305 -0.555 10.611 1.00 3.21
ATOM 1034 C SER 1 651 10.788 0.846 10.809 1.00 3.21
ATOM 1035 O SER 1 651 10.753 1.373 11.919 1.00 3.21
ATOM 1036 CB SER 1 651 11.543 -1.467 10.566 1.00 3.21
ATOM 1037 OG SER 1 651 12.442 -1.019 9.562 1.00 3.21
ATOM 1038 N GLU 1 652 11.247 1.482 9.715 1.00 3.30
ATOM 1039 CA GLU 1 652 11.786 2.811 9.744 1.00 3.30
ATOM 1040 C GLU 1 652 10.741 3.828 10.087 1.00 3.30
ATOM 1041 O GLU 1 652 11.018 4.810 10.772 1.00 3.30
ATOM 1042 CB GLU 1 652 12.417 3.215 8.399 1.00 3.30
ATOM 1043 CG GLU 1 652 13.164 4.548 8.446 1.00 3.30
ATOM 1044 CD GLU 1 652 13.852 4.745 7.102 1.00 3.30
ATOM 1045 OE1 GLU 1 652 14.492 3.772 6.620 1.00 3.30
ATOM 1046 OE2 GLU 1 652 13.746 5.866 6.538 1.00 3.30
ATOM 1047 N LEU 1 653 9.502 3.601 9.613 1.00 1.22
ATOM 1048 CA LEU 1 653 8.382 4.490 9.772 1.00 1.22
ATOM 1049 C LEU 1 653 7.999 4.675 11.205 1.00 1.22
ATOM 1050 O LEU 1 653 7.473 5.722 11.576 1.00 1.22
ATOM 1051 CB LEU 1 653 7.121 3.976 9.055 1.00 1.22
ATOM 1052 CG LEU 1 653 7.274 3.871 7.529 1.00 1.22
ATOM 1053 CD1 LEU 1 653 5.985 3.356 6.869 1.00 1.22
ATOM 1054 CD2 LEU 1 653 7.759 5.198 6.931 1.00 1.22
ATOM 1055 N HIS 1 654 8.239 3.664 12.056 1.00 0.94
ATOM 1056 CA HIS 1 654 7.780 3.733 13.412 1.00 0.94
ATOM 1057 C HIS 1 654 8.305 4.961 14.097 1.00 0.94
ATOM 1058 O HIS 1 654 7.566 5.632 14.816 1.00 0.94
ATOM 1059 CB HIS 1 654 8.210 2.509 14.238 1.00 0.94
ATOM 1060 CG HIS 1 654 7.684 1.227 13.664 1.00 0.94
ATOM 1061 ND1 HIS 1 654 6.369 0.824 13.747 1.00 0.94
ATOM 1062 CD2 HIS 1 654 8.323 0.263 12.946 1.00 0.94
ATOM 1063 CE1 HIS 1 654 6.279 -0.354 13.078 1.00 0.94
ATOM 1064 NE2 HIS 1 654 7.440 -0.735 12.578 1.00 0.94
ATOM 1065 N ARG 1 655 9.588 5.300 13.882 1.00 4.48
ATOM 1066 CA ARG 1 655 10.187 6.440 14.522 1.00 4.48
ATOM 1067 C ARG 1 655 9.540 7.715 14.072 1.00 4.48
ATOM 1068 O ARG 1 655 9.425 8.669 14.840 1.00 4.48
ATOM 1069 CB ARG 1 655 11.691 6.574 14.233 1.00 4.48
ATOM 1070 CG ARG 1 655 12.538 5.463 14.856 1.00 4.48
ATOM 1071 CD ARG 1 655 14.043 5.712 14.741 1.00 4.48
ATOM 1072 NE ARG 1 655 14.368 6.866 15.627 1.00 4.48
ATOM 1073 CZ ARG 1 655 15.669 7.202 15.868 1.00 4.48
ATOM 1074 NH1 ARG 1 655 15.961 8.258 16.682 1.00 4.48
ATOM 1075 NH2 ARG 1 655 16.677 6.484 15.293 1.00 4.48
ATOM 1076 N LEU 1 656 9.101 7.757 12.802 1.00 6.60

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ATOM  1077  CA  LEU 1 656      8.539   8.936  12.207  1.00  6.60
ATOM  1078  C   LEU 1 656      7.300   9.335  12.952  1.00  6.60
ATOM  1079  O   LEU 1 656      6.991  10.521  13.063  1.00  6.60
ATOM  1080  CB  LEU 1 656      8.207   8.718  10.718  1.00  6.60
ATOM  1081  CG  LEU 1 656      7.801   9.993   9.959  1.00  6.60
ATOM  1082  CD1 LEU 1 656      8.927  11.038   9.999  1.00  6.60
ATOM  1083  CD2 LEU 1 656      7.394   9.665   8.514  1.00  6.60
ATOM  1084  N   GLN 1 657      6.552   8.349  13.484  1.00  4.61
ATOM  1085  CA  GLN 1 657      5.373   8.650  14.248  1.00  4.61
ATOM  1086  C   GLN 1 657      4.426   9.452  13.422  1.00  4.61
ATOM  1087  O   GLN 1 657      4.006  10.537  13.822  1.00  4.61
ATOM  1088  CB  GLN 1 657      5.670   9.464  15.521  1.00  4.61
ATOM  1089  CG  GLN 1 657      6.537   8.726  16.543  1.00  4.61
ATOM  1090  CD  GLN 1 657      5.673   7.683  17.234  1.00  4.61
ATOM  1091  OE1 GLN 1 657      6.155   6.910  18.062  1.00  4.61
ATOM  1092  NE2 GLN 1 657      4.358   7.659  16.892  1.00  4.61
ATOM  1093  N   VAL 1 658      4.057   8.932  12.237  1.00  4.09
ATOM  1094  CA  VAL 1 658      3.151   9.662  11.405  1.00  4.09
ATOM  1095  C   VAL 1 658      1.751   9.432  11.857  1.00  4.09
ATOM  1096  O   VAL 1 658      1.415   8.383  12.406  1.00  4.09
ATOM  1097  CB  VAL 1 658      3.196   9.282   9.954  1.00  4.09
ATOM  1098  CG1 VAL 1 658      4.593   9.604   9.412  1.00  4.09
ATOM  1099  CG2 VAL 1 658      2.781   7.811   9.803  1.00  4.09
ATOM  1100  N   SER 1 659      0.893  10.447  11.648  1.00  5.48
ATOM  1101  CA  SER 1 659     -0.487  10.313  11.998  1.00  5.48
ATOM  1102  C   SER 1 659     -1.244  10.189  10.719  1.00  5.48
ATOM  1103  O   SER 1 659     -0.664  10.146   9.635  1.00  5.48
ATOM  1104  CB  SER 1 659     -1.056  11.510  12.768  1.00  5.48
ATOM  1105  OG  SER 1 659     -0.398  11.640  14.020  1.00  5.48
ATOM  1106  N   TYR 1 660     -2.582  10.134  10.816  1.00  4.14
ATOM  1107  CA  TYR 1 660     -3.380   9.977   9.642  1.00  4.14
ATOM  1108  C   TYR 1 660     -3.203  11.111   8.680  1.00  4.14
ATOM  1109  O   TYR 1 660     -3.173  10.886   7.474  1.00  4.14
ATOM  1110  CB  TYR 1 660     -4.869   9.731   9.952  1.00  4.14
ATOM  1111  CG  TYR 1 660     -5.313  10.667  11.021  1.00  4.14
ATOM  1112  CD1 TYR 1 660     -4.992  10.401  12.333  1.00  4.14
ATOM  1113  CD2 TYR 1 660     -6.192  11.686  10.751  1.00  4.14
ATOM  1114  CE1 TYR 1 660     -5.513  11.159  13.354  1.00  4.14
ATOM  1115  CE2 TYR 1 660     -6.718  12.451  11.766  1.00  4.14
ATOM  1116  CZ  TYR 1 660     -6.383  12.184  13.071  1.00  4.14
ATOM  1117  OH  TYR 1 660     -6.940  12.949  14.117  1.00  4.14
ATOM  1118  N   GLU 1 661     -3.055  12.357   9.166  1.00  3.59
ATOM  1119  CA  GLU 1 661     -2.906  13.461   8.257  1.00  3.59
ATOM  1120  C   GLU 1 661     -1.654  13.326   7.442  1.00  3.59
ATOM  1121  O   GLU 1 661     -1.658  13.567   6.235  1.00  3.59
ATOM  1122  CB  GLU 1 661     -2.847  14.820   8.973  1.00  3.59
ATOM  1123  CG  GLU 1 661     -1.677  14.957   9.948  1.00  3.59
ATOM  1124  CD  GLU 1 661     -1.767  16.345  10.567  1.00  3.59
ATOM  1125  OE1 GLU 1 661     -1.886  17.329   9.790  1.00  3.59
ATOM  1126  OE2 GLU 1 661     -1.728  16.440  11.822  1.00  3.59
ATOM  1127  N   GLU 1 662     -0.542  12.935   8.085  1.00  1.15
ATOM  1128  CA  GLU 1 662      0.708  12.809   7.393  1.00  1.15
ATOM  1129  C   GLU 1 662      0.611  11.716   6.372  1.00  1.15
ATOM  1130  O   GLU 1 662      1.114  11.856   5.259  1.00  1.15
ATOM  1131  CB  GLU 1 662      1.866  12.534   8.369  1.00  1.15
ATOM  1132  CG  GLU 1 662      2.138  13.747   9.268  1.00  1.15
ATOM  1133  CD  GLU 1 662      3.040  13.341  10.425  1.00  1.15
ATOM  1134  OE1 GLU 1 662      2.691  12.356  11.130  1.00  1.15
ATOM  1135  OE2 GLU 1 662      4.085  14.016  10.624  1.00  1.15
ATOM  1136  N   TYR 1 663     -0.048  10.591   6.720  1.00  6.52
ATOM  1137  CA  TYR 1 663     -0.196   9.526   5.767  1.00  6.52
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ATOM  1138  C   TYR 1 663    -1.042   9.982   4.620  1.00  6.52
ATOM  1139  O   TYR 1 663    -0.767   9.640   3.472  1.00  6.52
ATOM  1140  CB  TYR 1 663    -0.819   8.241   6.339  1.00  6.52
ATOM  1141  CG  TYR 1 663    -1.054   7.337   5.175  1.00  6.52
ATOM  1142  CD1 TYR 1 663    -0.005   6.939   4.378  1.00  6.52
ATOM  1143  CD2 TYR 1 663    -2.288   6.761   4.971  1.00  6.52
ATOM  1144  CE1 TYR 1 663    -0.205   6.071   3.331  1.00  6.52
ATOM  1145  CE2 TYR 1 663    -2.484   5.855   3.955  1.00  6.52
ATOM  1146  CZ  TYR 1 663    -1.445   5.526   3.115  1.00  6.52
ATOM  1147  OH  TYR 1 663    -1.644   4.624   2.049  1.00  6.52
ATOM  1148  N   LEU 1 664    -2.101  10.772   4.896  1.00  4.94
ATOM  1149  CA  LEU 1 664    -2.936  11.261   3.833  1.00  4.94
ATOM  1150  C   LEU 1 664    -2.160  12.062   2.863  1.00  4.94
ATOM  1151  O   LEU 1 664    -2.253  11.872   1.652  1.00  4.94
ATOM  1152  CB  LEU 1 664    -3.980  12.302   4.252  1.00  4.94
ATOM  1153  CG  LEU 1 664    -5.336  11.712   4.558  1.00  4.94
ATOM  1154  CD1 LEU 1 664    -5.727  10.909   3.315  1.00  4.94
ATOM  1155  CD2 LEU 1 664    -5.408  11.006   5.915  1.00  4.94
ATOM  1156  N   CYS 1 665    -1.380  12.996   3.409  1.00  0.94
ATOM  1157  CA  CYS 1 665    -0.635  13.934   2.643  1.00  0.94
ATOM  1158  C   CYS 1 665     0.294  13.182   1.757  1.00  0.94
ATOM  1159  O   CYS 1 665     0.441  13.492   0.576  1.00  0.94
ATOM  1160  CB  CYS 1 665     0.222  14.789   3.581  1.00  0.94
ATOM  1161  SG  CYS 1 665    -0.788  15.819   4.692  1.00  0.94
ATOM  1162  N   MET 1 666     0.948  12.155   2.317  1.00  4.36
ATOM  1163  CA  MET 1 666     1.880  11.401   1.544  1.00  4.36
ATOM  1164  C   MET 1 666     1.150  10.699   0.442  1.00  4.36
ATOM  1165  O   MET 1 666     1.642  10.625  -0.683  1.00  4.36
ATOM  1166  CB  MET 1 666     2.668  10.379   2.382  1.00  4.36
ATOM  1167  CG  MET 1 666     1.864   9.172   2.858  1.00  4.36
ATOM  1168  SD  MET 1 666     2.829   8.023   3.882  1.00  4.36
ATOM  1169  CE  MET 1 666     4.183   7.920   2.678  1.00  4.36
ATOM  1170  N   LYS 1 667    -0.059  10.178   0.729  1.00  2.57
ATOM  1171  CA  LYS 1 667    -0.804   9.480  -0.281  1.00  2.57
ATOM  1172  C   LYS 1 667    -1.119  10.417  -1.402  1.00  2.57
ATOM  1173  O   LYS 1 667    -1.000  10.056  -2.572  1.00  2.57
ATOM  1174  CB  LYS 1 667    -2.168   8.953   0.189  1.00  2.57
ATOM  1175  CG  LYS 1 667    -2.117   7.815   1.204  1.00  2.57
ATOM  1176  CD  LYS 1 667    -3.513   7.385   1.660  1.00  2.57
ATOM  1177  CE  LYS 1 667    -4.251   6.536   0.622  1.00  2.57
ATOM  1178  NZ  LYS 1 667    -5.555   6.092   1.163  1.00  2.57
ATOM  1179  N   THR 1 668    -1.533  11.654  -1.069  1.00  5.21
ATOM  1180  CA  THR 1 668    -1.916  12.584  -2.089  1.00  5.21
ATOM  1181  C   THR 1 668    -0.743  12.889  -2.960  1.00  5.21
ATOM  1182  O   THR 1 668    -0.876  12.992  -4.177  1.00  5.21
ATOM  1183  CB  THR 1 668    -2.435  13.893  -1.555  1.00  5.21
ATOM  1184  OG1 THR 1 668    -1.418  14.575  -0.837  1.00  5.21
ATOM  1185  CG2 THR 1 668    -3.633  13.612  -0.634  1.00  5.21
ATOM  1186  N   LEU 1 669     0.456  13.042  -2.378  1.00  0.92
ATOM  1187  CA  LEU 1 669     1.555  13.381  -3.230  1.00  0.92
ATOM  1188  C   LEU 1 669     1.838  12.252  -4.172  1.00  0.92
ATOM  1189  O   LEU 1 669     2.136  12.473  -5.344  1.00  0.92
ATOM  1190  CB  LEU 1 669     2.847  13.743  -2.480  1.00  0.92
ATOM  1191  CG  LEU 1 669     3.977  14.146  -3.444  1.00  0.92
ATOM  1192  CD1 LEU 1 669     3.543  15.317  -4.339  1.00  0.92
ATOM  1193  CD2 LEU 1 669     5.270  14.473  -2.686  1.00  0.92
ATOM  1194  N   LEU 1 670     1.738  11.000  -3.686  1.00  0.69
ATOM  1195  CA  LEU 1 670     2.018   9.865  -4.520  1.00  0.69
ATOM  1196  C   LEU 1 670     1.049   9.837  -5.661  1.00  0.69
ATOM  1197  O   LEU 1 670     1.430   9.611  -6.810  1.00  0.69
ATOM  1198  CB  LEU 1 670     1.861   8.535  -3.763  1.00  0.69
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ATOM  1199  CG  LEU 1 670     2.854   8.365  -2.599  1.00  0.69
ATOM  1200  CD1 LEU 1 670     2.651   7.018  -1.890  1.00  0.69
ATOM  1201  CD2 LEU 1 670     4.305   8.572  -3.066  1.00  0.69
ATOM  1202  N   LEU 1 671    -0.240  10.082  -5.368  1.00  3.54
ATOM  1203  CA  LEU 1 671    -1.272  10.024  -6.364  1.00  3.54
ATOM  1204  C   LEU 1 671    -1.070  11.102  -7.383  1.00  3.54
ATOM  1205  O   LEU 1 671    -1.261  10.883  -8.577  1.00  3.54
ATOM  1206  CB  LEU 1 671    -2.678  10.108  -5.728  1.00  3.54
ATOM  1207  CG  LEU 1 671    -3.861  10.063  -6.716  1.00  3.54
ATOM  1208  CD1 LEU 1 671    -5.177   9.741  -5.994  1.00  3.54
ATOM  1209  CD2 LEU 1 671    -3.993  11.377  -7.493  1.00  3.54
ATOM  1210  N   LEU 1 672    -0.642  12.284  -6.918  1.00  5.01
ATOM  1211  CA  LEU 1 672    -0.396  13.478  -7.671  1.00  5.01
ATOM  1212  C   LEU 1 672     0.765  13.403  -8.606  1.00  5.01
ATOM  1213  O   LEU 1 672     1.018  14.367  -9.325  1.00  5.01
ATOM  1214  CB  LEU 1 672    -0.250  14.727  -6.797  1.00  5.01
ATOM  1215  CG  LEU 1 672    -1.602  15.358  -6.418  1.00  5.01
ATOM  1216  CD1 LEU 1 672    -2.591  14.356  -5.807  1.00  5.01
ATOM  1217  CD2 LEU 1 672    -1.363  16.565  -5.508  1.00  5.01
ATOM  1218  N   SER 1 673     1.564  12.322  -8.549  1.00  4.46
ATOM  1219  CA  SER 1 673     2.677  12.205  -9.450  1.00  4.46
ATOM  1220  C   SER 1 673     2.229  12.452 -10.854  1.00  4.46
ATOM  1221  O   SER 1 673     1.485  11.670 -11.444  1.00  4.46
ATOM  1222  CB  SER 1 673     3.371  10.834  -9.381  1.00  4.46
ATOM  1223  OG  SER 1 673     2.450   9.808  -9.715  1.00  4.46
ATOM  1224  N   SER 1 674     2.710  13.573 -11.422  1.00  4.03
ATOM  1225  CA  SER 1 674     2.324  14.023 -12.726  1.00  4.03
ATOM  1226  C   SER 1 674     3.197  13.391 -13.750  1.00  4.03
ATOM  1227  O   SER 1 674     2.937  12.281 -14.209  1.00  4.03
ATOM  1228  CB  SER 1 674     2.464  15.545 -12.902  1.00  4.03
ATOM  1229  OG  SER 1 674     1.589  16.226 -12.016  1.00  4.03
ATOM  1230  N   VAL 1 675     4.265  14.110 -14.135  1.00  4.27
ATOM  1231  CA  VAL 1 675     5.158  13.662 -15.158  1.00  4.27
ATOM  1232  C   VAL 1 675     5.648  12.258 -14.953  1.00  4.27
ATOM  1233  O   VAL 1 675     6.039  11.636 -15.940  1.00  4.27
ATOM  1234  CB  VAL 1 675     6.348  14.565 -15.353  1.00  4.27
ATOM  1235  CG1 VAL 1 675     7.204  14.599 -14.077  1.00  4.27
ATOM  1236  CG2 VAL 1 675     7.113  14.081 -16.596  1.00  4.27
ATOM  1237  N   PRO 1 676     5.668  11.678 -13.779  1.00  2.47
ATOM  1238  CA  PRO 1 676     6.142  10.328 -13.718  1.00  2.47
ATOM  1239  C   PRO 1 676     5.180   9.425 -14.410  1.00  2.47
ATOM  1240  O   PRO 1 676     5.538   8.290 -14.721  1.00  2.47
ATOM  1241  CB  PRO 1 676     6.368  10.014 -12.235  1.00  2.47
ATOM  1242  CG  PRO 1 676     5.825  11.241 -11.479  1.00  2.47
ATOM  1243  CD  PRO 1 676     5.899  12.365 -12.518  1.00  2.47
ATOM  1244  N   LYS 1 677     3.953   9.909 -14.647  1.00  7.09
ATOM  1245  CA  LYS 1 677     2.953   9.130 -15.305  1.00  7.09
ATOM  1246  C   LYS 1 677     3.295   9.075 -16.754  1.00  7.09
ATOM  1247  O   LYS 1 677     3.876  10.009 -17.301  1.00  7.09
ATOM  1248  CB  LYS 1 677     1.565   9.786 -15.268  1.00  7.09
ATOM  1249  CG  LYS 1 677     0.945   9.990 -13.886  1.00  7.09
ATOM  1250  CD  LYS 1 677     0.660   8.694 -13.134  1.00  7.09
ATOM  1251  CE  LYS 1 677     1.641   8.443 -11.994  1.00  7.09
ATOM  1252  NZ  LYS 1 677     3.004   8.241 -12.528  1.00  7.09
ATOM  1253  N   ASP 1 678     2.936   7.960 -17.414  1.00  3.66
ATOM  1254  CA  ASP 1 678     3.159   7.842 -18.822  1.00  3.66
ATOM  1255  C   ASP 1 678     1.804   7.942 -19.448  1.00  3.66
ATOM  1256  O   ASP 1 678     0.919   7.138 -19.154  1.00  3.66
ATOM  1257  CB  ASP 1 678     3.754   6.479 -19.221  1.00  3.66
ATOM  1258  CG  ASP 1 678     4.010   6.465 -20.722  1.00  3.66
ATOM  1259  OD1 ASP 1 678     3.687   7.483 -21.392  1.00  3.66
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ATOM 1260 OD2 ASP 1 678 4.529 5.431 -21.220 1.00 3.66
ATOM 1261 N GLY 1 679 1.600 8.946 -20.323 1.00 0.72
ATOM 1262 CA GLY 1 679 0.337 9.069 -20.992 1.00 0.72
ATOM 1263 C GLY 1 679 -0.557 10.104 -20.372 1.00 0.72
ATOM 1264 O GLY 1 679 -1.593 10.440 -20.942 1.00 0.72
ATOM 1265 N LEU 1 680 -0.195 10.641 -19.189 1.00 3.91
ATOM 1266 CA LEU 1 680 -1.015 11.655 -18.577 1.00 3.91
ATOM 1267 C LEU 1 680 -1.041 12.859 -19.453 1.00 3.91
ATOM 1268 O LEU 1 680 0.005 13.396 -19.817 1.00 3.91
ATOM 1269 CB LEU 1 680 -0.504 12.083 -17.185 1.00 3.91
ATOM 1270 CG LEU 1 680 -0.962 11.201 -16.007 1.00 3.91
ATOM 1271 CD1 LEU 1 680 -2.274 11.711 -15.404 1.00 3.91
ATOM 1272 CD2 LEU 1 680 -1.132 9.738 -16.439 1.00 3.91
ATOM 1273 N LYS 1 681 -2.252 13.279 -19.873 1.00 9.62
ATOM 1274 CA LYS 1 681 -2.324 14.444 -20.700 1.00 9.62
ATOM 1275 C LYS 1 681 -2.135 15.726 -19.952 1.00 9.62
ATOM 1276 O LYS 1 681 -1.432 16.617 -20.426 1.00 9.62
ATOM 1277 CB LYS 1 681 -3.605 14.566 -21.542 1.00 9.62
ATOM 1278 CG LYS 1 681 -4.874 14.922 -20.780 1.00 9.62
ATOM 1279 CD LYS 1 681 -5.342 13.847 -19.810 1.00 9.62
ATOM 1280 CE LYS 1 681 -6.817 14.021 -19.474 1.00 9.62
ATOM 1281 NZ LYS 1 681 -7.616 13.820 -20.704 1.00 9.62
ATOM 1282 N SER 1 682 -2.741 15.867 -18.753 1.00 3.76
ATOM 1283 CA SER 1 682 -2.629 17.141 -18.102 1.00 3.76
ATOM 1284 C SER 1 682 -1.576 17.102 -17.041 1.00 3.76
ATOM 1285 O SER 1 682 -1.874 17.009 -15.851 1.00 3.76
ATOM 1286 CB SER 1 682 -3.935 17.597 -17.438 1.00 3.76
ATOM 1287 OG SER 1 682 -3.752 18.895 -16.898 1.00 3.76
ATOM 1288 N GLN 1 683 -0.300 17.189 -17.456 1.00 3.60
ATOM 1289 CA GLN 1 683 0.774 17.152 -16.511 1.00 3.60
ATOM 1290 C GLN 1 683 0.808 18.390 -15.668 1.00 3.60
ATOM 1291 O GLN 1 683 1.001 18.313 -14.457 1.00 3.60
ATOM 1292 CB GLN 1 683 2.158 17.009 -17.167 1.00 3.60
ATOM 1293 CG GLN 1 683 2.560 18.199 -18.039 1.00 3.60
ATOM 1294 CD GLN 1 683 3.940 17.908 -18.610 1.00 3.60
ATOM 1295 OE1 GLN 1 683 4.530 16.864 -18.336 1.00 3.60
ATOM 1296 NE2 GLN 1 683 4.475 18.857 -19.425 1.00 3.60
ATOM 1297 N GLU 1 684 0.603 19.567 -16.290 1.00 3.13
ATOM 1298 CA GLU 1 684 0.756 20.811 -15.586 1.00 3.13
ATOM 1299 C GLU 1 684 -0.201 21.003 -14.452 1.00 3.13
ATOM 1300 O GLU 1 684 0.216 21.351 -13.349 1.00 3.13
ATOM 1301 CB GLU 1 684 0.622 22.033 -16.511 1.00 3.13
ATOM 1302 CG GLU 1 684 1.772 22.148 -17.513 1.00 3.13
ATOM 1303 CD GLU 1 684 3.054 22.373 -16.723 1.00 3.13
ATOM 1304 OE1 GLU 1 684 2.967 22.482 -15.472 1.00 3.13
ATOM 1305 OE2 GLU 1 684 4.139 22.436 -17.362 1.00 3.13
ATOM 1306 N LEU 1 685 -1.509 20.769 -14.668 1.00 7.18
ATOM 1307 CA LEU 1 685 -2.427 21.022 -13.593 1.00 7.18
ATOM 1308 C LEU 1 685 -2.104 20.082 -12.491 1.00 7.18
ATOM 1309 O LEU 1 685 -2.183 20.414 -11.310 1.00 7.18
ATOM 1310 CB LEU 1 685 -3.919 20.860 -13.977 1.00 7.18
ATOM 1311 CG LEU 1 685 -4.434 19.429 -14.259 1.00 7.18
ATOM 1312 CD1 LEU 1 685 -4.558 18.563 -12.993 1.00 7.18
ATOM 1313 CD2 LEU 1 685 -5.752 19.480 -15.047 1.00 7.18
ATOM 1314 N PHE 1 686 -1.737 18.859 -12.885 1.00 3.83
ATOM 1315 CA PHE 1 686 -1.447 17.791 -11.989 1.00 3.83
ATOM 1316 C PHE 1 686 -0.251 18.129 -11.151 1.00 3.83
ATOM 1317 O PHE 1 686 -0.213 17.840 -9.954 1.00 3.83
ATOM 1318 CB PHE 1 686 -1.208 16.527 -12.809 1.00 3.83
ATOM 1319 CG PHE 1 686 -1.341 15.429 -11.852 1.00 3.83
ATOM 1320 CD1 PHE 1 686 -2.481 15.350 -11.090 1.00 3.83

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ATOM  1321  CD2 PHE 1 686     -0.486  14.369 -11.931  1.00  3.83
ATOM  1322  CE1 PHE 1 686     -2.676  14.293 -10.247  1.00  3.83
ATOM  1323  CE2 PHE 1 686     -0.708  13.282 -11.144  1.00  3.83
ATOM  1324  CZ  PHE 1 686     -1.751  13.284 -10.258  1.00  3.83
ATOM  1325  N   ASP 1 687      0.768  18.753 -11.768  1.00  4.20
ATOM  1326  CA  ASP 1 687      1.949  19.143 -11.056  1.00  4.20
ATOM  1327  C   ASP 1 687      1.566  20.206 -10.078  1.00  4.20
ATOM  1328  O   ASP 1 687      2.041  20.230  -8.943  1.00  4.20
ATOM  1329  CB  ASP 1 687      3.032  19.728 -11.978  1.00  4.20
ATOM  1330  CG  ASP 1 687      4.308  19.892 -11.165  1.00  4.20
ATOM  1331  OD1 ASP 1 687      5.331  20.338 -11.752  1.00  4.20
ATOM  1332  OD2 ASP 1 687      4.279  19.570  -9.948  1.00  4.20
ATOM  1333  N   GLU 1 688      0.669  21.115 -10.499  1.00  1.12
ATOM  1334  CA  GLU 1 688      0.259  22.192  -9.649  1.00  1.12
ATOM  1335  C   GLU 1 688     -0.378  21.601  -8.437  1.00  1.12
ATOM  1336  O   GLU 1 688     -0.161  22.052  -7.313  1.00  1.12
ATOM  1337  CB  GLU 1 688     -0.788  23.103 -10.312  1.00  1.12
ATOM  1338  CG  GLU 1 688     -0.249  23.904 -11.497  1.00  1.12
ATOM  1339  CD  GLU 1 688     -1.408  24.693 -12.086  1.00  1.12
ATOM  1340  OE1 GLU 1 688     -1.157  25.526 -12.997  1.00  1.12
ATOM  1341  OE2 GLU 1 688     -2.563  24.470 -11.635  1.00  1.12
ATOM  1342  N   ILE 1 689     -1.196  20.559  -8.634  1.00  3.95
ATOM  1343  CA  ILE 1 689     -1.864  19.967  -7.519  1.00  3.95
ATOM  1344  C   ILE 1 689     -0.849  19.371  -6.598  1.00  3.95
ATOM  1345  O   ILE 1 689     -0.917  19.555  -5.385  1.00  3.95
ATOM  1346  CB  ILE 1 689     -2.812  18.880  -7.932  1.00  3.95
ATOM  1347  CG1 ILE 1 689     -3.859  19.434  -8.913  1.00  3.95
ATOM  1348  CG2 ILE 1 689     -3.448  18.299  -6.659  1.00  3.95
ATOM  1349  CD1 ILE 1 689     -4.718  20.551  -8.321  1.00  3.95
ATOM  1350  N   ARG 1 690      0.153  18.658  -7.135  1.00  7.53
ATOM  1351  CA  ARG 1 690      1.086  18.025  -6.251  1.00  7.53
ATOM  1352  C   ARG 1 690      1.845  19.026  -5.444  1.00  7.53
ATOM  1353  O   ARG 1 690      2.016  18.847  -4.239  1.00  7.53
ATOM  1354  CB  ARG 1 690      2.112  17.131  -6.970  1.00  7.53
ATOM  1355  CG  ARG 1 690      3.021  17.870  -7.953  1.00  7.53
ATOM  1356  CD  ARG 1 690      4.037  16.952  -8.632  1.00  7.53
ATOM  1357  NE  ARG 1 690      4.936  16.430  -7.564  1.00  7.53
ATOM  1358  CZ  ARG 1 690      5.289  15.111  -7.550  1.00  7.53
ATOM  1359  NH1 ARG 1 690      6.109  14.637  -6.566  1.00  7.53
ATOM  1360  NH2 ARG 1 690      4.819  14.267  -8.514  1.00  7.53
ATOM  1361  N   MET 1 691      2.310  20.127  -6.064  1.00  8.51
ATOM  1362  CA  MET 1 691      3.098  21.007  -5.254  1.00  8.51
ATOM  1363  C   MET 1 691      2.254  21.587  -4.169  1.00  8.51
ATOM  1364  O   MET 1 691      2.743  21.819  -3.064  1.00  8.51
ATOM  1365  CB  MET 1 691      3.846  22.155  -5.971  1.00  8.51
ATOM  1366  CG  MET 1 691      3.084  23.466  -6.180  1.00  8.51
ATOM  1367  SD  MET 1 691      2.189  23.618  -7.747  1.00  8.51
ATOM  1368  CE  MET 1 691      3.673  23.884  -8.758  1.00  8.51
ATOM  1369  N   THR 1 692      0.958  21.838  -4.439  1.00  4.62
ATOM  1370  CA  THR 1 692      0.168  22.427  -3.398  1.00  4.62
ATOM  1371  C   THR 1 692      0.124  21.491  -2.231  1.00  4.62
ATOM  1372  O   THR 1 692      0.213  21.924  -1.083  1.00  4.62
ATOM  1373  CB  THR 1 692     -1.245  22.771  -3.789  1.00  4.62
ATOM  1374  OG1 THR 1 692     -1.808  23.642  -2.819  1.00  4.62
ATOM  1375  CG2 THR 1 692     -2.094  21.496  -3.868  1.00  4.62
ATOM  1376  N   TYR 1 693     -0.014  20.175  -2.487  1.00  1.13
ATOM  1377  CA  TYR 1 693     -0.051  19.248  -1.393  1.00  1.13
ATOM  1378  C   TYR 1 693      1.261  19.240  -0.685  1.00  1.13
ATOM  1379  O   TYR 1 693      1.294  19.257   0.542  1.00  1.13
ATOM  1380  CB  TYR 1 693     -0.396  17.808  -1.809  1.00  1.13
ATOM  1381  CG  TYR 1 693     -1.845  17.808  -2.157  1.00  1.13
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ATOM 1382 CD1 TYR 1 693 -2.271 18.338 -3.348 1.00 1.13
ATOM 1383 CD2 TYR 1 693 -2.785 17.299 -1.293 1.00 1.13
ATOM 1384 CE1 TYR 1 693 -3.600 18.367 -3.687 1.00 1.13
ATOM 1385 CE2 TYR 1 693 -4.123 17.333 -1.616 1.00 1.13
ATOM 1386 CZ TYR 1 693 -4.532 17.869 -2.814 1.00 1.13
ATOM 1387 OH TYR 1 693 -5.904 17.965 -3.131 1.00 1.13
ATOM 1388 N ILE 1 694 2.381 19.263 -1.426 1.00 0.61
ATOM 1389 CA ILE 1 694 3.674 19.185 -0.803 1.00 0.61
ATOM 1390 C ILE 1 694 3.869 20.332 0.139 1.00 0.61
ATOM 1391 O ILE 1 694 4.382 20.153 1.244 1.00 0.61
ATOM 1392 CB ILE 1 694 4.797 19.235 -1.797 1.00 0.61
ATOM 1393 CG1 ILE 1 694 4.708 18.050 -2.772 1.00 0.61
ATOM 1394 CG2 ILE 1 694 6.121 19.294 -1.016 1.00 0.61
ATOM 1395 CD1 ILE 1 694 5.631 18.187 -3.983 1.00 0.61
ATOM 1396 N LYS 1 695 3.463 21.547 -0.271 1.00 8.13
ATOM 1397 CA LYS 1 695 3.654 22.702 0.559 1.00 8.13
ATOM 1398 C LYS 1 695 2.868 22.556 1.822 1.00 8.13
ATOM 1399 O LYS 1 695 3.366 22.835 2.912 1.00 8.13
ATOM 1400 CB LYS 1 695 3.189 23.998 -0.126 1.00 8.13
ATOM 1401 CG LYS 1 695 3.567 25.267 0.640 1.00 8.13
ATOM 1402 CD LYS 1 695 5.066 25.573 0.615 1.00 8.13
ATOM 1403 CE LYS 1 695 5.917 24.542 1.359 1.00 8.13
ATOM 1404 NZ LYS 1 695 5.642 24.610 2.811 1.00 8.13
ATOM 1405 N GLU 1 696 1.609 22.098 1.705 1.00 1.25
ATOM 1406 CA GLU 1 696 0.766 21.945 2.853 1.00 1.25
ATOM 1407 C GLU 1 696 1.349 20.908 3.750 1.00 1.25
ATOM 1408 O GLU 1 696 1.299 21.027 4.973 1.00 1.25
ATOM 1409 CB GLU 1 696 -0.655 21.486 2.498 1.00 1.25
ATOM 1410 CG GLU 1 696 -1.425 22.546 1.722 1.00 1.25
ATOM 1411 CD GLU 1 696 -2.816 22.018 1.423 1.00 1.25
ATOM 1412 OE1 GLU 1 696 -3.532 22.684 0.629 1.00 1.25
ATOM 1413 OE2 GLU 1 696 -3.181 20.951 1.982 1.00 1.25
ATOM 1414 N LEU 1 697 1.913 19.842 3.161 1.00 8.40
ATOM 1415 CA LEU 1 697 2.441 18.787 3.970 1.00 8.40
ATOM 1416 C LEU 1 697 3.586 19.306 4.776 1.00 8.40
ATOM 1417 O LEU 1 697 3.701 19.017 5.967 1.00 8.40
ATOM 1418 CB LEU 1 697 2.977 17.603 3.151 1.00 8.40
ATOM 1419 CG LEU 1 697 1.981 17.123 2.084 1.00 8.40
ATOM 1420 CD1 LEU 1 697 2.257 15.678 1.640 1.00 8.40
ATOM 1421 CD2 LEU 1 697 0.530 17.468 2.462 1.00 8.40
ATOM 1422 N GLY 1 698 4.466 20.103 4.143 1.00 0.45
ATOM 1423 CA GLY 1 698 5.622 20.592 4.835 1.00 0.45
ATOM 1424 C GLY 1 698 5.201 21.455 5.979 1.00 0.45
ATOM 1425 O GLY 1 698 5.741 21.351 7.080 1.00 0.45
ATOM 1426 N LYS 1 699 4.211 22.333 5.748 1.00 5.59
ATOM 1427 CA LYS 1 699 3.791 23.224 6.787 1.00 5.59
ATOM 1428 C LYS 1 699 3.230 22.419 7.911 1.00 5.59
ATOM 1429 O LYS 1 699 3.441 22.737 9.079 1.00 5.59
ATOM 1430 CB LYS 1 699 2.680 24.193 6.357 1.00 5.59
ATOM 1431 CG LYS 1 699 1.342 23.489 6.155 1.00 5.59
ATOM 1432 CD LYS 1 699 0.150 24.428 6.129 1.00 5.59
ATOM 1433 CE LYS 1 699 0.256 25.462 5.020 1.00 5.59
ATOM 1434 NZ LYS 1 699 -0.767 26.488 5.248 1.00 5.59
ATOM 1435 N ALA 1 700 2.489 21.346 7.580 1.00 0.65
ATOM 1436 CA ALA 1 700 1.876 20.550 8.598 1.00 0.65
ATOM 1437 C ALA 1 700 2.941 19.933 9.443 1.00 0.65
ATOM 1438 O ALA 1 700 2.831 19.901 10.667 1.00 0.65
ATOM 1439 CB ALA 1 700 1.015 19.412 8.026 1.00 0.65
ATOM 1440 N ILE 1 701 4.017 19.433 8.810 1.00 3.82
ATOM 1441 CA ILE 1 701 5.036 18.790 9.585 1.00 3.82
ATOM 1442 C ILE 1 701 5.693 19.794 10.475 1.00 3.82

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ATOM  1443  O   ILE 1 701     6.075 19.481 11.602 1.00 3.82
ATOM  1444  CB  ILE 1 701     6.075 18.082  8.764 1.00 3.82
ATOM  1445  CG1 ILE 1 701     6.839 17.095  9.659 1.00 3.82
ATOM  1446  CG2 ILE 1 701     6.979 19.119  8.079 1.00 3.82
ATOM  1447  CD1 ILE 1 701     7.626 16.051  8.874 1.00 3.82
ATOM  1448  N   VAL 1 702     5.845 21.039  9.986 1.00 0.51
ATOM  1449  CA  VAL 1 702     6.428 22.062 10.798 1.00 0.51
ATOM  1450  C   VAL 1 702     5.517 22.229 11.968 1.00 0.51
ATOM  1451  O   VAL 1 702     5.964 22.385 13.104 1.00 0.51
ATOM  1452  CB  VAL 1 702     6.515 23.385 10.096 1.00 0.51
ATOM  1453  CG1 VAL 1 702     7.095 24.420 11.074 1.00 0.51
ATOM  1454  CG2 VAL 1 702     7.344 23.206  8.812 1.00 0.51
ATOM  1455  N   LYS 1 703     4.197 22.165 11.712 1.00 9.37
ATOM  1456  CA  LYS 1 703     3.230 22.326 12.756 1.00 9.37
ATOM  1457  C   LYS 1 703     3.514 21.258 13.752 1.00 9.37
ATOM  1458  O   LYS 1 703     3.431 21.497 14.955 1.00 9.37
ATOM  1459  CB  LYS 1 703     1.780 22.143 12.269 1.00 9.37
ATOM  1460  CG  LYS 1 703     0.715 22.521 13.305 1.00 9.37
ATOM  1461  CD  LYS 1 703     0.716 21.657 14.570 1.00 9.37
ATOM  1462  CE  LYS 1 703     0.197 20.237 14.342 1.00 9.37
ATOM  1463  NZ  LYS 1 703    -1.226 20.280 13.937 1.00 9.37
ATOM  1464  N   ARG 1 704     3.839 20.043 13.267 1.00 8.04
ATOM  1465  CA  ARG 1 704     4.206 18.988 14.163 1.00 8.04
ATOM  1466  C   ARG 1 704     5.501 19.453 14.723 1.00 8.04
ATOM  1467  O   ARG 1 704     6.557 19.224 14.134 1.00 8.04
ATOM  1468  CB  ARG 1 704     4.479 17.646 13.467 1.00 8.04
ATOM  1469  CG  ARG 1 704     3.235 17.002 12.861 1.00 8.04
ATOM  1470  CD  ARG 1 704     2.385 16.248 13.882 1.00 8.04
ATOM  1471  NE  ARG 1 704     1.223 15.686 13.146 1.00 8.04
ATOM  1472  CZ  ARG 1 704     0.363 14.832 13.771 1.00 8.04
ATOM  1473  NH1 ARG 1 704     0.560 14.486 15.077 1.00 8.04
ATOM  1474  NH2 ARG 1 704    -0.703 14.331 13.084 1.00 8.04
ATOM  1475  N   GLU 1 705     5.433 20.112 15.891 1.00 6.89
ATOM  1476  CA  GLU 1 705     6.571 20.722 16.502 1.00 6.89
ATOM  1477  C   GLU 1 705     7.717 19.793 16.543 1.00 6.89
ATOM  1478  O   GLU 1 705     7.541 18.584 16.667 1.00 6.89
ATOM  1479  CB  GLU 1 705     6.312 21.210 17.939 1.00 6.89
ATOM  1480  CG  GLU 1 705     5.415 22.446 18.000 1.00 6.89
ATOM  1481  CD  GLU 1 705     6.174 23.576 17.320 1.00 6.89
ATOM  1482  OE1 GLU 1 705     5.603 24.693 17.201 1.00 6.89
ATOM  1483  OE2 GLU 1 705     7.339 23.332 16.906 1.00 6.89
ATOM  1484  N   GLY 1 706     8.927 20.362 16.413 1.00 2.21
ATOM  1485  CA  GLY 1 706    10.141 19.610 16.420 1.00 2.21
ATOM  1486  C   GLY 1 706    10.330 19.086 17.800 1.00 2.21
ATOM  1487  O   GLY 1 706    11.162 18.208 18.022 1.00 2.21
ATOM  1488  N   ASN 1 707     9.576 19.640 18.769 1.00 3.74
ATOM  1489  CA  ASN 1 707     9.717 19.183 20.118 1.00 3.74
ATOM  1490  C   ASN 1 707     9.444 17.717 20.094 1.00 3.74
ATOM  1491  O   ASN 1 707    10.295 16.908 20.458 1.00 3.74
ATOM  1492  CB  ASN 1 707     8.712 19.832 21.086 1.00 3.74
ATOM  1493  CG  ASN 1 707     9.135 19.488 22.509 1.00 3.74
ATOM  1494  OD1 ASN 1 707     8.484 19.885 23.475 1.00 3.74
ATOM  1495  ND2 ASN 1 707    10.260 18.739 22.647 1.00 3.74
ATOM  1496  N   SER 1 708     8.238 17.327 19.649 1.00 3.07
ATOM  1497  CA  SER 1 708     7.976 15.927 19.536 1.00 3.07
ATOM  1498  C   SER 1 708     8.722 15.483 18.319 1.00 3.07
ATOM  1499  O   SER 1 708     9.414 14.466 18.325 1.00 3.07
ATOM  1500  CB  SER 1 708     6.487 15.607 19.324 1.00 3.07
ATOM  1501  OG  SER 1 708     6.299 14.204 19.220 1.00 3.07
ATOM  1502  N   SER 1 709     8.607 16.282 17.242 1.00 4.34
ATOM  1503  CA  SER 1 709     9.228 15.993 15.988 1.00 4.34
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ATOM  1504  C   SER 1 709     10.693  16.280  16.079  1.00  4.34
ATOM  1505  O   SER 1 709     11.242  16.982  15.230  1.00  4.34
ATOM  1506  CB  SER 1 709      8.652  16.859  14.853  1.00  4.34
ATOM  1507  OG  SER 1 709      9.278  16.563  13.617  1.00  4.34
ATOM  1508  N   GLN 1 710     11.389  15.761  17.111  1.00  3.96
ATOM  1509  CA  GLN 1 710     12.803  15.981  17.041  1.00  3.96
ATOM  1510  C   GLN 1 710     13.402  14.857  16.284  1.00  3.96
ATOM  1511  O   GLN 1 710     13.900  13.888  16.857  1.00  3.96
ATOM  1512  CB  GLN 1 710     13.607  16.084  18.355  1.00  3.96
ATOM  1513  CG  GLN 1 710     13.732  17.498  18.931  1.00  3.96
ATOM  1514  CD  GLN 1 710     12.928  17.617  20.209  1.00  3.96
ATOM  1515  OE1 GLN 1 710     12.380  18.674  20.514  1.00  3.96
ATOM  1516  NE2 GLN 1 710     12.875  16.511  20.998  1.00  3.96
ATOM  1517  N   ASN 1 711     13.342  14.967  14.951  1.00  4.08
ATOM  1518  CA  ASN 1 711     13.976  14.014  14.103  1.00  4.08
ATOM  1519  C   ASN 1 711     14.772  14.907  13.220  1.00  4.08
ATOM  1520  O   ASN 1 711     14.246  15.879  12.682  1.00  4.08
ATOM  1521  CB  ASN 1 711     12.996  13.224  13.218  1.00  4.08
ATOM  1522  CG  ASN 1 711     13.739  12.049  12.597  1.00  4.08
ATOM  1523  OD1 ASN 1 711     13.346  10.895  12.759  1.00  4.08
ATOM  1524  ND2 ASN 1 711     14.845  12.343  11.864  1.00  4.08
ATOM  1525  N   TRP 1 712     16.076  14.630  13.069  1.00  4.56
ATOM  1526  CA  TRP 1 712     16.846  15.510  12.249  1.00  4.56
ATOM  1527  C   TRP 1 712     16.558  15.188  10.823  1.00  4.56
ATOM  1528  O   TRP 1 712     16.349  14.030  10.466  1.00  4.56
ATOM  1529  CB  TRP 1 712     18.366  15.377  12.449  1.00  4.56
ATOM  1530  CG  TRP 1 712     18.903  13.991  12.181  1.00  4.56
ATOM  1531  CD1 TRP 1 712     19.096  13.350  10.992  1.00  4.56
ATOM  1532  CD2 TRP 1 712     19.394  13.108  13.202  1.00  4.56
ATOM  1533  NE1 TRP 1 712     19.650  12.111  11.211  1.00  4.56
ATOM  1534  CE2 TRP 1 712     19.844  11.952  12.567  1.00  4.56
ATOM  1535  CE3 TRP 1 712     19.471  13.253  14.559  1.00  4.56
ATOM  1536  CZ2 TRP 1 712     20.375  10.915  13.280  1.00  4.56
ATOM  1537  CZ3 TRP 1 712     20.010  12.208  15.275  1.00  4.56
ATOM  1538  CH2 TRP 1 712     20.452  11.061  14.648  1.00  4.56
ATOM  1539  N   GLN 1 713     16.527  16.223   9.966  1.00  4.63
ATOM  1540  CA  GLN 1 713     16.349  15.980   8.566  1.00  4.63
ATOM  1541  C   GLN 1 713     14.980  15.395   8.370  1.00  4.63
ATOM  1542  O   GLN 1 713     14.782  14.579   7.474  1.00  4.63
ATOM  1543  CB  GLN 1 713     17.343  14.909   8.068  1.00  4.63
ATOM  1544  CG  GLN 1 713     18.778  15.071   8.596  1.00  4.63
ATOM  1545  CD  GLN 1 713     19.638  15.895   7.648  1.00  4.63
ATOM  1546  OE1 GLN 1 713     19.889  15.497   6.512  1.00  4.63
ATOM  1547  NE2 GLN 1 713     20.121  17.070   8.134  1.00  4.63
ATOM  1548  N   ARG 1 714     13.987  15.802   9.188  1.00  3.83
ATOM  1549  CA  ARG 1 714     12.701  15.167   9.100  1.00  3.83
ATOM  1550  C   ARG 1 714     11.971  15.323   7.801  1.00  3.83
ATOM  1551  O   ARG 1 714     11.537  14.331   7.218  1.00  3.83
ATOM  1552  CB  ARG 1 714     11.716  15.608  10.193  1.00  3.83
ATOM  1553  CG  ARG 1 714     10.353  14.928  10.041  1.00  3.83
ATOM  1554  CD  ARG 1 714      9.426  15.134  11.235  1.00  3.83
ATOM  1555  NE  ARG 1 714      9.949  14.285  12.341  1.00  3.83
ATOM  1556  CZ  ARG 1 714      9.284  13.149  12.699  1.00  3.83
ATOM  1557  NH1 ARG 1 714      9.786  12.343  13.678  1.00  3.83
ATOM  1558  NH2 ARG 1 714      8.109  12.828  12.083  1.00  3.83
ATOM  1559  N   PHE 1 715     11.811  16.556   7.285  1.00  7.35
ATOM  1560  CA  PHE 1 715     10.994  16.649   6.108  1.00  7.35
ATOM  1561  C   PHE 1 715     11.615  15.939   4.948  1.00  7.35
ATOM  1562  O   PHE 1 715     10.968  15.128   4.287  1.00  7.35
ATOM  1563  CB  PHE 1 715     10.643  18.095   5.701  1.00  7.35
ATOM  1564  CG  PHE 1 715     11.864  18.861   5.318  1.00  7.35
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ATOM  1565 CD1 PHE 1 715    12.296 18.874  4.011 1.00 7.35
ATOM  1566 CD2 PHE 1 715    12.497 19.665  6.236 1.00 7.35
ATOM  1567 CE1 PHE 1 715    13.350 19.671  3.630 1.00 7.35
ATOM  1568 CE2 PHE 1 715    13.555 20.459  5.862 1.00 7.35
ATOM  1569 CZ  PHE 1 715    13.977 20.472  4.554 1.00 7.35
ATOM  1570 N   TYR 1 716    12.905 16.199  4.687 1.00 4.17
ATOM  1571 CA  TYR 1 716    13.554 15.554  3.588 1.00 4.17
ATOM  1572 C   TYR 1 716    13.721 14.089  3.821 1.00 4.17
ATOM  1573 O   TYR 1 716    13.701 13.300  2.878 1.00 4.17
ATOM  1574 CB  TYR 1 716    14.874 16.225  3.162 1.00 4.17
ATOM  1575 CG  TYR 1 716    15.608 16.683  4.370 1.00 4.17
ATOM  1576 CD1 TYR 1 716    15.188 17.824  5.012 1.00 4.17
ATOM  1577 CD2 TYR 1 716    16.814 16.131  4.723 1.00 4.17
ATOM  1578 CE1 TYR 1 716    15.914 18.386  6.031 1.00 4.17
ATOM  1579 CE2 TYR 1 716    17.552 16.698  5.733 1.00 4.17
ATOM  1580 CZ  TYR 1 716    17.109 17.820  6.391 1.00 4.17
ATOM  1581 OH  TYR 1 716    17.871 18.391  7.430 1.00 4.17
ATOM  1582 N   GLN 1 717    13.892 13.661  5.083 1.00 4.45
ATOM  1583 CA  GLN 1 717    14.034 12.252  5.290 1.00 4.45
ATOM  1584 C   GLN 1 717    12.760 11.597  4.856 1.00 4.45
ATOM  1585 O   GLN 1 717    12.790 10.543  4.227 1.00 4.45
ATOM  1586 CB  GLN 1 717    14.289 11.853  6.756 1.00 4.45
ATOM  1587 CG  GLN 1 717    13.128 12.151  7.705 1.00 4.45
ATOM  1588 CD  GLN 1 717    13.537 11.704  9.101 1.00 4.45
ATOM  1589 OE1 GLN 1 717    12.744 11.748 10.041 1.00 4.45
ATOM  1590 NE2 GLN 1 717    14.812 11.253  9.242 1.00 4.45
ATOM  1591 N   LEU 1 718    11.612 12.225  5.182 1.00 0.89
ATOM  1592 CA  LEU 1 718    10.315 11.703  4.853 1.00 0.89
ATOM  1593 C   LEU 1 718    10.116 11.696  3.366 1.00 0.89
ATOM  1594 O   LEU 1 718     9.529 10.760  2.823 1.00 0.89
ATOM  1595 CB  LEU 1 718     9.173 12.524  5.478 1.00 0.89
ATOM  1596 CG  LEU 1 718     7.772 11.987  5.137 1.00 0.89
ATOM  1597 CD1 LEU 1 718     7.570 10.569  5.700 1.00 0.89
ATOM  1598 CD2 LEU 1 718     6.674 12.963  5.589 1.00 0.89
ATOM  1599 N   THR 1 719    10.607 12.736  2.666 1.00 4.49
ATOM  1600 CA  THR 1 719    10.417 12.802  1.244 1.00 4.49
ATOM  1601 C   THR 1 719    11.120 11.627  0.650 1.00 4.49
ATOM  1602 O   THR 1 719    10.716 11.101 -0.385 1.00 4.49
ATOM  1603 CB  THR 1 719    10.957 14.047  0.599 1.00 4.49
ATOM  1604 OG1 THR 1 719    10.426 14.178 -0.712 1.00 4.49
ATOM  1605 CG2 THR 1 719    12.487 13.952  0.516 1.00 4.49
ATOM  1606 N   LYS 1 720    12.203 11.191  1.313 1.00 8.13
ATOM  1607 CA  LYS 1 720    12.989 10.077  0.874 1.00 8.13
ATOM  1608 C   LYS 1 720    12.109  8.864  0.840 1.00 8.13
ATOM  1609 O   LYS 1 720    12.278  7.996 -0.013 1.00 8.13
ATOM  1610 CB  LYS 1 720    14.177  9.812  1.819 1.00 8.13
ATOM  1611 CG  LYS 1 720    15.149  8.724  1.356 1.00 8.13
ATOM  1612 CD  LYS 1 720    14.561  7.313  1.350 1.00 8.13
ATOM  1613 CE  LYS 1 720    14.315  6.750  2.752 1.00 8.13
ATOM  1614 NZ  LYS 1 720    13.746  5.387  2.658 1.00 8.13
ATOM  1615 N   LEU 1 721    11.139  8.777  1.770 1.00 3.53
ATOM  1616 CA  LEU 1 721    10.246  7.652  1.836 1.00 3.53
ATOM  1617 C   LEU 1 721     9.467  7.564  0.564 1.00 3.53
ATOM  1618 O   LEU 1 721     9.163  6.476  0.080 1.00 3.53
ATOM  1619 CB  LEU 1 721     9.203  7.760  2.965 1.00 3.53
ATOM  1620 CG  LEU 1 721     9.775  7.642  4.388 1.00 3.53
ATOM  1621 CD1 LEU 1 721    10.758  8.774  4.697 1.00 3.53
ATOM  1622 CD2 LEU 1 721     8.647  7.568  5.426 1.00 3.53
ATOM  1623 N   LEU 1 722     9.113  8.720 -0.014 1.00 4.47
ATOM  1624 CA  LEU 1 722     8.339  8.721 -1.217 1.00 4.47
ATOM  1625 C   LEU 1 722     9.128  7.983 -2.250 1.00 4.47
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ATOM  1626  O   LEU 1 722     8.576   7.213  -3.035  1.00  4.47
ATOM  1627  CB  LEU 1 722     8.075  10.143  -1.733  1.00  4.47
ATOM  1628  CG  LEU 1 722     7.237  10.990  -0.759  1.00  4.47
ATOM  1629  CD1 LEU 1 722     7.970  11.234   0.569  1.00  4.47
ATOM  1630  CD2 LEU 1 722     6.785  12.297  -1.417  1.00  4.47
ATOM  1631  N   ASP 1 723    10.455   8.197  -2.256  1.00  4.04
ATOM  1632  CA  ASP 1 723    11.333   7.563  -3.195  1.00  4.04
ATOM  1633  C   ASP 1 723    11.247   6.081  -3.008  1.00  4.04
ATOM  1634  O   ASP 1 723    11.102   5.331  -3.973  1.00  4.04
ATOM  1635  CB  ASP 1 723    12.801   7.981  -2.965  1.00  4.04
ATOM  1636  CG  ASP 1 723    13.697   7.406  -4.055  1.00  4.04
ATOM  1637  OD1 ASP 1 723    14.413   8.214  -4.705  1.00  4.04
ATOM  1638  OD2 ASP 1 723    13.684   6.163  -4.258  1.00  4.04
ATOM  1639  N   SER 1 724    11.308   5.619  -1.747  1.00  3.24
ATOM  1640  CA  SER 1 724    11.287   4.209  -1.498  1.00  3.24
ATOM  1641  C   SER 1 724     9.986   3.653  -1.977  1.00  3.24
ATOM  1642  O   SER 1 724     9.938   2.558  -2.534  1.00  3.24
ATOM  1643  CB  SER 1 724    11.446   3.845  -0.009  1.00  3.24
ATOM  1644  OG  SER 1 724    10.310   4.264   0.732  1.00  3.24
ATOM  1645  N   MET 1 725     8.890   4.407  -1.776  1.00  0.77
ATOM  1646  CA  MET 1 725     7.590   3.949  -2.165  1.00  0.77
ATOM  1647  C   MET 1 725     7.516   3.774  -3.652  1.00  0.77
ATOM  1648  O   MET 1 725     6.920   2.815  -4.138  1.00  0.77
ATOM  1649  CB  MET 1 725     6.465   4.916  -1.756  1.00  0.77
ATOM  1650  CG  MET 1 725     6.331   5.076  -0.241  1.00  0.77
ATOM  1651  SD  MET 1 725     4.967   6.152   0.289  1.00  0.77
ATOM  1652  CE  MET 1 725     3.672   4.931  -0.072  1.00  0.77
ATOM  1653  N   HIS 1 726     8.098   4.697  -4.438  1.00  3.69
ATOM  1654  CA  HIS 1 726     8.018   4.491  -5.855  1.00  3.69
ATOM  1655  C   HIS 1 726     8.835   3.300  -6.224  1.00  3.69
ATOM  1656  O   HIS 1 726     8.536   2.585  -7.177  1.00  3.69
ATOM  1657  CB  HIS 1 726     8.434   5.689  -6.730  1.00  3.69
ATOM  1658  CG  HIS 1 726     9.861   6.124  -6.617  1.00  3.69
ATOM  1659  ND1 HIS 1 726    10.251   7.298  -6.014  1.00  3.69
ATOM  1660  CD2 HIS 1 726    10.990   5.583  -7.148  1.00  3.69
ATOM  1661  CE1 HIS 1 726    11.586   7.412  -6.215  1.00  3.69
ATOM  1662  NE2 HIS 1 726    12.083   6.392  -6.892  1.00  3.69
ATOM  1663  N   GLU 1 727     9.922   3.054  -5.483  1.00  3.10
ATOM  1664  CA  GLU 1 727    10.722   1.912  -5.796  1.00  3.10
ATOM  1665  C   GLU 1 727     9.893   0.682  -5.611  1.00  3.10
ATOM  1666  O   GLU 1 727     9.911  -0.216  -6.453  1.00  3.10
ATOM  1667  CB  GLU 1 727    11.945   1.794  -4.872  1.00  3.10
ATOM  1668  CG  GLU 1 727    12.968   2.911  -5.081  1.00  3.10
ATOM  1669  CD  GLU 1 727    13.728   2.599  -6.360  1.00  3.10
ATOM  1670  OE1 GLU 1 727    14.682   3.355  -6.684  1.00  3.10
ATOM  1671  OE2 GLU 1 727    13.365   1.595  -7.029  1.00  3.10
ATOM  1672  N   VAL 1 728     9.116   0.615  -4.512  1.00  3.54
ATOM  1673  CA  VAL 1 728     8.362  -0.578  -4.262  1.00  3.54
ATOM  1674  C   VAL 1 728     7.337  -0.786  -5.333  1.00  3.54
ATOM  1675  O   VAL 1 728     7.119  -1.913  -5.772  1.00  3.54
ATOM  1676  CB  VAL 1 728     7.677  -0.623  -2.919  1.00  3.54
ATOM  1677  CG1 VAL 1 728     8.755  -0.522  -1.828  1.00  3.54
ATOM  1678  CG2 VAL 1 728     6.576   0.440  -2.837  1.00  3.54
ATOM  1679  N   VAL 1 729     6.684   0.294  -5.803  1.00  3.39
ATOM  1680  CA  VAL 1 729     5.675   0.117  -6.810  1.00  3.39
ATOM  1681  C   VAL 1 729     6.279  -0.428  -8.067  1.00  3.39
ATOM  1682  O   VAL 1 729     5.694  -1.291  -8.720  1.00  3.39
ATOM  1683  CB  VAL 1 729     4.943   1.375  -7.186  1.00  3.39
ATOM  1684  CG1 VAL 1 729     5.919   2.329  -7.879  1.00  3.39
ATOM  1685  CG2 VAL 1 729     3.762   1.002  -8.099  1.00  3.39
ATOM  1686  N   GLU 1 730     7.477   0.063  -8.441  1.00  1.12
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ATOM 1687 CA GLU 1 730 8.090 -0.357 -9.663 1.00 1.12
ATOM 1688 C GLU 1 730 8.377 -1.815 -9.564 1.00 1.12
ATOM 1689 O GLU 1 730 8.113 -2.579 -10.490 1.00 1.12
ATOM 1690 CB GLU 1 730 9.431 0.350 -9.936 1.00 1.12
ATOM 1691 CG GLU 1 730 9.310 1.849 -10.229 1.00 1.12
ATOM 1692 CD GLU 1 730 10.714 2.390 -10.474 1.00 1.12
ATOM 1693 OE1 GLU 1 730 10.842 3.618 -10.731 1.00 1.12
ATOM 1694 OE2 GLU 1 730 11.680 1.583 -10.410 1.00 1.12
ATOM 1695 N ASN 1 731 8.908 -2.238 -8.405 1.00 3.09
ATOM 1696 CA ASN 1 731 9.277 -3.607 -8.203 1.00 3.09
ATOM 1697 C ASN 1 731 8.062 -4.472 -8.272 1.00 3.09
ATOM 1698 O ASN 1 731 8.100 -5.581 -8.801 1.00 3.09
ATOM 1699 CB ASN 1 731 9.937 -3.838 -6.836 1.00 3.09
ATOM 1700 CG ASN 1 731 10.529 -5.236 -6.849 1.00 3.09
ATOM 1701 OD1 ASN 1 731 9.829 -6.227 -7.053 1.00 3.09
ATOM 1702 ND2 ASN 1 731 11.870 -5.318 -6.641 1.00 3.09
ATOM 1703 N LEU 1 732 6.935 -3.981 -7.738 1.00 1.26
ATOM 1704 CA LEU 1 732 5.742 -4.771 -7.713 1.00 1.26
ATOM 1705 C LEU 1 732 5.349 -5.051 -9.132 1.00 1.26
ATOM 1706 O LEU 1 732 4.895 -6.146 -9.456 1.00 1.26
ATOM 1707 CB LEU 1 732 4.593 -4.049 -6.971 1.00 1.26
ATOM 1708 CG LEU 1 732 3.312 -4.871 -6.685 1.00 1.26
ATOM 1709 CD1 LEU 1 732 2.279 -4.010 -5.941 1.00 1.26
ATOM 1710 CD2 LEU 1 732 2.700 -5.502 -7.945 1.00 1.26
ATOM 1711 N LEU 1 733 5.537 -4.073 -10.034 1.00 6.33
ATOM 1712 CA LEU 1 733 5.142 -4.289 -11.394 1.00 6.33
ATOM 1713 C LEU 1 733 5.868 -5.480 -11.943 1.00 6.33
ATOM 1714 O LEU 1 733 5.287 -6.307 -12.642 1.00 6.33
ATOM 1715 CB LEU 1 733 5.480 -3.096 -12.307 1.00 6.33
ATOM 1716 CG LEU 1 733 5.063 -3.298 -13.777 1.00 6.33
ATOM 1717 CD1 LEU 1 733 3.536 -3.380 -13.924 1.00 6.33
ATOM 1718 CD2 LEU 1 733 5.696 -2.234 -14.689 1.00 6.33
ATOM 1719 N ASN 1 734 7.172 -5.615 -11.663 1.00 4.20
ATOM 1720 CA ASN 1 734 7.856 -6.750 -12.213 1.00 4.20
ATOM 1721 C ASN 1 734 7.377 -8.043 -11.629 1.00 4.20
ATOM 1722 O ASN 1 734 7.196 -9.035 -12.335 1.00 4.20
ATOM 1723 CB ASN 1 734 9.398 -6.679 -12.092 1.00 4.20
ATOM 1724 CG ASN 1 734 9.854 -6.616 -10.639 1.00 4.20
ATOM 1725 OD1 ASN 1 734 10.239 -5.552 -10.159 1.00 4.20
ATOM 1726 ND2 ASN 1 734 9.831 -7.775 -9.927 1.00 4.20
ATOM 1727 N TYR 1 735 7.136 -8.093 -10.314 1.00 7.65
ATOM 1728 CA TYR 1 735 6.749 -9.366 -9.802 1.00 7.65
ATOM 1729 C TYR 1 735 5.394 -9.717 -10.306 1.00 7.65
ATOM 1730 O TYR 1 735 5.118 -10.881 -10.597 1.00 7.65
ATOM 1731 CB TYR 1 735 6.652 -9.443 -8.283 1.00 7.65
ATOM 1732 CG TYR 1 735 6.449 -10.889 -7.992 1.00 7.65
ATOM 1733 CD1 TYR 1 735 7.537 -11.677 -7.696 1.00 7.65
ATOM 1734 CD2 TYR 1 735 5.188 -11.455 -7.945 1.00 7.65
ATOM 1735 CE1 TYR 1 735 7.377 -12.989 -7.317 1.00 7.65
ATOM 1736 CE2 TYR 1 735 5.026 -12.770 -7.578 1.00 7.65
ATOM 1737 CZ TYR 1 735 6.118 -13.531 -7.238 1.00 7.65
ATOM 1738 OH TYR 1 735 5.951 -14.875 -6.842 1.00 7.65
ATOM 1739 N CYS 1 736 4.507 -8.714 -10.433 1.00 4.30
ATOM 1740 CA CYS 1 736 3.158 -9.054 -10.756 1.00 4.30
ATOM 1741 C CYS 1 736 3.081 -9.771 -12.053 1.00 4.30
ATOM 1742 O CYS 1 736 2.369 -10.767 -12.164 1.00 4.30
ATOM 1743 CB CYS 1 736 2.192 -7.856 -10.780 1.00 4.30
ATOM 1744 SG CYS 1 736 2.518 -6.684 -12.120 1.00 4.30
ATOM 1745 N PHE 1 737 3.823 -9.323 -13.075 1.00 7.73
ATOM 1746 CA PHE 1 737 3.655 -10.052 -14.290 1.00 7.73
ATOM 1747 C PHE 1 737 4.160 -11.453 -14.158 1.00 7.73

ATOM 1748 O PHE 1 737 3.507 -12.390 -14.611 1.00 7.73
ATOM 1749 CB PHE 1 737 4.273 -9.389 -15.540 1.00 7.73
ATOM 1750 CG PHE 1 737 5.754 -9.302 -15.437 1.00 7.73
ATOM 1751 CD1 PHE 1 737 6.355 -8.226 -14.824 1.00 7.73
ATOM 1752 CD2 PHE 1 737 6.542 -10.220 -16.092 1.00 7.73
ATOM 1753 CE1 PHE 1 737 7.722 -8.082 -14.847 1.00 7.73
ATOM 1754 CE2 PHE 1 737 7.911 -10.092 -16.101 1.00 7.73
ATOM 1755 CZ PHE 1 737 8.503 -9.023 -15.476 1.00 7.73
ATOM 1756 N GLN 1 738 5.315 -11.656 -13.493 1.00 7.23
ATOM 1757 CA GLN 1 738 5.836 -12.990 -13.454 1.00 7.23
ATOM 1758 C GLN 1 738 4.860 -13.857 -12.729 1.00 7.23
ATOM 1759 O GLN 1 738 4.605 -14.996 -13.114 1.00 7.23
ATOM 1760 CB GLN 1 738 7.208 -13.107 -12.762 1.00 7.23
ATOM 1761 CG GLN 1 738 7.177 -12.981 -11.240 1.00 7.23
ATOM 1762 CD GLN 1 738 7.120 -14.405 -10.704 1.00 7.23
ATOM 1763 OE1 GLN 1 738 7.186 -14.645 -9.500 1.00 7.23
ATOM 1764 NE2 GLN 1 738 7.013 -15.395 -11.631 1.00 7.23
ATOM 1765 N THR 1 739 4.283 -13.340 -11.637 1.00 5.24
ATOM 1766 CA THR 1 739 3.338 -14.132 -10.912 1.00 5.24
ATOM 1767 C THR 1 739 2.092 -14.330 -11.715 1.00 5.24
ATOM 1768 O THR 1 739 1.507 -15.413 -11.725 1.00 5.24
ATOM 1769 CB THR 1 739 2.953 -13.519 -9.596 1.00 5.24
ATOM 1770 OG1 THR 1 739 2.945 -12.102 -9.699 1.00 5.24
ATOM 1771 CG2 THR 1 739 3.949 -13.970 -8.515 1.00 5.24
ATOM 1772 N PHE 1 740 1.665 -13.276 -12.430 1.00 6.82
ATOM 1773 CA PHE 1 740 0.434 -13.258 -13.161 1.00 6.82
ATOM 1774 C PHE 1 740 0.463 -14.242 -14.278 1.00 6.82
ATOM 1775 O PHE 1 740 -0.558 -14.842 -14.609 1.00 6.82
ATOM 1776 CB PHE 1 740 0.130 -11.872 -13.756 1.00 6.82
ATOM 1777 CG PHE 1 740 -1.308 -11.852 -14.142 1.00 6.82
ATOM 1778 CD1 PHE 1 740 -1.724 -12.340 -15.358 1.00 6.82
ATOM 1779 CD2 PHE 1 740 -2.246 -11.343 -13.272 1.00 6.82
ATOM 1780 CE1 PHE 1 740 -3.055 -12.316 -15.701 1.00 6.82
ATOM 1781 CE2 PHE 1 740 -3.577 -11.318 -13.609 1.00 6.82
ATOM 1782 CZ PHE 1 740 -3.985 -11.804 -14.827 1.00 6.82
ATOM 1783 N LEU 1 741 1.647 -14.447 -14.877 1.00 5.17
ATOM 1784 CA LEU 1 741 1.718 -15.298 -16.022 1.00 5.17
ATOM 1785 C LEU 1 741 1.219 -16.654 -15.648 1.00 5.17
ATOM 1786 O LEU 1 741 0.458 -17.260 -16.398 1.00 5.17
ATOM 1787 CB LEU 1 741 3.155 -15.433 -16.573 1.00 5.17
ATOM 1788 CG LEU 1 741 3.290 -16.235 -17.890 1.00 5.17
ATOM 1789 CD1 LEU 1 741 3.002 -17.735 -17.715 1.00 5.17
ATOM 1790 CD2 LEU 1 741 2.455 -15.594 -19.010 1.00 5.17
ATOM 1791 N ASP 1 742 1.605 -17.172 -14.469 1.00 6.55
ATOM 1792 CA ASP 1 742 1.164 -18.507 -14.199 1.00 6.55
ATOM 1793 C ASP 1 742 0.007 -18.588 -13.252 1.00 6.55
ATOM 1794 O ASP 1 742 0.168 -18.330 -12.059 1.00 6.55
ATOM 1795 CB ASP 1 742 2.282 -19.432 -13.678 1.00 6.55
ATOM 1796 CG ASP 1 742 2.836 -18.875 -12.374 1.00 6.55
ATOM 1797 OD1 ASP 1 742 2.616 -17.665 -12.100 1.00 6.55
ATOM 1798 OD2 ASP 1 742 3.494 -19.654 -11.634 1.00 6.55
ATOM 1799 N LYS 1 743 -1.188 -18.919 -13.811 1.00 7.11
ATOM 1800 CA LYS 1 743 -2.427 -19.213 -13.129 1.00 7.11
ATOM 1801 C LYS 1 743 -3.536 -18.292 -13.532 1.00 7.11
ATOM 1802 O LYS 1 743 -3.327 -17.101 -13.755 1.00 7.11
ATOM 1803 CB LYS 1 743 -2.353 -19.214 -11.590 1.00 7.11
ATOM 1804 CG LYS 1 743 -3.579 -19.800 -10.895 1.00 7.11
ATOM 1805 CD LYS 1 743 -3.308 -20.161 -9.434 1.00 7.11
ATOM 1806 CE LYS 1 743 -2.225 -21.231 -9.278 1.00 7.11
ATOM 1807 NZ LYS 1 743 -2.007 -21.537 -7.847 1.00 7.11
ATOM 1808 N THR 1 744 -4.764 -18.848 -13.631 1.00 3.77

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ATOM  1809 CA  THR 1 744     -5.932 -18.071 -13.934  1.00  3.77
ATOM  1810 C   THR 1 744     -6.606 -18.018 -12.601  1.00  3.77
ATOM  1811 O   THR 1 744     -5.925 -17.857 -11.590  1.00  3.77
ATOM  1812 CB  THR 1 744     -6.839 -18.721 -14.948  1.00  3.77
ATOM  1813 OG1 THR 1 744     -6.106 -18.987 -16.136  1.00  3.77
ATOM  1814 CG2 THR 1 744     -7.995 -17.762 -15.299  1.00  3.77
ATOM  1815 N   MET 1 745     -7.948 -18.136 -12.517  1.00 12.59
ATOM  1816 CA  MET 1 745     -8.413 -18.065 -11.172  1.00 12.59
ATOM  1817 C   MET 1 745     -9.878 -18.181 -10.986  1.00 12.59
ATOM  1818 O   MET 1 745    -10.676 -17.804 -11.842  1.00 12.59
ATOM  1819 CB  MET 1 745     -8.183 -16.711 -10.536  1.00 12.59
ATOM  1820 CG  MET 1 745     -9.189 -15.659 -11.022  1.00 12.59
ATOM  1821 SD  MET 1 745     -9.788 -14.502  -9.750  1.00 12.59
ATOM  1822 CE  MET 1 745    -10.941 -13.605 -10.832  1.00 12.59
ATOM  1823 N   SER 1 746    -10.262 -18.777  -9.844  1.00  4.73
ATOM  1824 CA  SER 1 746    -11.605 -18.590  -9.414  1.00  4.73
ATOM  1825 C   SER 1 746    -11.447 -17.285  -8.692  1.00  4.73
ATOM  1826 O   SER 1 746    -11.988 -16.252  -9.084  1.00  4.73
ATOM  1827 CB  SER 1 746    -12.061 -19.649  -8.395  1.00  4.73
ATOM  1828 OG  SER 1 746    -13.407 -19.413  -8.007  1.00  4.73
ATOM  1829 N   ILE 1 747    -10.646 -17.343  -7.603  1.00  6.94
ATOM  1830 CA  ILE 1 747    -10.266 -16.253  -6.747  1.00  6.94
ATOM  1831 C   ILE 1 747     -8.902 -15.708  -7.066  1.00  6.94
ATOM  1832 O   ILE 1 747     -8.586 -14.569  -6.729  1.00  6.94
ATOM  1833 CB  ILE 1 747    -10.217 -16.660  -5.303  1.00  6.94
ATOM  1834 CG1 ILE 1 747     -9.984 -15.428  -4.414  1.00  6.94
ATOM  1835 CG2 ILE 1 747     -9.141 -17.749  -5.149  1.00  6.94
ATOM  1836 CD1 ILE 1 747    -11.153 -14.445  -4.422  1.00  6.94
ATOM  1837 N   GLU 1 748     -8.062 -16.506  -7.750  1.00  5.83
ATOM  1838 CA  GLU 1 748     -6.665 -16.191  -7.900  1.00  5.83
ATOM  1839 C   GLU 1 748     -6.317 -14.839  -8.467  1.00  5.83
ATOM  1840 O   GLU 1 748     -5.542 -14.112  -7.851  1.00  5.83
ATOM  1841 CB  GLU 1 748     -5.904 -17.242  -8.728  1.00  5.83
ATOM  1842 CG  GLU 1 748     -4.393 -17.188  -8.502  1.00  5.83
ATOM  1843 CD  GLU 1 748     -4.115 -17.849  -7.157  1.00  5.83
ATOM  1844 OE1 GLU 1 748     -4.360 -19.080  -7.041  1.00  5.83
ATOM  1845 OE2 GLU 1 748     -3.656 -17.133  -6.228  1.00  5.83
ATOM  1846 N   PHE 1 749     -6.846 -14.431  -9.636  1.00  0.97
ATOM  1847 CA  PHE 1 749     -6.471 -13.137 -10.126  1.00  0.97
ATOM  1848 C   PHE 1 749     -7.707 -12.328 -10.320  1.00  0.97
ATOM  1849 O   PHE 1 749     -8.441 -12.492 -11.293  1.00  0.97
ATOM  1850 CB  PHE 1 749     -5.729 -13.184 -11.471  1.00  0.97
ATOM  1851 CG  PHE 1 749     -4.441 -13.886 -11.218  1.00  0.97
ATOM  1852 CD1 PHE 1 749     -4.391 -15.260 -11.210  1.00  0.97
ATOM  1853 CD2 PHE 1 749     -3.294 -13.173 -10.959  1.00  0.97
ATOM  1854 CE1 PHE 1 749     -3.209 -15.915 -10.956  1.00  0.97
ATOM  1855 CE2 PHE 1 749     -2.109 -13.822 -10.701  1.00  0.97
ATOM  1856 CZ  PHE 1 749     -2.066 -15.196 -10.702  1.00  0.97
ATOM  1857 N   PRO 1 750     -7.925 -11.440  -9.397  1.00  2.67
ATOM  1858 CA  PRO 1 750     -9.095 -10.620  -9.417  1.00  2.67
ATOM  1859 C   PRO 1 750     -9.079  -9.888 -10.712  1.00  2.67
ATOM  1860 O   PRO 1 750     -7.998  -9.566 -11.200  1.00  2.67
ATOM  1861 CB  PRO 1 750     -8.924  -9.612  -8.279  1.00  2.67
ATOM  1862 CG  PRO 1 750     -7.545  -9.932  -7.664  1.00  2.67
ATOM  1863 CD  PRO 1 750     -6.833 -10.743  -8.759  1.00  2.67
ATOM  1864 N   GLU 1 751    -10.261  -9.636 -11.291  1.00  5.68
ATOM  1865 CA  GLU 1 751    -10.318  -8.882 -12.502  1.00  5.68
ATOM  1866 C   GLU 1 751     -9.848  -7.504 -12.174  1.00  5.68
ATOM  1867 O   GLU 1 751     -9.093  -6.895 -12.931  1.00  5.68
ATOM  1868 CB  GLU 1 751    -11.743  -8.770 -13.073  1.00  5.68
ATOM  1869 CG  GLU 1 751    -12.741  -8.112 -12.116  1.00  5.68
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ATOM  1870  CD  GLU 1 751    -13.010  -9.085 -10.976  1.00  5.68
ATOM  1871  OE1 GLU 1 751    -13.346 -10.263 -11.271  1.00  5.68
ATOM  1872  OE2 GLU 1 751    -12.865  -8.669  -9.796  1.00  5.68
ATOM  1873  N   MET 1 752    -10.275  -6.984 -11.009  1.00  5.28
ATOM  1874  CA  MET 1 752     -9.934  -5.644 -10.636  1.00  5.28
ATOM  1875  C   MET 1 752     -8.448  -5.558 -10.471  1.00  5.28
ATOM  1876  O   MET 1 752     -7.819  -4.609 -10.932  1.00  5.28
ATOM  1877  CB  MET 1 752    -10.589  -5.214  -9.312  1.00  5.28
ATOM  1878  CG  MET 1 752    -10.778  -3.701  -9.185  1.00  5.28
ATOM  1879  SD  MET 1 752     -9.265  -2.716  -9.345  1.00  5.28
ATOM  1880  CE  MET 1 752    -10.099  -1.122  -9.091  1.00  5.28
ATOM  1881  N   LEU 1 753     -7.840  -6.568  -9.818  1.00  0.87
ATOM  1882  CA  LEU 1 753     -6.422  -6.511  -9.613  1.00  0.87
ATOM  1883  C   LEU 1 753     -5.745  -6.551 -10.937  1.00  0.87
ATOM  1884  O   LEU 1 753     -4.771  -5.837 -11.174  1.00  0.87
ATOM  1885  CB  LEU 1 753     -5.856  -7.665  -8.770  1.00  0.87
ATOM  1886  CG  LEU 1 753     -4.331  -7.554  -8.569  1.00  0.87
ATOM  1887  CD1 LEU 1 753     -3.962  -6.286  -7.787  1.00  0.87
ATOM  1888  CD2 LEU 1 753     -3.750  -8.831  -7.940  1.00  0.87
ATOM  1889  N   ALA 1 754     -6.263  -7.386 -11.852  1.00  0.70
ATOM  1890  CA  ALA 1 754     -5.656  -7.499 -13.142  1.00  0.70
ATOM  1891  C   ALA 1 754     -5.733  -6.157 -13.790  1.00  0.70
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HETATM 1978  H100STR   1      -2.698 -8.429 -4.720  1.00  0.00
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CONECT 1963 1962
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CONECT 1964 1961 1965 1977
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CONECT 1976 1966
CONECT 1977 1964 1978
CONECT 1978 1977
CONECT 1979 1955
MASTER     0  0  0  0  0  0  0  0 1979  1  27  19
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(81) Designated States *(national)*: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW.

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Published:
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28 December 2000

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 00/52050 A3

(54) Title: HOMOLOGY MODELS OF THE GLUCOCORTICOID RECEPTOR

(57) Abstract: A method of designing a homology model of the ligand binding domain of a glucocorticoid receptor wherein the homology model may be displayed as a three-dimensional image, the method comprising: (i) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, estrogen or progesterone receptor; (ii) modifying said x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domains of the glucocorticoid receptor on the one hand and the thyroid, estrogen, or progesterone receptor on the other hand; (iii) verifying the accuracy of the homology model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (iv) if required modifying the homology model for greater consistency with those binding properties.

INTERNATIONAL SEARCH REPORT

Int tional Application No
PCT/GB 00/00727

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K14/705

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G06F C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 56812 A (PIKE ASHLEY CHARLES WILLIAM ;BZOZOWSKI ANDRZEJI MAREK (GB); HUBBAR) 17 December 1998 (1998-12-17) page 3, paragraph 1 page 13, paragraph 3 page 28, paragraph 4 claims 13,53,54,56 ---	1-13, 17-20
X	WO 97 21993 A (UNIV CALIFORNIA) 19 June 1997 (1997-06-19) abstract; claims 10-12,23,29-31,38-45 page 3, paragraph 1 page 10, line 19 - line 27 page 29, line 24 -page 30, line 13 --- -/--	1-13, 17-20

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
3 August 2000	15.08.00

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Filloy García, E

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INTERNATIONAL SEARCH REPORT

Inte ional Application No
PCT/GB 00/00727

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 99 50658 A (GREENE GEOFFREY L ;AGARD DAVID A (US); ARCH DEV CORP (US); KUSHNER) 7 October 1999 (1999-10-07) abstract; claims 1-71 ---	1-13, 17-20
P,X	WO 99 26966 A (APRILETTI JAMES W ;FLETTERICK ROBERT J (US); BAXTER JOHN D (US); K) 3 June 1999 (1999-06-03) abstract; claims 8,17,19 page 3, paragraph 1 - paragraph 2 ---	1-13, 17-20
A	ANSTEAD G M ET AL: "The estradiol pharmacophore: Ligand structure-estrogen receptor binding affinity relationships and a model for the receptor binding site" STEROIDS: STRUCTURE, FUNCTION, AND REGULATION,US,ELSEVIER SCIENCE PUBLISHERS, NEW YORK, NY, vol. 62, no. 3, 1 March 1997 (1997-03-01), pages 268-303, XP004057108 ISSN: 0039-128X abstract ---	1-13, 17-20
A	R C J RIBEIRO ET AL: "Mechanisms of Thyroid Hormone Action: Insights from X-ray Crystallographic and Functional Studies" RECENT PROGRESS IN HORMONE RESEARCH,US,ACADEMIC PRESS, NEW YORK, NY, vol. 53, no. 53, 1998, pages 351-394-394, XP002101079 ISSN: 0079-9963 abstract page 373, paragraph 4 page 377, paragraph 2 - paragraph 3 ---	1-13, 17-20
A	BRZOZOWSKI A ET AL: "Molecular basis of agonism and antagonism in the oestrogen receptor" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, no. 389, 16 October 1997 (1997-10-16), pages 753-758, XP002075907 ISSN: 0028-0836 page 757, left-hand column, paragraph 4 -right-hand column, paragraph 2 ---	1-13, 17-20
A	BOURGUET W ET AL: "Crystal structure of the ligand-binding domain of the human nuclear receptor RXR-alpha" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, no. 375, 1 July 1995 (1995-07-01), pages 377-382, XP002075905 ISSN: 0028-0836 page 379, right-hand column, paragraph 3 -----	1-13, 17-20

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/GB 00/00727

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 14-16
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 14-16

Claims 14-16 refer to a glucocorticoid agonist/antagonist without giving a true technical characterisation. Consequently, the scope of said claims is ambiguous and vague. No meaningful search can be carried out for such claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int tional Application No
PCT/GB 00/00727

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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